SUPPLEMENTARY TABLE S11

Transcript ID	Base Mean	log2 Fold-Change M:F	log -fold change SE	Statistic	p-value	FDR	Module membership	Gene Correlation to Male	GSPvalue	Gene Ontology	Arabidopsis homolog	Arabidopsis Symbol	Arabidopsis Description	Salix gene description
Sapur.016G293900.2	23.56843842	-1.305412868	0.067535265	-19.3294	3.04E-83	2.78E-82	black	-0.59107255	3.66E-16	GO:0016020	AT1G33265.1		Transmembrane proteins 14C	transmembrane protein 14C
Sapur.016G145800.1	1123.812019	-0.704844446	0.036650616	-19.2314	2.02E-82	1.82E-81	black	-0.851003191	3.31E-45	GO:0003676	AT1G51510.1	Y14	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA-binding protein RBM8A RNA recognition motif protein
Sapur.005G149500.1	172.150132	-0.840094252	0.044708722	-18.7904	9.05E-79	7.74E-78	black	-0.839273369	7.29E-43	GO:0003676,GO:0017069,GO:0000398	AT1G21320.2		nucleotide binding;nucleic acid binding	RNA-binding protein with multiple splicing protein, putative
Sapur.010G205500.1	167.0812601	-0.874182415	0.04705308	-18.5786	4.78E-77	3.99E-76	black	-0.831923851	1.73E-41		AT1G16790.1		ribosomal protein-related	hypothetical protein
Sapur.004G170400.1	426.3086412	-1.284436824	0.071388171	-17.9923	2.24E-72	1.75E-71	black	-0.842377615	1.83E-43	GO:0006414,GO:0003746,GO:0043043,GO:0005737	AT3G08740.1		elongation factor P (EF-P) family protein	elongation factor P
Sapur.002G006700.1	446.8872606	-1.261190715	0.070440681	-17.9043	1.09E-71	8.43E-71	black	-0.846003083	3.49E-44	GO:0006396	AT1G20580.1		Small nuclear ribonucleoprotein family protein	small nuclear ribonucleoprotein Sm protein D3
Sapur.010G147400.1	913.6818735	-0.559583072	0.031473616	-17.7794	1.02E-70	7.77E-70	black	-0.809434365	1.15E-37	GO:0005515,GO:0042393,GO:0006355	AT5G05610.2	AL1	alfin-like 1	PHD finger protein
Sapur.016G215800.1	211.4276984	-0.698691722	0.040737364	-17.1511	6.16E-66	4.36E-65	black	-0.8108713	6.77E-38		AT5G40570.1		Surfeit locus protein 2 (SURF2)	surfeit locus protein
Sapur.005G201200.1	706.8631866	-1.024277064	0.061097012	-16.7648	4.42E-63	2.99E-62	black	-0.825435311	2.49E-40	GO:0006396	AT1G20580.1		Small nuclear ribonucleoprotein family protein	small nuclear ribonucleoprotein Sm protein D3
Sapur.016G064800.1	491.7734777	-1.139627601	0.068568901	-16.6202	4.98E-62	3.32E-61	black	-0.817095352	6.56E-39		AT5G06360.1		Ribosomal protein S8e family protein	NA
Sapur.15WG072500.1	382.4935288	-0.781277832	0.048416101	-16.1367	1.41E-58	8.88E-58	black	-0.818620069	3.65E-39	GO:0003676	AT5G61030.1	GR-RBP3	glycine-rich RNA-binding protein 3	RNA recognition motif 2 in yeast gar2-like protein
Sapur.017G099000.1	189.571667	-1.009945526	0.062718968	-16.1027	2.44E-58	1.53E-57	black	-0.833640981	8.35E-42	GO:0019843,GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G16740.1		Ribosomal protein L20	50S ribosomal protein L20
Sapur.008G150400.1	866.3909516	-1.052652732	0.065569081	-16.0541	5.35E-58	3.34E-57	black	-0.819715783	2.39E-39		AT1G70600.1		Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L27a
Sapur.006G003900.1	317.6622394	-0.577775628	0.036055232	-16.0247	8.59E-58	5.35E-57	black	-0.760248639	7.70E-31		AT5G47680.1			tRNA (guanine(37)-N(1))-methyltransferase
Sapur.009G056500.1	285.6752159	-0.844487512	0.052857883	-15.9766	1.86E-57	1.15E-56	black	-0.828185877	8.13E-41		AT1G65700.3		Small nuclear ribonucleoprotein family protein	U6 snRNA-associated-like-Smprotein LSM8
Sapur.002G049200.1	3885.002981	-0.506533087	0.03201169	-15.8234	2.15E-56	1.31E-55	black	-0.791646979	5.49E-35		AT4G02450.1		HSP20-like chaperones superfamily protein	HSP90 co-chaperone, putative
Sapur.014G103200.1	1066.980522	-1.064833234	0.067351516	-15.8101	2.65E-56	1.61E-55	black	-0.818826737	3.37E-39	GO:0030532,GO:0008380	AT2G47640.3		Small nuclear ribonucleoprotein family protein	small nuclear ribonucleoprotein Sm protein D2
Sapur.014G043300.1	2310.49738	-0.598711346	0.037902873	-15.7959	3.32E-56	2.02E-55	black	-0.797132323	8.75E-36	GO:0006412,GO:0005840,GO:0003735	AT4G16720.1		Ribosomal protein L23/L15e family protein	60S ribosomal protein L15
Sapur.010G084600.1	378.8421678	-1.349311311	0.087777372	-15.372	2.52E-53	1.47E-52	black	-0.830390615	3.27E-41	GO:0006457,GO:0005737	AT1G23100.1		GroES-like family protein	10 kDa chaperonin
Sapur.013G116500.1	1165.467232	-1.039146331	0.068228392	-15.2304	2.22E-52	1.27E-51	black	-0.79658129	1.05E-35	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G34620.1	SSR16	small subunit ribosomal protein 16	30S ribosomal protein S16
Sapur.007G123000.1	480.7805675	-0.789852718	0.052008117	-15.1871	4.31E-52	2.45E-51	black	-0.808868533	1.41E-37		AT2G33845.1		Nucleic acid-binding, OB-fold-like protein	OB fold SoSSB-OBF: A subfamily protein, putative
Sapur.014G063500.1	203.2836743	-0.640713463	0.042188912	-15.1868	4.33E-52	2.46E-51	black	-0.767258103	1.04E-31		AT1G01730.1			hypothetical protein
Sapur.003G135500.1	199.8417967	-0.722624962	0.048599707	-14.8689	5.25E-50	2.87E-49	black	-0.76623098	1.40E-31	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G80620.1		S15/NS1, RNA-binding protein	NA
Sapur.007G087000.1	1248.91845	-0.719232247	0.048464615	-14.8404	8.03E-50	4.39E-49	black	-0.784295128	5.93E-34	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G10360.1	EMB3010,RPS6B	Ribosomal protein S6e	40S ribosomal protein S6
Sapur.005G008700.1	146.4801471	-1.101186447	0.074832474	-14.7154	5.14E-49	2.77E-48	black	-0.806096243	3.83E-37		AT5G26800.1			NA
Sapur.004G074600.1	2144.568813	-0.658170508	0.045123657	-14.5859	3.45E-48	1.84E-47	black	-0.772577214	2.18E-32		AT3G62870.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L7a
Sapur.018G028600.1	1473.078791	0.835215937	0.057313217	14.57283	4.18E-48	2.22E-47	black	0.752696179	6.17E-30		AT2G25660.1	emb2410	embryo defective 2410	embryo defective 2410 protein
Sapur.15WG008600.1	263.0177275	-0.77369944	0.053252798	-14.5288	7.96E-48	4.21E-47	black	-0.773746722	1.53E-32		AT5G24314.1	PDE225,PTAC7	plastid transcriptionally active7	plastid transcriptionally active protein, putative
Sapur.016G000800.1	633.1713977	-0.602847648	0.04152233	-14.5186	9.23E-48	4.87E-47	black	-0.779716638	2.49E-33	GO:0015934,GO:0006412,GO:0003735	AT5G64670.1		Ribosomal protein L18e/L15 superfamily protein	ribosomal protein L15
Sapur.019G056000.1	1152.96778	-0.671363235	0.046263272	-14.5118	1.02E-47	5.38E-47	black	-0.772109627	2.50E-32		AT1G08580.1			hypothetical protein
Sapur.007G085200.1	1279.241548	-0.819262429	0.057619305	-14.2185	7.03E-46	3.59E-45	black	-0.72578939	5.77E-27	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G65220.1		Ribosomal L29 family protein	50S ribosomal protein L29
Sapur.005G082000.1	43.60120739	-1.279981037	0.090440755	-14.1527	1.80E-45	9.12E-45	black	-0.761937236	4.79E-31	GO:0006412,GO:0005840,GO:0003735	AT4G35490.1	MRPL11	mitochondrial ribosomal protein L11	50S ribosomal protein L11
Sapur.014G127400.1	1016.871493	0.71351266	0.050608183	14.09876	3.86E-45	1.95E-44	black	0.708963059	2.79E-25	GO:0006511	AT4G15420.1		Ubiquitin fusion degradation UFD1 family protein	ubiquitin fusion degradation protein
Sapur.011G044700.1	960.3015422	-0.953345957	0.067791743	-14.0629	6.42E-45	3.23E-44	black	-0.790257944	8.67E-35	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G29070.1		Ribosomal protein L34	ribosomal protein L34
Sapur.003G063200.2	22.38798994	-1.221771213	0.087182098	-14.014	1.28E-44	6.39E-44	black	-0.535669712	4.87E-13		AT2G35500.1	SKL2	shikimate kinase like 2	shikimate kinase-like protein
Sapur.005G130800.1	1723.273284	0.919070117	0.065910272	13.94426	3.41E-44	1.69E-43	black	0.737843528	2.99E-28		AT4G30100.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	tRNA-splicing endonuclease positive effector-like protein
Sapur.014G076000.1	641.1384977	0.777009846	0.055913744	13.89658	6.64E-44	3.28E-43	black	0.770622797	3.89E-32		AT3G61690.1		nucleotidyltransferases	nucleotidyltransferase
Sapur.017G068200.1	1066.908286	-0.97407922	0.070310087	-13.854	1.20E-43	5.90E-43	black	-0.76860305	7.04E-32	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G26880.1		Ribosomal protein L34e superfamily protein	60S ribosomal protein L34
Sapur.T045100.1	393.7108675	-0.581580648	0.042026722	-13.8384	1.50E-43	7.34E-43	black	-0.763516331	3.06E-31		AT3G07510.1			transmembrane protein, putative
Sapur.010G204000.2	8.060494274	5.311054131	0.387060915	13.72149	7.55E-43	3.66E-42	black	0.468751218	5.96E-10		AT1G51560.1		Pyridoxamine 5\'-phosphate oxidase family protein	pyridoxamine 5'-phosphate oxidase family protein
Sapur.006G125200.1	73.65272106	-0.877816645	0.064461647	-13.6177	3.14E-42	1.51E-41	black	-0.742422576	9.29E-29		AT1G55160.1			transmembrane protein, putative
Sapur.003G053000.1	2368.996223	-0.635858352	0.046884461	-13.5622	6.71E-42	3.19E-41	black	-0.733113809	9.73E-28	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G10950.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L37a
Sapur.005G071400.1	432.8558205	-0.567267924	0.0419836	-13.5117	1.33E-41	6.34E-41	black	-0.757691572	1.57E-30		AT5G23290.1	PFD5	prefoldin 5	prefoldin subunit 5, putative
Sapur.005G021500.1	254.7477013	0.829625706	0.061490816	13.49186	1.75E-41	8.27E-41	black	0.742574121	8.93E-29	GO:0008270	AT3G62900.1		CW-type Zinc Finger	CW-type zinc finger protein
Sapur.007G032200.1	259.7612866	-1.06967741	0.079496803	-13.4556	2.85E-41	1.35E-40	black	-0.749705761	1.38E-29		AT4G37090.1			hypothetical protein
Sapur.009G076300.1	617.9634245	-0.512482137	0.038264254	-13.3932	6.62E-41	3.11E-40	black	-0.761365674	5.63E-31	GO:0046983,GO:0006351,GO:0003899	AT2G15430.1	NRPB3.NRPD3.NRPE3A.RBP	DNA-directed RNA polymerase family protein	DNA-directed RNA polymerase II subunit RPB3
Sapur.001G092400.1	410.1146261	-0.421189086	0.031943666	-13.1854	1.07E-39	4.89E-39	black	-0.721374456	1.64E-26		AT2G45640.1	ATSAP18,SAP18	SIN3 associated polypeptide P18	histone deacetylase complex subunit SAP18
Sapur.012G020800.1	93.22740056	-0.890142595	0.067741752	-13.1402	1.94E-39	8.84E-39	black	-0.702929442	1.05E-24		AT5G52960.1			DUF3143 family protein
Sapur.010G035700.1	115.4415633	-0.857642329	0.065294948	-13.1349	2.08E-39	9.48E-39	black	-0.749997905	1.27E-29	GO:0006412,GO:0005840,GO:0003735	AT5G09510.1		Ribosomal protein S19 family protein	40S ribosomal protein S15
Sapur.004G010300.1	192.5184691	-0.451665433	0.034471226	-13.1027	3.18E-39	1.45E-38	black	-0.697587364	3.30E-24		AT4G04780.1	MED21	mediator 21	mediator of RNA polymerase II transcription subunit 21
Sapur.016G195000.1	203.8511866	-1.138933904	0.087372819	-13.0353	7.70E-39	3.47E-38	black	-0.736628221	4.05E-28	GO:0003676	AT4G13850.1	ATGRP2,GR-RBP2,GRP2	glycine-rich RNA-binding protein 2	eukaryotic RNA-binding protein RBM24 RNA recognition motif protein
Sapur.002G067300.1	205.7131902	-0.574074002	0.044081223	-13.0231	9.04E-39	4.07E-38	black	-0.724319292	8.19E-27		AT1G48200.1			hypothetical protein
Sapur.T050600.1	99.13633386	-0.646882724	0.049751015	-13.0024	1.19E-38	5.32E-38	black	-0.704107477	8.12E-25	GO:0003676,GO:0006810,GO:0005622	AT5G43960.1		Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain	Ras GTPase-activating protein-binding protein
Sapur.017G008800.1	87.78023634	-0.947523493	0.072962955	-12.9864	1.46E-38	6.55E-38	black	-0.722746843	1.19E-26		AT1G06720.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.002G124300.1	1337.517236	0.653202322	0.050561151	12.91906	3.51E-38	1.56E-37	black	0.730258185	1.96E-27	GO:0003824,GO:0005515	AT2G42010.1	PLDBETA,PLDBETA1	phospholipase D beta 1	phospholipase D
Sapur.001G133800.1	982.7049908	-0.842087184	0.065300561	-12.8956	4.77E-38	2.12E-37	black	-0.763008376	3.53E-31	GO:0006412,GO:0005840,GO:0005622,GO:0003735,GO:0015935	AT1G72370.1	AP40,P40,RP40,RPSAA	40s ribosomal protein SA	40S ribosomal protein Sa protein
Sapur.001G144300.1	772.5371472	0.621127088	0.048188948	12.88941	5.16E-38	2.29E-37	black	0.749972563	1.28E-29		AT5G20030.1		Plant Tudor-like RNA-binding protein	agenet domain protein
Sapur.016G225000.2	17.75533306	-1.250866606	0.097124259	-12.879	5.91E-38	2.62E-37	black	-0.622879425	3.03E-18	GO:0008168	AT1G29790.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.010G064800.1	3540.035993	-0.746015817	0.057955703	-12.8722	6.46E-38	2.86E-37	black	-0.743835249	6.45E-29	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G34670.1		Ribosomal protein S3Ae	40S ribosomal protein S3a
Sapur.008G007800.1	2269.235892	-0.850764175	0.066139248	-12.8632	7.25E-38	3.21E-37	black	-0.738367416	2.62E-28	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G64140.1	RPS28	ribosomal protein S28	40S ribosomal protein S28
Sapur.008G088200.1	512.9442141	-1.142002025	0.088804653	-12.8597	7.59E-38	3.36E-37	black	-0.749398449	1.49E-29		AT5G08180.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	H/ACA ribonucleoprotein complex subunit 2
Sapur.001G023700.1	190.802384	-1.36147525	0.10592501	-12.8532	8.25E-38	3.65E-37	black	-0.693722125	7.43E-24	GO:0045454,GO:0015035,GO:0006662	AT3G06730.1	TRX P,TRX z	Thioredoxin z	thioredoxin-like protein CITRX protein
Sapur.009G037000.1	111.4833279	-0.933619072	0.073024276	-12.7851	1.99E-37	8.72E-37	black	-0.705001979	6.68E-25	GO:0005515.GO:0003723.GO:0016070.GO:0051028.GO:0045292.GO:0005846.GO:000033	AT2G13540.1	ABH1,ATCBP80,CBP80,ENS	ARM repeat superfamily protein	nuclear cap-binding protein
Sapur.15ZG050500.1	287.5255515	0.661138969	0.05185044	12.75088	3.08E-37	1.35E-36	black	0.733497958	8.84E-28	GO:0007165,GO:0005515,GO:0043531	AT1G27170.2		transmembrane receptors;ATP binding	TIR-NBS-LRR resistance protein
Sapur.15WG000400.1	1261.554663	-0.557342784	0.043772854	-12.7326	3.90E-37	1.70E-36	black	-0.735121585	5.91E-28	GO:0005515	AT5G24650.1		Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	import inner membrane translocase subunit Tim17, putative
Sapur.008G123600.1	646.084405	-0.741861583	0.058674899	-12.6436	1.21E-36	5.25E-36	black	-0.750649624	1.07E-29	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G28060.1		Ribosomal protein S24e family protein	40S ribosomal protein S24
Sapur.012G072300.1	2206.82811	0.517396682	0.040962235	12.63107	1.42E-36	6.15E-36	black	0.755374959	2.97E-30	GO:0009378,GO:0006310,GO:0006281,GO:0005515	AT4G02480.1		AAA-type ATPase family protein	AAA family ATPase
Sapur.017G082500.1	922.0925096	-0.746717034	0.059151676	-12.6238	1.56E-36	6.74E-36	black	-0.735427239	5.48E-28		AT3G62870.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	NA
Sapur.15WG026500.1	2885.367571	-0.582701886	0.04616885	-12.6211	1.62E-36	6.97E-36	black	-0.730819117	1.71E-27	GO:0003723,GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G07090.1		Ribosomal protein S4 (RPS4A) family protein	40S ribosomal protein S4
Sapur.011G051000.1	1264.175047	-0.562685943	0.04475736	-12.5719	3.01E-36	1.29E-35	black	-0.732064538	1.26E-27	GO:0006412,GO:0005840,GO:0003735	AT2G34480.1		Ribosomal protein L18ae/LX family protein	60S ribosomal protein L18a
Sapur.016G278000.1	1024.511212	-0.61185325	0.048754878	-12.5496	4.00E-36	1.71E-35	black	-0.758224522	1.36E-30		AT1G50900.1		Ankyrin repeat family protein	LHCP translocation defect protein
Sapur.012G056300.1	3223.480358	-0.415056432	0.033155848	-12.5183	5.93E-36	2.53E-35	black	-0.728258309	3.19E-27	GO:0003723	AT5G35530.1		Ribosomal protein S3 family protein	40S ribosomal protein S3
Sapur.016G144200.1	328.5126401	-0.584503765	0.046701336	-12.5158	6.12E-36	2.61E-35	black	-0.75583408	2.62E-30	GO:0003723	AT5G12410.1		THUMP domain-containing protein	THUMP domain protein
Sapur.001G168900.1	466.757446	-0.488988194	0.03909897	-12.5064	6.89E-36	2.93E-35	black	-0.700614802	1.73E-24		AT5G64160.1			plant/MHJ24-14 protein, putative
Sapur.005G111600.1	152.0988659	-0.685367973	0.054909862	-12.4817	9.40E-36	3.99E-35	black	-0.703066225	1.02E-24		AT5G64816.2			transmembrane protein, putative
Sapur.017G007500.1	829.9283671	-0.592069478	0.047505822	-12.4631	1.19E-35	5.02E-35	black	-0.769481916	5.44E-32		AT2G33845.1		Nucleic acid-binding, OB-fold-like protein	single-stranded DNA-binding protein, putative
Sapur.006G174700.1	351.2049512	-0.937616464	0.075292731	-12.4529	1.35E-35	5.70E-35	black	-0.709179336	2.66E-25		AT2G37400.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR protein
Sapur.001G027800.1	2561.687788	-0.616229056	0.049773172	-12.3807	3.32E-35	1.39E-34	black	-0.724429999	7.97E-27		AT3G12390.1		Nascent polypeptide-associated complex (NAC), alpha subunit family protein	nascent polypeptide-associated complex subunit alpha-like protein
Sapur.002G044500.1	70.05636647	-0.964386783	0.077898939	-12.38	3.35E-35	1.41E-34	black	-0.710302172	2.07E-25	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G32060.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	NA
Sapur.010G197700.1	214.9499479	-0.732481817	0.059182499	-12.3767	3.50E-35	1.47E-34	black	-0.745220825	4.49E-29	GO:0005759	AT4G32605.1		Mitochondrial glycoprotein family protein	glycoprotein
Sapur.014G102900.1	1254.724585	-0.807455056	0.065362426	-12.3535	4.66E-35	1.95E-34	black	-0.740944811	1.36E-28	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G05560.2		Ribosomal L22e protein family	60S ribosomal protein L22, putative
Sapur.003G046800.1	358.668339	-0.716527834	0.058471089	-12.2544	1.59E-34	6.58E-34	black	-0.710823225	1.84E-25	GO:0006412,GO:0005840,GO:0003735	AT4G16720.1		Ribosomal protein L23/L15e family protein	60S ribosomal protein L15
Sapur.002G114900.1	1841.310472	-0.700146033	0.057773812	-12.1187	8.40E-34	3.43E-33	black	-0.696804592	3.89E-24	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G23740.1	RPS11-BETA	ribosomal protein S11-beta	40S ribosomal protein S11
Sapur.15WG032600.1	5318.722034	-0.523284271	0.043688577	-11.9776	4.66E-33	1.87E-32	black	-0.723680193	9.53E-27	GO:0005515	AT1G18080.1	ATARCA.RACK1A.RACK1A A	Transducin/WD40 repeat-like superfamily protein	guanine nucleotide-binding protein subunit beta-like protein
Sapur.001G140900.1	1151.729371	-0.811132277	0.067828002	-11.9587	5.85E-33	2.35E-32	black	-0.714215564	8.56E-26	GO:0006412,GO:0005840,GO:0003735	AT4G16720.1		Ribosomal protein L23/L15e family protein	ribosomal protein L15
Sapur.009G127600.1	2604.729497	-0.561056315	0.04708968	-11.9146	9.93E-33	3.97E-32	black	-0.693477143	7.82E-24	GO:0015934,GO:0006412,GO:0003735				ribosomal protein L32
Sapur.004G142300.1	2293.742104	-0.612959747	0.051651046	-11.8673	1.75E-32	6.96E-32	black	-0.705076389	6.57E-25		AT3G44750.1	ATHD2A,HD2A,HDA3,HDT1	histone deacetylase 3	type 2 histone deacetylase
Sapur.016G137900.1	314.3796945	-0.710111685	0.059973978	-11.8403	2.42E-32	9.57E-32	black	-0.713782709	9.45E-26		AT5G52370.1			hypothetical protein
Sapur.007G083700.1	2754.18911	0.789151546	0.066715662	11.82858	2.78E-32	1.10E-31	black	0.682523917	7.30E-23	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT4G39850.1	ACN2.AtABCD1.CTS.PED3.P	peroxisomal ABC transporter 1	ABC transporter D family protein
Sapur.002G122300.1	95.72261816	-0.657038187	0.05554945	-11.828	2.80E-32	1.11E-31	black	-0.704740883	7.07E-25	GO:0006457,GO:0003755,GO:0000413	AT1G01940.1		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.006G084600.1	2735.203182	-0.516708287	0.043696932	-11.8248	2.91E-32	1.15E-31	black	-0.717272732	4.25E-26	GO:0003723,GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G58420.1		Ribosomal protein S4 (RPS4A) family protein	40S ribosomal protein S4
Sapur.004G148400.1	2624.381848	-0.567436272	0.048028151	-11.8147	3.28E-32	1.30E-31	black	-0.714990683	7.18E-26	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G77940.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L30
Sapur.002G025400.1	1042.159322	-0.683392206	0.058018723	-11.7788	5.02E-32	1.97E-31	black	-0.662591565	3.34E-21	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G75350.1	emb2184	Ribosomal protein L31	50S ribosomal protein L31
Sapur.016G191300.1	2605.794518	-0.706535659	0.059985585	-11.7784	5.04E-32	1.98E-31	black	-0.714348795	8.31E-26	GO:0006412,GO:0005840,GO:0003735,GO:0015934	AT5G48760.2		Ribosomal protein L13 family protein	60S ribosomal protein L13a
Sapur.018G087200.1	1017.076043	-0.999160996	0.084945545	-11.7624	6.10E-32	2.39E-31	black	-0.693021137	8.60E-24	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G31985.1		Ribosomal protein L39 family protein	60S ribosomal protein L39
Sapur.008G071900.1	75.49825109	-0.982197408	0.083615033	-11.7467	7.35E-32	2.88E-31	black	-0.687381527	2.74E-23		AT1G26660.1		Prefoldin chaperone subunit family protein	prefoldin, alpha subunit
Sapur.005G161000.1	1565.654773	-0.742511774	0.063341298	-11.7224	9.79E-32	3.83E-31	black	-0.715602164	6.24E-26	GO:0006412,GO:0005840,GO:0003735	AT2G34480.1		Ribosomal protein L18ae/LX family protein	60S ribosomal protein L18a
Sapur.007G002500.1	1962.103581	0.571008463	0.048723482	11.71937	1.01E-31	3.97E-31	black	0.703256573	9.77E-25	GO:0008270.GO:0005515.GO:0006355.GO:0005634.GO:0004402.GO:0003712.GO:001657	AT1G79000.1	ATHAC1.ATHPCAT2.HAC1.P	histone acetyltransferase of the CBP family 1	histone acetyltransferase HAC12
Sapur.004G074500.1	3540.623926	-0.583924851	0.049957621	-11.6884	1.46E-31	5.69E-31	black	-0.691463168	1.19E-23		AT3G62870.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L7a
Sapur.014G091900.1	3235.28574	-0.660188385	0.056557274	-11.6729	1.75E-31	6.82E-31	black	-0.720013838	2.25E-26	GO:0006412,GO:0005840,GO:0003735	AT2G47110.1	UBQ6	ubiquitin 6	ubiquitin-40S ribosomal protein S27a
Sapur.012G044700.1	2485.31724	-0.593188198	0.050922513	-11.6488	2.33E-31	9.01E-31	black	-0.720757439	1.90E-26	GO:0003676	AT5G61030.1	GR-RBP3	glycine-rich RNA-binding protein 3	heterogeneous nuclear ribonucleoprotein G RNA recognition motif protein
Sapur.016G070900.1	2841.640113	-0.728431016	0.06260474	-11.6354	2.72E-31	1.05E-30	black	-0.734426059	7.03E-28	GO:0006412,GO:0005840,GO:0003735	AT3G52590.1	EMB2167.ERD16.HAP4.UBC	ubiquitin extension protein 1	ubiquitin-60S ribosomal L40 fusion protein
Sapur.003G160300.1	321.7544479	-0.608000895	0.052262061	-11.6337	2.78E-31	1.07E-30	black	-0.715920158	5.80E-26		AT3G57930.1			metal tolerance protein, putative
Sapur.008G052200.1	3772.814389	-0.634345798	0.054527868	-11.6334	2.79E-31	1.08E-30	black	-0.714988244	7.18E-26	GO:0042254,GO:0005622	AT2G40010.1		Ribosomal protein L10 family protein	60S acidic ribosomal protein P0
Sapur.15WG102300.1	702.8259322	-0.74605575	0.064211459	-11.6187	3.31E-31	1.28E-30	black	-0.679221509	1.40E-22	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G56670.1		Ribosomal protein S30 family protein	40S ribosomal protein S30
Sapur.007G037100.1	302.6627101	-0.797175439	0.068701775	-11.6034	3.96E-31	1.53E-30	black	-0.716722711	4.83E-26	GO:0008097,GO:0006412,GO:0005840,GO:0003735	AT5G66860.1		Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain	50S ribosomal protein L25
Sapur.002G126400.1	967.3044576	-0.647468849	0.055919779	-11.5785	5.29E-31	2.04E-30	black	-0.673581931	4.21E-22		AT4G01310.1		Ribosomal L5P family protein	50S ribosomal protein L5
Sapur.002G167700.1	1168.643624	-0.832056912	0.071966106	-11.5618	6.44E-31	2.47E-30	black	-0.703559079	9.15E-25	GO:0006412,GO:0005840,GO:0003735	AT2G47110.2	UBQ6	ubiquitin 6	ubiquitin/ribosomal protein S27a
Sapur.014G058000.1	47.49358837	-0.942674994	0.081696616	-11.5387	8.42E-31	3.22E-30	black	-0.682498002	7.34E-23		AT1G01860.1	PFC1	Ribosomal RNA adenine dimethylase family protein	ribosomal RNA small subunit methyltransferase A
Sapur.013G057600.1	217.4590033	-0.890469366	0.077266081	-11.5247	9.90E-31	3.78E-30	black	-0.664183937	2.49E-21		AT3G03773.1		HSP20-like chaperones superfamily protein	p23 co-chaperone protein
Sapur.016G116900.1	84.8963723	-0.645607795	0.056035582	-11.5214	1.03E-30	3.93E-30	black	-0.68034743	1.13E-22		AT2G25570.3		binding	Sel1 domain protein
Sapur.016G080600.1	3966.518747	-0.526103282	0.045898415	-11.4623	2.04E-30	7.74E-30	black	-0.693332133	8.06E-24	GO:0006412,GO:0005840,GO:0003735	AT3G09630.1		Ribosomal protein L4/L1 family	60S ribosomal protein L4-1
Sapur.001G182500.1	200.7593176	-0.680327406	0.059356491	-11.4617	2.05E-30	7.79E-30	black	-0.68411644	5.31E-23	GO:0006412,GO:0003735	AT4G37660.1		Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein	ribosomal protein L7/L12 carboxy-terminal domain protein
Sapur.006G172700.1	296.1268155	-1.027930604	0.08992173	-11.4314	2.91E-30	1.10E-29	black	-0.730245803	1.97E-27		AT3G11500.1		Small nuclear ribonucleoprotein family protein	small nuclear ribonucleoprotein G, putative
Sapur.001G114500.1	16.74144341	-1.106249319	0.09686484	-11.4205	3.30E-30	1.25E-29	black	-0.665174068	2.07E-21		AT1G32310.1			hypothetical protein
Sapur.014G009800.1	209.911268	-0.580523654	0.050843994	-11.4177	3.41E-30	1.29E-29	black	-0.702241201	1.22E-24		AT5G65860.2		ankyrin repeat family protein	arginine N-methyltransferase
Sapur.017G082400.1	1399.331432	-0.494231315	0.04330319	-11.4133	3.59E-30	1.35E-29	black	-0.674356513	3.63E-22		AT3G62870.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L7a
Sapur.006G022500.1	592.2064455	-0.416108782	0.036535865	-11.389	4.74E-30	1.78E-29	black	-0.64009858	1.79E-19		AT3G12390.1		Nascent polypeptide-associated complex (NAC), alpha subunit family protein	nascent polypeptide associated complex protein alpha
Sapur.012G082000.1	1482.922448	-0.687359933	0.060365554	-11.3866	4.88E-30	1.83E-29	black	-0.701436423	1.45E-24	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G26880.1		Ribosomal protein L34e superfamily protein	60S ribosomal protein L34
Sapur.016G124300.1	8791.67637	0.694446238	0.061139617	11.35837	6.74E-30	2.53E-29	black	0.680542454	1.08E-22	GO:0016020,GO:0006075,GO:0003843,GO:0000148	AT2G31960.2	ATGSL03,ATGSL3,GSL03	glucan synthase-like 3	callose synthase
Sapur.013G043500.1	850.6862068	0.527740601	0.046463931	11.35807	6.76E-30	2.54E-29	black	0.690218305	1.54E-23	GO:0005634	AT1G08620.1	PKDM7D	Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein	transcription factor jumonji family protein
Sapur.012G024100.1	1455.708894	-0.711891629	0.062766717	-11.3419	8.14E-30	3.05E-29	black	-0.693354099	8.03E-24	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G16780.1		Ribosomal protein L19e family protein	ribosomal protein L19
Sapur.014G038900.1	783.1336576	0.57248563	0.050536192	11.32823	9.51E-30	3.55E-29	black	0.699374548	2.25E-24	GO:0003676	AT2G44710.1		RNA-binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.T049500.1	736.244808	-0.609172413	0.054025419	-11.2757	1.73E-29	6.44E-29	black	-0.682446665	7.42E-23	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G18100.1		Ribosomal protein L32e	60S ribosomal protein L32, putative
Sapur.006G172800.2	125.8433918	1.819822964	0.161612775	11.26039	2.06E-29	7.65E-29	black	0.36812716	2.10E-06	GO:0007165	AT5G22400.1		Rho GTPase activating protein with PAK-box/P21-Rho-binding domain	Rho GTPase-activating protein
Sapur.016G210300.1	67.39730169	-1.004724729	0.089256823	-11.2566	2.15E-29	7.99E-29	black	-0.691395206	1.21E-23	GO:0016020	AT5G40770.1	ATPHB3,PHB3	prohibitin 3	prohibitin
Sapur.005G168500.1	222.5118442	-0.676082899	0.06024618	-11.222	3.18E-29	1.18E-28	black	-0.668870694	1.04E-21		AT4G04614.1			hypothetical protein
Sapur.008G124900.1	264.9729594	-0.658288538	0.058957988	-11.1654	6.02E-29	2.22E-28	black	-0.708423807	3.14E-25	GO:0051082,GO:0016272,GO:0006457	AT3G22480.1	PDF2	prefoldin 2	prefoldin subunit 2
Sapur.009G043500.1	5683.946917	-0.564236027	0.050666212	-11.1363	8.35E-29	3.06E-28	black	-0.691544569	1.17E-23	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G59240.1		Ribosomal protein S8e family protein	40S ribosomal protein S8
Sapur.017G086300.1	129.4152304	-0.610436935	0.054837082	-11.1318	8.78E-29	3.22E-28	black	-0.649731177	3.39E-20		AT5G49550.1			biogenesis of lysosome-related organelles complex-1 subunit 2
Sapur.002G110200.1	41.2686862	-0.93281981	0.083856823	-11.124	9.59E-29	3.51E-28	black	-0.663029741	3.08E-21					transmembrane protein, putative
Sapur.005G156800.1	1812.129127	-0.366571014	0.032961925	-11.121	9.91E-29	3.63E-28	black	-0.66436291	2.41E-21		AT4G02450.1		HSP20-like chaperones superfamily protein	ripening regulated protein DDTFR8, putative
Sapur.017G009700.1	77.99573961	-0.824016642	0.074263892	-11.0958	1.31E-28	4.80E-28	black	-0.66236473	3.49E-21		AT5G44170.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ribosomal protein L11 methyltransferase
Sapur.016G116400.1	3039.644136	-0.590295483	0.053506258	-11.0323	2.67E-28	9.70E-28	black	-0.680939095	1.00E-22	GO:0006412,GO:0005840,GO:0003735	AT3G52580.1		Ribosomal protein S11 family protein	40S ribosomal protein S14
Sapur.008G047400.1	1618.561675	-0.318788638	0.028896031	-11.0323	2.67E-28	9.70E-28	black	-0.659390763	6.02E-21	GO:0003676,GO:0005852,GO:0005737,GO:0003743	AT3G11400.1	ATEIF3G1,EIF3G1	eukaryotic translation initiation factor 3G1	eukaryotic translation initiation factor 3 subunit G
Sapur.016G059200.1	3846.945008	-0.523210601	0.047465682	-11.0229	2.96E-28	1.07E-27	black	-0.68762861	2.61E-23	GO:0006412	AT2G37270.2	ATRPS5B,RPS5B	ribosomal protein 5B	40S ribosomal protein S5, putative
Sapur.008G142500.1	2088.34503	-0.595928047	0.054088448	-11.0177	3.14E-28	1.14E-27	black	-0.699290794	2.29E-24	GO:0006412,GO:0005840,GO:0003735,GO:0015934	AT1G67430.1		Ribosomal protein L22p/L17e family protein	60S ribosomal protein L17
Sapur.010G152000.1	721.0148682	-0.868608354	0.078993298	-10.996	4.00E-28	1.45E-27	black	-0.684258115	5.16E-23	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G07070.1		Ribosomal protein L35Ae family protein	60S ribosomal protein L35a
Sapur.006G120600.1	1344.121695	0.577767958	0.052627699	10.9784	4.85E-28	1.75E-27	black	0.67402769	3.87E-22	GO:0016459,GO:0005524,GO:0003774,GO:0005515	AT5G20490.1	ATXIK,XI-17,XIK	Myosin family protein with Dil domain	myosin XI, putative
Sapur.005G092400.1	2067.693761	-0.614557996	0.056065888	-10.9614	5.86E-28	2.11E-27	black	-0.702106632	1.25E-24	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G36130.1		Ribosomal protein L2 family	60S ribosomal protein L2
Sapur.006G184700.1	16.60349008	-1.365513503	0.125492679	-10.8812	1.42E-27	5.06E-27	black	-0.64574394	6.80E-20		AT4G33100.1			protein phosphatase 2C, putative
Sapur.008G102000.1	1550.888168	0.553750658	0.050951718	10.86814	1.63E-27	5.84E-27	black	0.663433708	2.86E-21	GO:0005515	AT1G15130.1		Endosomal targeting BRO1-like domain-containing protein	mammalian alix-like protein interacting Bro1-like domain protein
Sapur.005G047500.1	98.40384736	1.034512897	0.095214494	10.86508	1.69E-27	6.03E-27	black	0.621410073	3.83E-18		AT2G13650.1	GONST1	golgi nucleotide sugar transporter 1	NA
Sapur.002G102200.1	274.9669415	-0.474363342	0.043730873	-10.8473	2.05E-27	7.31E-27	black	-0.639958129	1.83E-19		AT1G45230.1		Protein of unknown function (DUF3223)	DCL protein
Sapur.014G024200.1	31.20490079	-0.817140878	0.07537433	-10.8411	2.20E-27	7.82E-27	black	-0.654006884	1.59E-20	GO:0055114,GO:0006788,GO:0004392	AT2G26550.2	HO2	heme oxygenase 2	heme oxygenase
Sapur.15WG023500.1	1349.632915	-0.594223118	0.054867726	-10.8301	2.48E-27	8.81E-27	black	-0.644190543	8.89E-20		AT1G17880.1	ATBTF3,BTF3	basic transcription factor 3	transcription factor-BTF3-like protein
Sapur.003G101700.1	706.3469321	-0.37442999	0.034659839	-10.803	3.33E-27	1.18E-26	black	-0.674287649	3.68E-22		AT1G64350.1	SEH1H	Transducin/WD40 repeat-like superfamily protein	nucleoporin seh1
Sapur.001G188900.1	1174.363767	-0.279961288	0.025984966	-10.774	4.57E-27	1.61E-26	black	-0.636577201	3.24E-19	GO:0005515,GO:0042393,GO:0006355	AT2G02470.1	AL6	alfin-like 6	PHD finger ALFIN-like protein
Sapur.004G048600.1	550.1203534	0.663663841	0.061707568	10.75498	5.61E-27	1.98E-26	black	0.629867758	9.82E-19		AT1G73210.1		Protein of unknown function (DUF789)	DUF789 family protein
Sapur.005G036400.1	450.1518932	0.454519024	0.042409575	10.71737	8.44E-27	2.96E-26	black	0.666778874	1.53E-21	GO:0006468,GO:0004672	AT1G08720.1	ATEDR1,EDR1	Protein kinase superfamily protein	MAP kinase
Sapur.002G112400.1	618.194525	-0.350444355	0.03277107	-10.6937	1.09E-26	3.81E-26	black	-0.656363889	1.04E-20	GO:0005634	AT1G02140.1	HAP1,MAGO,MEE63	mago nashi family protein	mago nashi-like protein
Sapur.005G031800.1	436.0384471	0.487660164	0.045649999	10.68259	1.23E-26	4.29E-26	black	0.64602504	6.47E-20		AT1G54710.1	ATATG18H,ATG18H	homolog of yeast autophagy 18 (ATG18) H	breast carcinoma amplified sequence protein, putative
Sapur.15WG151100.1	2071.631763	-0.553472658	0.051816446	-10.6814	1.24E-26	4.34E-26	black	-0.641708815	1.36E-19	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G53740.2		Ribosomal protein L36e family protein	60S ribosomal protein L36
Sapur.008G030700.1	114.7355511	0.973823984	0.091188381	10.67926	1.27E-26	4.44E-26	black	0.657695367	8.19E-21					NA
Sapur.012G024200.1	35.3288466	-0.826573997	0.077409139	-10.678	1.29E-26	4.50E-26	black	-0.617589896	6.99E-18	GO:0006284	AT3G07930.3		DNA glycosylase superfamily protein	base excision DNA repair protein, HhH-GPD family protein
Sapur.006G146200.1	171.2849718	-0.662623441	0.06224057	-10.6462	1.82E-26	6.32E-26	black	-0.629364744	1.07E-18		AT4G30845.1			transmembrane protein, putative
Sapur.016G132700.1	2595.35662	-0.689723263	0.064858321	-10.6343	2.06E-26	7.17E-26	black	-0.715683795	6.13E-26		AT2G28900.1	ATOEP16-1.ATOEP16-L.OEP	outer plastid envelope protein 16-1	amino acid selective channel protein
Sapur.010G202200.1	174.7256377	-0.580614085	0.054648338	-10.6246	2.29E-26	7.94E-26	black	-0.619977979	4.80E-18		AT3G21200.1	PGR7	proton gradient regulation 7	glutamyl-tRNA reductase-binding protein
Sapur.006G092800.1	44.82292552	-0.82123138	0.077469182	-10.6007	2.96E-26	1.02E-25	black	-0.634311193	4.72E-19	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G54210.1		Ribosomal protein L17 family protein	50S ribosomal protein L17
Sapur.007G078500.1	2368.511153	-0.636816575	0.060242208	-10.5709	4.06E-26	1.40E-25	black	-0.67084862	7.11E-22	GO:0015934,GO:0006412,GO:0003735	AT3G49910.1		Translation protein SH3-like family protein	60S ribosomal protein L26
Sapur.006G176700.1	599.7010531	-0.468706765	0.044466111	-10.5408	5.60E-26	1.93E-25	black	-0.65743742	8.58E-21		AT5G02740.1		Ribosomal protein S24e family protein	hypothetical protein
Sapur.008G032200.1	229.1957544	-0.754394147	0.071606024	-10.5353	5.94E-26	2.04E-25	black	-0.699643313	2.13E-24		AT2G35790.1			transmembrane protein, putative
Sapur.016G070700.1	3739.636181	-0.710163424	0.067460601	-10.5271	6.48E-26	2.22E-25	black	-0.671760619	5.97E-22	GO:0019843,GO:0005622,GO:0003723	AT5G39850.1		Ribosomal protein S4	40S ribosomal protein S9
Sapur.016G107600.1	3779.191005	-0.517753572	0.049272198	-10.508	7.93E-26	2.72E-25	black	-0.671947107	5.77E-22	GO:0003723,GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G58420.1		Ribosomal protein S4 (RPS4A) family protein	40S ribosomal protein S4
Sapur.018G090100.1	651.7485347	-0.691364739	0.065903929	-10.4905	9.55E-26	3.26E-25	black	-0.668435175	1.12E-21	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G23740.1	RPS11-BETA	ribosomal protein S11-beta	40S ribosomal protein S11
Sapur.018G009700.1	314.3137674	-0.495187106	0.047230159	-10.4846	1.02E-25	3.48E-25	black	-0.649658733	3.43E-20	GO:0007264,GO:0005525	AT2G24765.1	ARF3,ARL1,ATARL1	ADP-ribosylation factor 3	ADP-ribosylation factor(Arf)/Arf-like (Arl) small GTPase family protein
Sapur.010G206200.1	451.5121758	-0.524567973	0.050051889	-10.4805	1.06E-25	3.63E-25	black	-0.666129355	1.73E-21		AT5G63670.1	SPT42	SPT4 homolog 2	transcription elongation factor SPT4
Sapur.017G055900.1	16.35627471	-0.934797085	0.0896103	-10.4318	1.77E-25	6.03E-25	black	-0.659676511	5.71E-21					NA
Sapur.017G095400.1	2172.464883	-0.645084455	0.061963358	-10.4107	2.21E-25	7.51E-25	black	-0.668643032	1.08E-21	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G02560.2		Ribosomal protein S7e family protein	40S ribosomal protein S7, putative
Sapur.012G012800.1	254.4412947	-0.559261998	0.053771496	-10.4007	2.46E-25	8.33E-25	black	-0.644412061	8.56E-20		AT4G22000.1			hypothetical protein
Sapur.009G127700.1	358.4041025	0.3806862	0.036670464	10.38128	3.02E-25	1.02E-24	black	0.665193775	2.06E-21	GO:0030127,GO:0008270,GO:0006888,GO:0006886	AT2G27460.1		sec23/sec24 transport family protein	Sec23/Sec24 transport family protein, putative
Sapur.013G035600.1	3314.032826	-0.657804212	0.063384121	-10.3781	3.12E-25	1.05E-24	black	-0.676808679	2.25E-22	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G28060.1		Ribosomal protein S24e family protein	40S ribosomal protein S24
Sapur.005G119400.1	513.4436956	-0.539691112	0.052203292	-10.3383	4.73E-25	1.59E-24	black	-0.653201675	1.83E-20		AT4G38100.1			NA
Sapur.013G047300.2	61.18548508	1.030397923	0.099689112	10.33611	4.84E-25	1.63E-24	black	0.579540943	1.83E-15		AT3G04240.1	SEC	Tetratricopeptide repeat (TPR)-like superfamily protein	UDP-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase, putative
Sapur.010G122400.1	97.96726138	-0.676775322	0.065511021	-10.3307	5.12E-25	1.72E-24	black	-0.604773293	4.95E-17		AT1G26460.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.014G097100.1	348.174452	-0.615186197	0.05954975	-10.3306	5.12E-25	1.72E-24	black	-0.663406571	2.88E-21		AT1G47820.2			NA
Sapur.016G071400.1	1856.512017	-0.653752994	0.063322664	-10.3242	5.48E-25	1.84E-24	black	-0.690337775	1.50E-23		AT3G11500.1		Small nuclear ribonucleoprotein family protein	small nuclear ribonucleoprotein G, putative
Sapur.010G087600.1	120.688656	-0.60586338	0.058695692	-10.3221	5.60E-25	1.88E-24	black	-0.630113208	9.44E-19	GO:0016887,GO:0005524,GO:0016020	AT2G01320.2		ABC-2 type transporter family protein	ABC transporter family protein
Sapur.014G119900.1	276.2893421	-0.689694406	0.066970772	-10.2984	7.16E-25	2.40E-24	black	-0.630528151	8.82E-19		AT1G60710.1	ATB2	NAD(P)-linked oxidoreductase superfamily protein	aldo/keto reductase family protein
Sapur.017G039700.1	121.403989	-0.654035752	0.063563227	-10.2895	7.86E-25	2.63E-24	black	-0.636818033	3.11E-19	GO:0003676	AT5G65260.1		RNA-binding (RRM/RBD/RNP motifs) family protein	polyadenylate-binding family protein
Sapur.013G114000.2	30.04417937	-0.737994322	0.071744525	-10.2864	8.11E-25	2.72E-24	black	-0.352704109	5.88E-06	GO:0015031,GO:0006457	AT2G30695.1			hypothetical protein
Sapur.008G126500.1	5609.582277	-0.475322906	0.046235139	-10.2806	8.62E-25	2.89E-24	black	-0.643776896	9.55E-20	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G34670.1		Ribosomal protein S3Ae	NA
Sapur.018G031300.1	40.8184668	-0.663538469	0.064622432	-10.2679	9.83E-25	3.28E-24	black	-0.610738336	2.01E-17		AT3G10740.1	ARAF,ARAF1,ASD1,ATASD1	alpha-L-arabinofuranosidase 1	NA
Sapur.002G161900.1	459.4355673	-0.333649091	0.032505079	-10.2645	1.02E-24	3.40E-24	black	-0.608938781	2.65E-17		AT3G54170.1	ATFIP37,FIP37	FKBP12 interacting protein 37	FKBP12-interacting protein of 37 kDa protein
Sapur.006G112400.1	1339.924606	-0.374521512	0.036636954	-10.2225	1.57E-24	5.22E-24	black	-0.642208496	1.25E-19	GO:0005852,GO:0005737,GO:0003743	AT4G33250.1	ATTIF3K1,EIF3K,TIF3K1	eukaryotic translation initiation factor 3K	eukaryotic translation initiation factor 3 subunit K
Sapur.006G159800.1	866.9936438	-0.794714512	0.077791841	-10.2159	1.68E-24	5.59E-24	black	-0.622468482	3.24E-18	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G09590.1		Translation protein SH3-like family protein	60S ribosomal protein L21
Sapur.006G017200.1	1225.913012	-0.761260855	0.074588952	-10.2061	1.86E-24	6.18E-24	black	-0.661547834	4.05E-21	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G15000.1		Ribosomal L27e protein family	60S ribosomal protein L27
Sapur.006G072100.1	1093.263553	-0.659343488	0.06472504	-10.1868	2.27E-24	7.51E-24	black	-0.668782992	1.05E-21		AT5G02160.1			transmembrane protein, putative
Sapur.15WG131300.1	394.6799021	-0.611680952	0.060064708	-10.1837	2.34E-24	7.76E-24	black	-0.641674336	1.37E-19	GO:0016192,GO:0016021	AT1G04760.1	ATVAMP726,VAMP726	vesicle-associated membrane protein 726	vesicle-associated membrane protein, putative
Sapur.003G066400.1	236.4140065	-0.428172577	0.042047994	-10.1829	2.36E-24	7.82E-24	black	-0.646633549	5.83E-20	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G45590.1		Ribosomal protein L35	50S ribosomal protein L35
Sapur.013G134100.1	218.103368	-0.547183344	0.05398392	-10.136	3.82E-24	1.26E-23	black	-0.661289888	4.25E-21	GO:0016226,GO:0008199	AT4G03240.1	ATFH,FH	frataxin homolog	iron donor protein CyaY
Sapur.018G013900.1	405.5038561	-0.502374008	0.049600155	-10.1285	4.13E-24	1.36E-23	black	-0.669012333	1.01E-21	GO:0008152,GO:0003824	AT4G31810.1		ATP-dependent caseinolytic (Clp) protease/crotonase family protein	enoyl-CoA hydratase
Sapur.005G064400.1	1171.223186	-0.703624842	0.069602769	-10.1092	5.03E-24	1.65E-23	black	-0.657074022	9.16E-21	GO:0015934,GO:0006412,GO:0003735	AT3G49910.1		Translation protein SH3-like family protein	60S ribosomal protein L26
Sapur.018G030300.1	1648.218108	-0.722981428	0.071553361	-10.1041	5.30E-24	1.74E-23	black	-0.651159737	2.64E-20	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G15250.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L37, putative
Sapur.018G102400.1	628.9317772	-0.595395477	0.058956666	-10.0989	5.59E-24	1.83E-23	black	-0.685560956	3.97E-23	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G20180.2		Ribosomal protein L36	ribosomal protein L36
Sapur.001G021500.1	1023.315339	-0.720676079	0.071440655	-10.0878	6.26E-24	2.05E-23	black	-0.653864456	1.63E-20	GO:0006412,GO:0005840,GO:0003735	AT2G47110.2	UBQ6	ubiquitin 6	NA
Sapur.014G002000.1	1065.761375	-0.590047765	0.058524456	-10.0821	6.63E-24	2.17E-23	black	-0.680203334	1.16E-22	GO:0055085,GO:0005741	AT3G20000.1	TOM40	translocase of the outer mitochondrial membrane 40	import receptor subunit TOM40
Sapur.016G176400.1	2127.307037	-0.627403835	0.062276364	-10.0745	7.16E-24	2.34E-23	black	-0.638669358	2.28E-19	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G33865.1		Ribosomal protein S14p/S29e family protein	40S ribosomal protein S29
Sapur.008G131700.1	105.9705526	-0.801463333	0.079589405	-10.07	7.50E-24	2.45E-23	black	-0.652465861	2.09E-20	GO:0006412,GO:0005840,GO:0003735	AT5G09510.1		Ribosomal protein S19 family protein	40S ribosomal protein S15
Sapur.007G031900.1	921.4915339	-0.514486605	0.051132179	-10.0619	8.14E-24	2.65E-23	black	-0.619000597	5.60E-18		AT2G23670.1	YCF37	homolog of Synechocystis YCF37	hypothetical protein
Sapur.010G060800.1	1292.170587	-0.641566739	0.063880842	-10.0432	9.84E-24	3.20E-23	black	-0.646535613	5.93E-20	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G28060.1		Ribosomal protein S24e family protein	40S ribosomal protein S24
Sapur.002G157300.1	590.3362394	-0.713736539	0.071159349	-10.0301	1.12E-23	3.65E-23	black	-0.641811058	1.34E-19	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G05560.1		Ribosomal L22e protein family	60S ribosomal protein L22, putative
Sapur.018G113100.1	1056.940835	-0.604719583	0.060520375	-9.992	1.65E-23	5.34E-23	black	-0.633692328	5.24E-19	GO:0006412,GO:0005840,GO:0003735	AT2G37190.1		Ribosomal protein L11 family protein	60S ribosomal protein L12
Sapur.017G042900.1	4458.852336	-0.479002507	0.048087369	-9.96109	2.26E-23	7.27E-23	black	-0.653256954	1.82E-20	GO:0006412,GO:0005840,GO:0003735,GO:0015934	AT3G07110.1		Ribosomal protein L13 family protein	60S ribosomal protein L13a
Sapur.15WG111800.1	2498.595332	-0.608086067	0.061082911	-9.95509	2.40E-23	7.71E-23	black	-0.66334297	2.91E-21	GO:0006412,GO:0005840,GO:0003735,GO:0015934	AT1G67430.1		Ribosomal protein L22p/L17e family protein	60S ribosomal protein L17
Sapur.017G122400.1	2683.539236	-0.545176418	0.054822935	-9.94431	2.67E-23	8.59E-23	black	-0.662574245	3.36E-21		AT4G25740.1		RNA binding Plectin/S10 domain-containing protein	plectin/S10 domain protein
Sapur.006G118300.1	793.59074	0.429329518	0.043214404	9.934871	2.94E-23	9.43E-23	black	0.629866749	9.82E-19		AT5G35560.1		DENN (AEX-3) domain-containing protein	DENN (AEX-3) domain protein
Sapur.T050900.1	145.8319192	-0.803869389	0.081021911	-9.92163	3.35E-23	1.08E-22	black	-0.632348754	6.54E-19	GO:0006886,GO:0005741	AT5G43970.1	ATTOM22-V.TOM22-V.TOM	translocase of outer membrane 22-V	import receptor subunit Tom22
Sapur.014G063300.1	113.7671631	-1.025559138	0.10348164	-9.91054	3.75E-23	1.20E-22	black	-0.628709601	1.19E-18		AT2G45860.1			hypothetical protein
Sapur.011G045000.1	38.68698227	0.652871396	0.065960574	9.897904	4.25E-23	1.36E-22	black	0.618547049	6.01E-18					NA
Sapur.005G207400.1	1951.910461	0.417041449	0.042198778	9.882785	4.94E-23	1.58E-22	black	0.646927951	5.54E-20	GO:0005634,GO:0003677	AT1G20980.1	ATSPL14.FBR6.SPL14.SPL1R	squamosa promoter binding protein-like 14	squamosa promoter-binding-like protein
Sapur.007G094800.1	1920.223297	-0.616673267	0.062454371	-9.87398	5.40E-23	1.72E-22	black	-0.65321258	1.83E-20	GO:0042651,GO:0015979,GO:0009522,GO:0005516	AT5G64040.1	PSAN	photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN)	photosystem I reaction center subunit N
Sapur.006G102200.1	862.9534438	-0.330560588	0.033485063	-9.87188	5.51E-23	1.76E-22	black	-0.640998037	1.54E-19		AT2G36930.1		zinc finger (C2H2 type) family protein	zinc finger-like protein
Sapur.016G194900.1	1811.406996	-0.732918658	0.074292373	-9.86533	5.88E-23	1.88E-22	black	-0.662668101	3.30E-21	GO:0003676	AT4G13850.1	ATGRP2,GR-RBP2,GRP2	glycine-rich RNA-binding protein 2	RNA-binding protein 42 (RBM42)-like RNA recognition motif protein
Sapur.15WG118200.1	405.9687826	-0.793322686	0.080426754	-9.86392	5.97E-23	1.90E-22	black	-0.682940053	6.72E-23		AT5G50810.1	TIM8	translocase inner membrane subunit 8	import inner membrane translocase subunit Tim8
Sapur.006G140900.1	486.2305572	-0.648954	0.065992057	-9.83382	8.05E-23	2.56E-22	black	-0.67438004	3.61E-22	GO:0005681,GO:0000398	AT2G18740.1		Small nuclear ribonucleoprotein family protein	small nuclear ribonucleoprotein E
Sapur.002G077600.1	176.7267475	-0.615790158	0.062637451	-9.83102	8.28E-23	2.63E-22	black	-0.619053425	5.56E-18		AT1G78190.1		Trm112p-like protein	TRM112-like protein
Sapur.15WG139000.1	3882.000356	-0.38555125	0.039228326	-9.82839	8.50E-23	2.70E-22	black	-0.63858073	2.31E-19	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G00100.1	ATRPS13A.PFL2.RPS13.RPS1	ribosomal protein S13A	40S ribosomal protein S13
Sapur.15WG122100.1	1078.346237	-0.773631233	0.079341118	-9.7507	1.83E-22	5.78E-22	black	-0.640783728	1.59E-19	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G26880.1		Ribosomal protein L34e superfamily protein	60S ribosomal protein L34
Sapur.005G202500.1	8015.184289	-0.586814787	0.060303632	-9.731	2.22E-22	7.00E-22	black	-0.62895044	1.14E-18		AT1G20693.2	HMG BETA 1.HMGB2.NFD0	high mobility group B2	HMG (high mobility group) box protein
Sapur.008G035000.1	657.3234098	-0.369740374	0.038005143	-9.72869	2.27E-22	7.16E-22	black	-0.6404606	1.68E-19		AT3G55005.1	TON1B	tonneau 1b (TON1b)	FGFR1 oncogene partner
Sapur.016G292700.1	457.3959117	-0.506037906	0.052047994	-9.72252	2.42E-22	7.60E-22	black	-0.652148499	2.21E-20		AT1G73940.1			hypothetical protein
Sapur.006G136300.1	49.69301651	-0.668614677	0.068773377	-9.722	2.43E-22	7.64E-22	black	-0.596808727	1.60E-16		AT2G18940.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.001G065800.1	119.8577884	-0.429673866	0.044399867	-9.67737	3.76E-22	1.18E-21	black	-0.602699818	6.75E-17		AT5G16950.1			histone acetyltransferase type B subunit, putative
Sapur.006G040000.1	2923.686206	-0.422721301	0.043883097	-9.6329	5.81E-22	1.81E-21	black	-0.642497406	1.19E-19	GO:0006412,GO:0005840,GO:0003735,GO:0003723	AT3G57490.1		Ribosomal protein S5 family protein	40S ribosomal protein S2
Sapur.007G051400.1	9.848316207	-1.163592247	0.120852654	-9.62819	6.08E-22	1.89E-21	black	-0.639892404	1.85E-19	GO:0015934,GO:0006412,GO:0003735	AT3G49910.1		Translation protein SH3-like family protein	60S ribosomal protein L26
Sapur.012G111500.1	2.353797478	-1.879971167	0.195510498	-9.6157	6.86E-22	2.14E-21	black	-0.613759759	1.27E-17		AT3G58660.1		Ribosomal protein L1p/L10e family	ribosomal protein .1/L10e family protein
Sapur.003G012900.3	6.672194093	1.347297495	0.140744078	9.572676	1.04E-21	3.23E-21	black	0.511470789	7.63E-12		AT1G68140.1		Protein of unknown function (DUF1644)	DUF1644 family protein
Sapur.001G054200.1	2832.201226	-0.545022709	0.056938553	-9.57212	1.05E-21	3.25E-21	black	-0.639490156	1.98E-19	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G61110.1	ARS27A,RS27A	ribosomal protein S27	40S ribosomal protein S27
Sapur.009G024100.1	2408.249047	-0.600700732	0.06282154	-9.56202	1.15E-21	3.58E-21	black	-0.646507228	5.96E-20		AT5G57290.1		60S acidic ribosomal protein family	NA
Sapur.002G114400.1	1834.266734	-0.569006494	0.059526916	-9.55881	1.19E-21	3.69E-21	black	-0.607507934	3.29E-17	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G10950.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L37a
Sapur.006G188500.1	486.8034506	-0.579899493	0.060691425	-9.55488	1.24E-21	3.83E-21	black	-0.586980128	6.52E-16		AT5G60340.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	adenylate kinase
Sapur.013G101100.1	695.8369807	-0.53108668	0.055616478	-9.54909	1.31E-21	4.04E-21	black	-0.6270289	1.56E-18	GO:0006412,GO:0005840,GO:0003735	AT4G16720.1		Ribosomal protein L23/L15e family protein	60S ribosomal protein L15
Sapur.005G016400.1	108.7693429	-0.700624992	0.073403984	-9.54478	1.36E-21	4.21E-21	black	-0.615587206	9.55E-18	GO:0004857				NA

Sapur.014G033700.1	1213.895414	-0.410864309	0.043083308	-9.53651	1.48E-21	4.56E-21	black	-0.604809776	4.93E-17	GO:0006457,GO:0005737	AT3G60210.1		GroES-like family protein	chaperonin 10
Sapur.017G073500.1	2125.059786	0.329472765	0.034727572	9.487354	2.37E-21	7.28E-21	black	0.638705474	2.26E-19	GO:0016567,GO:0004842,GO:0034450,GO:0006511,GO:0000151	AT5G15400.1		U-box domain-containing protein	ubiquitin conjugation factor E4, putative
Sapur.15WG145700.1	78.69391213	-0.791282662	0.083485257	-9.47811	2.59E-21	7.94E-21	black	-0.583924057	1.00E-15	GO:0006351,GO:0003899,GO:0003677	AT5G51940.1	NRPB6A,NRPD6A,NRPE6A	RNA polymerase Rpb6	DNA-directed RNA polymerase
Sapur.005G058700.1	169.4624186	-0.53852232	0.056828086	-9.47634	2.63E-21	8.08E-21	black	-0.615880077	9.12E-18	GO:0006412,GO:0005840,GO:0003735	AT4G39880.1		Ribosomal protein L23/L15e family protein	ribosomal protein L23
Sapur.018G006000.1	246.8441657	-0.591274283	0.062473222	-9.46444	2.95E-21	9.04E-21	black	-0.670615119	7.43E-22	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G31460.1		Ribosomal L28 family	ribosomal protein L28
Sapur.017G115500.1	2941.689467	-0.50509464	0.053499237	-9.44116	3.69E-21	1.13E-20	black	-0.608647946	2.77E-17	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G16780.1		Ribosomal protein L19e family protein	ribosomal protein L19
Sapur.001G170100.1	174.4053914	-0.548532775	0.058171913	-9.42951	4.12E-21	1.26E-20	black	-0.600238142	9.70E-17					transmembrane protein, putative
Sapur.016G157200.1	3174.048651	-0.519214399	0.055220884	-9.4025	5.33E-21	1.62E-20	black	-0.644046184	9.11E-20	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G74050.1		Ribosomal protein L6 family protein	60S ribosomal protein L6
Sapur.018G051600.1	127.9086497	0.593787059	0.063209631	9.393933	5.78E-21	1.76E-20	black	0.662989814	3.11E-21					NA
Sapur.019G091000.1	94.63106115	-0.795821161	0.084736297	-9.39174	5.90E-21	1.79E-20	black	-0.652007571	2.27E-20		AT2G43780.2			transmembrane protein, putative
Sapur.008G037600.1	982.5274098	-0.687001126	0.073173815	-9.38862	6.08E-21	1.85E-20	black	-0.610373545	2.13E-17	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G39390.1		Ribosomal L29 family protein	60S ribosomal protein L35
Sapur.010G203400.1	1920.477083	-0.60869028	0.064888591	-9.38054	6.56E-21	1.99E-20	black	-0.644532059	8.38E-20	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G23390.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L44
Sapur.003G005500.1	810.5258419	-0.604099814	0.064399334	-9.38053	6.56E-21	1.99E-20	black	-0.632058941	6.86E-19		AT5G57290.1		60S acidic ribosomal protein family	60S acidic ribosomal protein P3, putative
Sapur.009G099000.1	117.7159507	-0.685564776	0.073188977	-9.36705	7.46E-21	2.26E-20	black	-0.599595894	1.07E-16		AT2G21290.1			30S ribosomal protein S31, putative
Sapur.006G051500.1	54.60848962	0.93511643	0.099883835	9.36204	7.82E-21	2.37E-20	black	0.571389924	5.50E-15	GO:0016157,GO:0005985	AT5G20280.1	ATSPS1F,SPS1F	sucrose phosphate synthase 1F	sucrose phosphate synthase
Sapur.004G164100.1	293.2721432	-0.384951676	0.041239137	-9.33462	1.01E-20	3.06E-20	black	-0.617112902	7.53E-18	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G56940.1		Ribosomal protein S16 family protein	30S ribosomal protein S16
Sapur.005G168300.1	794.4520761	-0.397981389	0.042710967	-9.31801	1.19E-20	3.57E-20	black	-0.612687512	1.49E-17	GO:0006468,GO:0005524,GO:0004672,GO:0004674	AT5G26110.1		Protein kinase superfamily protein	Kae1-associated kinase Bud32
Sapur.004G062500.1	152.0114719	-0.661997481	0.071087215	-9.31247	1.25E-20	3.76E-20	black	-0.586735744	6.75E-16		AT4G09460.1	AtMYB6,MYB6	myb domain protein 6	MYB-like transcription factor 6, putative
Sapur.008G025000.2	104.7097982	-0.739628954	0.079735267	-9.27606	1.76E-20	5.28E-20	black	-0.559293081	2.67E-14		AT3G10380.1	ATSEC8,SEC8	subunit of exocyst complex 8	SEC8 exocyst complex component specific domain protein
Sapur.002G070600.1	854.0477403	0.428248654	0.046200694	9.269312	1.87E-20	5.62E-20	black	0.582113156	1.28E-15	GO:0046488,GO:0016307	AT1G77740.1	PIP5K2	phosphatidylinositol-4-phosphate 5-kinase 2	phosphatidylinositol-4-phosphate 5-kinase
Sapur.011G097400.1	1542.039193	-0.373611222	0.040336939	-9.26226	2.00E-20	6.00E-20	black	-0.569335006	7.23E-15	GO:0003677	AT1G51060.1	HTA10	histone H2A 10	histone H2A
Sapur.011G084100.1	450.4393108	-0.310901381	0.033628879	-9.24507	2.35E-20	7.03E-20	black	-0.58495488	8.66E-16		AT5G53800.1			hypothetical protein
Sapur.003G104500.1	163.2353618	-0.782645714	0.084854655	-9.22337	2.88E-20	8.59E-20	black	-0.629307659	1.08E-18		AT5G42070.1			hypothetical protein
Sapur.004G065300.1	1166.798986	-0.258820827	0.028132053	-9.20021	3.57E-20	1.06E-19	black	-0.576298169	2.85E-15		AT1G66670.1	CLPP3,NCLPP3	CLP protease proteolytic subunit 3	ATP-dependent Clp protease proteolytic subunit
Sapur.013G012700.1	3369.097671	-0.474695117	0.05163918	-9.19254	3.84E-20	1.14E-19	black	-0.603514869	5.98E-17	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G05590.1	RPL18	ribosomal protein L18	60S ribosomal protein L18
Sapur.008G062300.1	707.0321515	-0.508441039	0.055509261	-9.15957	5.21E-20	1.54E-19	black	-0.644432033	8.53E-20		AT2G43810.1		Small nuclear ribonucleoprotein family protein	U6 snRNA-associated-like-Smprotein
Sapur.003G084000.1	617.1365769	-0.487700043	0.053255461	-9.15775	5.30E-20	1.57E-19	black	-0.611101279	1.90E-17		AT2G45640.1	ATSAP18,SAP18	SIN3 associated polypeptide P18	histone deacetylase complex subunit SAP18
Sapur.002G183100.1	722.6595936	-0.466605115	0.050953664	-9.15744	5.31E-20	1.57E-19	black	-0.577054561	2.57E-15		AT2G31410.1			hypothetical protein
Sapur.016G081700.1	3051.45034	-0.551413876	0.060310597	-9.1429	6.08E-20	1.80E-19	black	-0.628222953	1.28E-18	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G02960.1		Ribosomal protein S12/S23 family protein	ribosomal protein S23 component of cytosolic 80S ribosome and 40S small subunit
Sapur.014G129100.1	512.3833674	-0.498991482	0.054735252	-9.11646	7.76E-20	2.29E-19	black	-0.621325849	3.88E-18		AT5G55160.1	ATSUMO2 SUM2 SUMO 2 S	small ubiquitin-like modifier 2	small ubiquitin-related modifier
Sapur.002G098200.1	523.4182522	0.493875578	0.054209343	9.110525	8.20E-20	2.42E-19	black	0.590607483	3.91E-16	GO:0016020,GO:0006810,GO:0005215	AT1G47240.1	ATNRAMP2,NRAMP2	NRAMP metal ion transporter 2	metal transporter NRAMP2
Sapur.012G072600.1	1323.636614	-0.47112849	0.051751525	-9.10366	8.73E-20	2.57E-19	black	-0.645319274	7.32E-20	GO:0006412,GO:0005840,GO:0003735,GO:0015934	AT1G27400.1		Ribosomal protein L22p/L17e family protein	60S ribosomal protein L17
Sapur.001G107700.1	4729.530935	-0.48509268	0.053332364	-9.09565	9.40E-20	2.76E-19	black	-0.580475854	1.61E-15	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G49010.2	ATBBC1,BBC1,RSU2	breast basic conserved 1	60S ribosomal protein L13
Sapur.011G045900.1	1755.402221	-0.706264413	0.077804348	-9.07744	1.11E-19	3.26E-19	black	-0.596685014	1.63E-16	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G37600.1		Ribosomal protein L36e family protein	60S ribosomal protein L36
Sapur.001G079300.1	891.2178512	0.54175452	0.059786633	9.061466	1.29E-19	3.77E-19	black	0.555772325	4.17E-14		AT1G64140.1			transcription factor, putative
Sapur.017G075800.1	1912.865999	-0.44243664	0.048916902	-9.04466	1.50E-19	4.39E-19	black	-0.595828881	1.85E-16	GO:0006412,GO:0005840,GO:0003735	AT5G61170.1		Ribosomal protein S19e family protein	40S ribosomal protein S19
Sapur.016G218900.1	3519.160433	-0.457004229	0.050557382	-9.03932	1.58E-19	4.61E-19	black	-0.554064955	5.17E-14	GO:0006412,GO:0003735	AT3G27830.1	RPL12,RPL12-A	ribosomal protein L12-A	50S ribosomal protein L12
Sapur.016G212600.1	323.9650003	-0.349790199	0.038753355	-9.02606	1.78E-19	5.20E-19	black	-0.62121732	3.95E-18	GO:0043461	AT5G40660.1		ATP12 protein-related	ATP synthase F1 complex assembly factor 2
Sapur.006G062600.1	2264.348414	-0.584550575	0.064917161	-9.00456	2.17E-19	6.31E-19	black	-0.615587348	9.55E-18	GO:0006412,GO:0005840,GO:0003735	AT2G37190.1		Ribosomal protein L11 family protein	60S ribosomal protein L12
Sapur.009G029300.1	413.6473119	-0.564054684	0.062782404	-8.98428	2.60E-19	7.58E-19	black	-0.586919569	6.58E-16	GO:0045039	AT2G29530.2	TIM10	Tim10/DDP family zinc finger protein	import inner membrane translocase subunit Tim10
Sapur.010G024700.1	926.6227429	-0.530127287	0.059027126	-8.98108	2.68E-19	7.80E-19	black	-0.597669527	1.41E-16		AT1G70600.1		Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L27a
Sapur.014G119500.1	1469.987897	-0.552692529	0.061558985	-8.97826	2.75E-19	8.00E-19	black	-0.615717903	9.35E-18	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G29390.1		Ribosomal protein S30 family protein	40S ribosomal protein S30
Sapur.15WG148100.1	1370.401676	-0.54664015	0.060986593	-8.96328	3.15E-19	9.15E-19	black	-0.589481261	4.58E-16		AT2G36620.1	RPL24A	ribosomal protein L24	60S ribosomal protein L24
Sapur.016G087000.1	693.5803622	-0.514116366	0.057369668	-8.96147	3.20E-19	9.30E-19	black	-0.601890721	7.60E-17		AT3G09860.1			hypothetical protein
Sapur.007G045400.2	14.54573035	-1.19530103	0.133728222	-8.93829	3.95E-19	1.14E-18	black	-0.556493437	3.81E-14		AT5G67240.1	SDN3	small RNA degrading nuclease 3	small RNA degrading nuclease
Sapur.018G051300.1	3270.632788	-0.578799687	0.064796844	-8.93253	4.16E-19	1.20E-18	black	-0.597651689	1.42E-16	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G19740.1		Ribosomal protein L31e family protein	60S ribosomal protein L31
Sapur.003G131800.1	549.0712833	-0.27913092	0.031292625	-8.92002	4.66E-19	1.35E-18	black	-0.569356724	7.21E-15	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT3G24050.1	GATA1	GATA transcription factor 1	GATA transcription factor
Sapur.017G093700.1	373.2019397	-0.670686759	0.075245795	-8.91328	4.95E-19	1.43E-18	black	-0.631403245	7.64E-19		AT5G16060.1		Cytochrome c oxidase biogenesis protein Cmc1-like	cytochrome C oxidase biogenesis Cmc1-like protein
Sapur.014G013500.1	37.76016619	-0.679881463	0.076322498	-8.90801	5.20E-19	1.50E-18	black	-0.581637916	1.37E-15		AT3G46630.1		Protein of unknown function (DUF3223)	DCL protein, putative
Sapur.014G046400.1	645.8181947	-0.215500362	0.024210563	-8.90109	5.53E-19	1.59E-18	black	-0.547571632	1.16E-13	GO:0005789	AT2G45140.1	PVA12	plant VAP homolog 12	vesicle-associated membrane protein, putative
Sapur.006G201500.1	2334.865817	-0.539039129	0.060582814	-8.89756	5.71E-19	1.64E-18	black	-0.585803995	7.69E-16	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G15250.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L37
Sapur.013G069900.1	13.88657478	-1.005567903	0.113163607	-8.88597	6.34E-19	1.82E-18	black	-0.566425704	1.06E-14	GO:0008270	AT5G17790.1	VAR3	zinc finger (Ran-binding) family protein	zinc finger protein VAR3, putative
Sapur.006G224700.1	488.9953449	1.206313256	0.136186822	8.857783	8.16E-19	2.34E-18	black	0.519592971	3.10E-12	GO:0046872,GO:0000166	AT2G24520.1	AHA5,HA5	H(+)-ATPase 5	plasma membrane H+-ATPase
Sapur.009G062500.1	308.898448	-0.474740405	0.053598214	-8.85739	8.19E-19	2.35E-18	black	-0.590935506	3.73E-16		AT5G61220.1		LYR family of Fe/S cluster biogenesis protein	catalytic/oxidoreductase, acting on NADH or NADPH protein
Sapur.008G136900.1	1190.718934	-0.629138902	0.071102703	-8.84831	8.89E-19	2.55E-18	black	-0.599131371	1.14E-16	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G27090.1		Ribosomal protein L14	60S ribosomal protein L14, putative
Sapur.018G082500.1	533.3485527	-0.473516387	0.05356373	-8.84024	9.55E-19	2.74E-18	black	-0.59221716	3.10E-16		AT5G57990.1	UBP23	ubiquitin-specific protease 23	NA
Sapur.016G199600.1	204.5896366	-0.509491644	0.057704102	-8.82938	1.05E-18	3.01E-18	black	-0.582724735	1.18E-15		AT1G27435.1			hypothetical protein
Sapur.013G016800.1	554.3893165	-0.556179502	0.06312567	-8.81067	1.24E-18	3.55E-18	black	-0.596585496	1.65E-16	GO:0005515	AT1G65030.1		Transducin/WD40 repeat-like superfamily protein	NA
Sapur.012G008600.1	996.5578499	-0.692162617	0.078875627	-8.77537	1.70E-18	4.85E-18	black	-0.588541706	5.23E-16		AT5G24510.1		60S acidic ribosomal protein family	60S acidic ribosomal protein P1, putative
Sapur.010G058600.1	2865.945526	-0.575563466	0.065781893	-8.74957	2.14E-18	6.08E-18	black	-0.601232257	8.38E-17	GO:0006412,GO:0005840,GO:0003735	AT5G18380.1		Ribosomal protein S5 domain 2-like superfamily protein	40S ribosomal protein S16
Sapur.004G088500.1	1295.607053	-0.429653808	0.049224075	-8.72853	2.58E-18	7.31E-18	black	-0.5809587	1.51E-15	GO:0006412	ATCG00900.1		Ribosomal protein S7p/S5e family protein	30S ribosomal protein S7
Sapur.018G068400.1	834.8067954	-0.582609369	0.06679047	-8.72294	2.71E-18	7.68E-18	black	-0.586404095	7.07E-16		AT4G30220.1	RUXF	small nuclear ribonucleoprotein F	small nuclear ribonucleoprotein F
Sapur.016G137600.1	317.2936142	-0.622678854	0.071550815	-8.70261	3.24E-18	9.17E-18	black	-0.60582691	4.23E-17	GO:0045039	AT2G29530.2	TIM10	Tim10/DDP family zinc finger protein	import inner membrane translocase subunit Tim10
Sapur.010G113900.1	860.5889963	-0.526136818	0.06060459	-8.68147	3.91E-18	1.10E-17	black	-0.594215212	2.33E-16		AT3G06610.1		DNA-binding enhancer protein-related	huntingtin-interacting protein K
Sapur.016G201300.1	83.12850742	-0.637954307	0.073540151	-8.67491	4.14E-18	1.17E-17	black	-0.556344492	3.88E-14		AT3G62870.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	NA
Sapur.001G056100.1	4145.080043	-0.430489397	0.049657067	-8.66925	4.35E-18	1.23E-17	black	-0.607427303	3.33E-17	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G09590.1		Translation protein SH3-like family protein	60S ribosomal protein L21
Sapur.008G038600.1	3084.729722	-0.613328595	0.070807461	-8.66192	4.64E-18	1.31E-17	black	-0.620598611	4.35E-18	GO:0006412,GO:0005840,GO:0003735	AT3G55280.1	RPL23AB	ribosomal protein L23AB	60S ribosomal protein L23a
Sapur.001G186100.1	239.5558166	-0.535470384	0.061847654	-8.65789	4.81E-18	1.35E-17	black	-0.636575426	3.24E-19		AT5G39600.1			39S ribosomal protein L53/MRP-L53
Sapur.002G193500.1	2718.063692	-0.603625288	0.069897686	-8.63584	5.83E-18	1.64E-17	black	-0.605310272	4.57E-17	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G18100.1		Ribosomal protein L32e	60S ribosomal protein L32
Sapur.005G095500.1	94.7595505	-0.457653455	0.053047612	-8.62722	6.29E-18	1.76E-17	black	-0.609694458	2.36E-17		AT5G49410.2			plant/F2P9-19 protein, putative
Sapur.002G189500.1	690.5627324	-0.337257846	0.03909324	-8.62701	6.30E-18	1.77E-17	black	-0.589368669	4.66E-16	GO:0005515	AT3G07170.1		Sterile alpha motif (SAM) domain-containing protein	SAM domain protein
Sapur.004G044100.1	3156.42882	-0.452510738	0.05246905	-8.62434	6.45E-18	1.81E-17	black	-0.635473368	3.89E-19	GO:0006412,GO:0005840,GO:0003735	AT2G34480.1		Ribosomal protein L18ae/LX family protein	NA
Sapur.006G034700.1	283.1314136	-0.462612898	0.053680662	-8.61787	6.82E-18	1.91E-17	black	-0.587775698	5.83E-16		AT3G57320.1			hypothetical protein
Sapur.016G125200.1	1349.256234	-0.395566656	0.04594694	-8.60921	7.36E-18	2.06E-17	black	-0.588564508	5.22E-16		AT2G44310.1		Calcium-binding EF-hand family protein	calcium-binding EF-hand protein
Sapur.003G026400.1	242.1441305	-0.496979645	0.057773244	-8.60225	7.82E-18	2.19E-17	black	-0.57385183	3.96E-15		AT3G27750.1			transmembrane protein, putative
Sapur.004G161200.1	147.0336872	-0.38759353	0.045081286	-8.59766	8.14E-18	2.28E-17	black	-0.572688296	4.63E-15	GO:0005515,GO:0043562,GO:0009744	AT2G28060.1		5\'-AMP-activated protein kinase beta-2 subunit protein	SNF1-related kinase regulatory subunit beta-2
Sapur.016G274600.1	1083.061314	-0.392655401	0.045708415	-8.59044	8.66E-18	2.42E-17	black	-0.551851264	6.83E-14	GO:0003677	AT4G27230.2	HTA2	histone H2A 2	histone H2A
Sapur.016G069600.1	785.0305172	0.456243373	0.053115599	8.589631	8.72E-18	2.44E-17	black	0.577050903	2.57E-15		AT3G11560.4		LETM1-like protein	LETM1-like protein
Sapur.010G193800.1	1012.355269	-0.531253524	0.061972138	-8.57246	1.01E-17	2.83E-17	black	-0.612515892	1.53E-17		AT4G39200.2		Ribosomal protein S25 family protein	40S ribosomal protein S25, putative
Sapur.008G014000.1	936.4964268	0.415334563	0.048579392	8.549604	1.24E-17	3.44E-17	black	0.587232805	6.29E-16		AT5G22450.1			hypothetical protein
Sapur.008G033400.1	1220.515371	-0.462437447	0.054242959	-8.5253	1.52E-17	4.23E-17	black	-0.637487919	2.78E-19	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G02960.1		Ribosomal protein S12/S23 family protein	ribosomal protein S23 component of cytosolic 80S ribosome and 40S small subunit
Sapur.15WG110300.1	1085.0066	-0.352689749	0.041423463	-8.51425	1.68E-17	4.64E-17	black	-0.58718074	6.34E-16	GO:0004017,GO:0019205,GO:0006139,GO:0005524	AT5G63400.1	ADK1	adenylate kinase 1	adenylate kinase
Sapur.005G174800.1	3745.850972	-0.462954889	0.054509958	-8.49303	2.01E-17	5.57E-17	black	-0.59394869	2.42E-16	GO:0006412,GO:0005840,GO:0003735	AT5G09500.1		Ribosomal protein S19 family protein	NA
Sapur.004G001400.1	11.78180659	-0.76913025	0.090571905	-8.49193	2.03E-17	5.62E-17	black	-0.574034903	3.86E-15		AT1G05000.1		Phosphotyrosine protein phosphatases superfamily protein	NA
Sapur.008G139400.1	1701.861093	-0.564861129	0.066638262	-8.47653	2.32E-17	6.41E-17	black	-0.60309392	6.36E-17	GO:0006412,GO:0005840,GO:0003735	AT2G33370.1		Ribosomal protein L14p/L23e family protein	60S ribosomal protein L23
Sapur.012G017400.1	123.8723256	-0.560438078	0.066146405	-8.47269	2.40E-17	6.62E-17	black	-0.594241105	2.32E-16		AT4G29660.1	EMB2752	embryo defective 2752	transmembrane protein, putative
Sapur.006G153900.1	1460.420925	-0.595034823	0.070300691	-8.46414	2.58E-17	7.11E-17	black	-0.581387945	1.42E-15	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G31985.1		Ribosomal protein L39 family protein	NA
Sapur.001G011700.1	396.4283799	-0.364170915	0.043056228	-8.45803	2.72E-17	7.49E-17	black	-0.62134219	3.87E-18		AT3G57930.1			metal tolerance protein, putative
Sapur.009G075400.1	114.9055817	-0.364399248	0.04317815	-8.43944	3.19E-17	8.76E-17	black	-0.546991974	1.25E-13		AT2G15270.1			DUF1168 family protein
Sapur.009G049500.1	4310.149028	-0.472933561	0.056190866	-8.41656	3.88E-17	1.06E-16	black	-0.618967416	5.63E-18	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G19740.1		Ribosomal protein L31e family protein	60S ribosomal protein L31
Sapur.016G063900.1	1336.73716	-0.458547487	0.054715181	-8.38063	5.26E-17	1.44E-16	black	-0.581236669	1.45E-15		AT1G70600.1		Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L27a
Sapur.016G015600.1	2178.3837	-0.531111926	0.063396495	-8.37762	5.40E-17	1.47E-16	black	-0.59795932	1.35E-16	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G15000.1		Ribosomal L27e protein family	60S ribosomal protein L27
Sapur.006G174400.1	933.5865873	-0.53774979	0.064189976	-8.37747	5.41E-17	1.48E-16	black	-0.572745819	4.59E-15	GO:0006412,GO:0005840,GO:0003735	AT3G55280.1	RPL23AB	ribosomal protein L23AB	60S ribosomal protein L23a
Sapur.013G033900.1	142.0444712	-0.492067915	0.058762414	-8.37385	5.58E-17	1.52E-16	black	-0.579581209	1.82E-15		AT3G04950.1			SEC-C motif protein
Sapur.010G170000.1	591.4834236	0.38526253	0.046022026	8.371264	5.70E-17	1.55E-16	black	0.569425171	7.14E-15		AT5G13590.1			hypothetical protein
Sapur.002G191100.1	1269.056089	-0.515284666	0.061641711	-8.35935	6.31E-17	1.72E-16	black	-0.580430736	1.62E-15		AT3G07230.1		wound-responsive protein-related	NA
Sapur.002G188000.2	7.180068005	-0.933217403	0.111671928	-8.35678	6.45E-17	1.75E-16	black	-0.45454446	2.23E-09	GO:0006412,GO:0005840,GO:0003735,GO:0015934	AT5G48760.1		Ribosomal protein L13 family protein	60S ribosomal protein L13a
Sapur.004G044800.1	472.9765557	0.652107295	0.078111012	8.348468	6.92E-17	1.88E-16	black	0.552399212	6.38E-14	GO:0046983,GO:0003677,GO:0006355,GO:0005634,GO:0003700	AT4G18960.1	AG	K-box region and MADS-box transcription factor family protein	MADS-box transcription factor
Sapur.016G208500.1	2.965988264	-1.346937293	0.161541166	-8.33804	7.55E-17	2.05E-16	black	-0.105235404	0.189619982		AT4G17310.1			hypothetical protein
Sapur.016G113900.1	1149.773845	0.477875619	0.05731359	8.337911	7.56E-17	2.05E-16	black	0.568548202	8.02E-15	GO:0005515,GO:0016787	AT1G08420.1	BSL2	BRI1 suppressor 1 (BSU1)-like 2	serine/threonine-protein phosphatase
Sapur.009G061600.1	1653.864852	0.412603365	0.049553738	8.326382	8.34E-17	2.26E-16	black	0.570370337	6.30E-15	GO:0055114,GO:0016491,GO:0008152	AT2G14170.1	ALDH6B2	aldehyde dehydrogenase 6B2	methylmalonate-semialdehyde dehydrogenase (acylating)
Sapur.15WG120800.1	12497.01906	0.332459401	0.040003055	8.31085	9.50E-17	2.57E-16	black	0.564752142	1.32E-14	GO:0005515,GO:0016887,GO:0005524,GO:0019538	AT5G50920.1	ATHSP93-V.CLPC.CLPC1.DC	CLPC homologue 1	ATP-dependent Clp protease ATP-binding subunit clpA-like protein
Sapur.008G077000.1	277.4273465	-0.448141749	0.053960231	-8.30504	9.98E-17	2.70E-16	black	-0.584009216	9.88E-16	GO:0003676,GO:0006457,GO:0003755	AT1G13690.1	ATE1	ATPase E1	peptidyl-prolyl cis-trans isomerase E
Sapur.009G013300.1	1949.912912	-0.406045526	0.048935373	-8.29759	1.06E-16	2.87E-16	black	-0.571127006	5.70E-15	GO:0006412,GO:0005840,GO:0003735	AT3G52580.1		Ribosomal protein S11 family protein	40S ribosomal protein S14
Sapur.003G067700.1	1646.104593	0.649364923	0.078285698	8.294809	1.09E-16	2.94E-16	black	0.589566929	4.53E-16					NA
Sapur.011G056800.1	757.9992165	-0.498890974	0.060267658	-8.27792	1.25E-16	3.38E-16	black	-0.564324794	1.39E-14		AT1G30070.1		SGS domain-containing protein	SGS domain protein
Sapur.004G054600.1	2898.997198	-0.355015605	0.042951331	-8.26553	1.39E-16	3.75E-16	black	-0.550034767	8.56E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G16780.1		Ribosomal protein L19e family protein	ribosomal protein L19
Sapur.003G001500.1	36.99693373	-0.579061527	0.070119519	-8.25821	1.48E-16	3.98E-16	black	-0.56595218	1.13E-14	GO:0008152,GO:0003824	AT5G23230.1	NIC2	nicotinamidase 2	isochorismatase hydrolase
Sapur.005G017200.2	36.76254651	-0.630573706	0.076394404	-8.25419	1.53E-16	4.12E-16	black	-0.385977322	5.96E-07	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G27850.1		Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L18
Sapur.007G022300.1	178.0555516	-0.5818341	0.070541962	-8.24806	1.61E-16	4.33E-16	black	-0.552781918	6.08E-14	GO:0019843,GO:0006412,GO:0005840,GO:0003735	AT2G18400.1		ribosomal protein L6 family protein	ribosomal protein L6
Sapur.003G151900.3	2.355202564	-1.468298555	0.178629215	-8.21981	2.04E-16	5.46E-16	black	-0.589617545	4.50E-16		AT3G54430.1	SRS6	SHI-related sequence 6	zinc finger, LRP1 type protein, putative
Sapur.007G001100.1	291.7437824	-0.252242869	0.030711277	-8.21336	2.15E-16	5.76E-16	black	-0.548637346	1.02E-13	GO:0005515	AT2G19430.1	AtTHO6,DWA1,THO6	DWD (DDB1-binding WD40 protein) hypersensitive to ABA 1	NA
Sapur.004G114800.1	1162.429303	-0.238623637	0.029067224	-8.20937	2.22E-16	5.96E-16	black	-0.53798966	3.70E-13		AT1G11750.1	CLPP6,NCLPP1,NCLPP6	CLP protease proteolytic subunit 6	ATP-dependent Clp protease proteolytic subunit
Sapur.016G112500.1	1427.440755	0.49813545	0.060711785	8.204922	2.31E-16	6.18E-16	black	0.542258758	2.22E-13	GO:0030036,GO:0005856	AT2G38440.1	ATSCAR2.DIS3.ITB1.SCAR2.\	SCAR homolog 2	SCAR2
Sapur.011G066100.1	51.37699761	0.808072648	0.098650833	8.19124	2.59E-16	6.91E-16	black	0.517718133	3.83E-12					hypothetical protein
Sapur.008G072500.1	101.1814275	-0.488459779	0.059725105	-8.17847	2.87E-16	7.68E-16	black	-0.58330603	1.09E-15	GO:0051301,GO:0032955	AT1G69390.1	ARC12,ATMINE1,MINE1	homologue of bacterial MinE 1	cell division topological specificity factor MinE
Sapur.017G071400.1	3974.24597	0.445048775	0.054458258	8.172292	3.03E-16	8.07E-16	black	0.534279651	5.74E-13	GO:0030170	AT3G01120.1	ATCYS1,CGS,CGS1,MTO1	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	cystathionine gamma-synthase
Sapur.014G095600.1	1856.983844	-0.192415517	0.023594404	-8.15513	3.49E-16	9.29E-16	black	-0.535343181	5.06E-13		AT1G02560.1	CLPP5,NCLPP1,NCLPP5	nuclear encoded CLP protease 5	ATP-dependent Clp protease proteolytic subunit
Sapur.002G122100.1	871.8297429	-0.431818406	0.052979907	-8.15061	3.62E-16	9.63E-16	black	-0.576399227	2.81E-15	GO:0016829,GO:0008152	AT2G45440.1	DHDPS2	dihydrodipicolinate synthase	dihydrodipicolinate synthase
Sapur.004G108500.1	338.6409454	-0.45801792	0.056220384	-8.14683	3.74E-16	9.93E-16	black	-0.593755668	2.49E-16		AT1G49510.1	emb1273	embryo defective 1273	transmembrane protein, putative
Sapur.010G168700.1	2494.46039	-0.477106497	0.058608573	-8.14056	3.93E-16	1.05E-15	black	-0.569623978	6.95E-15	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G02610.1		Ribosomal L29 family protein	60S ribosomal protein L35
Sapur.009G050800.1	5395.488503	-0.381114606	0.047001466	-8.10857	5.12E-16	1.36E-15	black	-0.583003386	1.14E-15	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G74050.1		Ribosomal protein L6 family protein	60S ribosomal protein L6
Sapur.018G073800.1	870.5739949	0.353987994	0.043717265	8.097213	5.62E-16	1.49E-15	black	0.549196334	9.49E-14	GO:0019538	AT5G57710.1		Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein	101 kDa heat shock protein; HSP101-like protein
Sapur.016G057500.1	1831.326376	-0.527178415	0.065433336	-8.05673	7.84E-16	2.07E-15	black	-0.559517	2.59E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G57660.1		Translation protein SH3-like family protein	60S ribosomal protein L21
Sapur.013G116800.1	10454.39803	-0.380178435	0.047328503	-8.03276	9.53E-16	2.51E-15	black	-0.558706684	2.87E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735,GO:0008097	AT3G25520.1	ATL5,OLI5,PGY3,RPL5A	ribosomal protein L5	60S ribosomal protein L5
Sapur.T091300.1	740.042577	-0.29831959	0.037143671	-8.03151	9.63E-16	2.53E-15	black	-0.534676943	5.48E-13	GO:0016020	AT5G40770.1	ATPHB3,PHB3	prohibitin 3	prohibitin
Sapur.002G195400.1	16.69861504	-0.968642761	0.120611023	-8.03113	9.66E-16	2.54E-15	black	-0.521169933	2.60E-12					NA
Sapur.010G041600.1	467.3531714	-0.426110067	0.053206602	-8.00859	1.16E-15	3.04E-15	black	-0.57186694	5.16E-15		AT3G23325.1		Splicing factor 3B subunit 5/RDS3 complex subunit 10	splicing factor 3B subunit
Sapur.014G069300.1	1686.209712	0.416234654	0.051987977	8.006364	1.18E-15	3.10E-15	black	0.55855368	2.93E-14		AT4G01290.2			hypothetical protein
Sapur.005G028800.1	628.840466	-0.334994236	0.041889774	-7.99704	1.27E-15	3.34E-15	black	-0.582690786	1.19E-15	GO:0016021,GO:0008233,GO:0006465,GO:0005787	AT5G27430.1		Signal peptidase subunit	signal peptidase subunit protein
Sapur.006G076800.3	18.90286346	-0.66579507	0.083459694	-7.97744	1.49E-15	3.91E-15	black	-0.538611893	3.43E-13	GO:0005515	AT3G09250.1		Nuclear transport factor 2 (NTF2) family protein	SnoaL-like domain protein
Sapur.010G010900.2	11.24484812	-1.041862583	0.131329021	-7.93322	2.14E-15	5.56E-15	black	-0.047848448	0.551783744	GO:0016021	AT2G42770.1		Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	peroxisomal membrane protein, putative
Sapur.014G128300.1	23.98303451	-0.752948346	0.095040605	-7.92239	2.33E-15	6.06E-15	black	-0.597816053	1.38E-16	GO:0003676	AT3G08000.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in RNA-binding protein 28 (RBM28)-like protein
Sapur.007G015400.1	254.4731412	-0.511914137	0.064718622	-7.90984	2.58E-15	6.70E-15	black	-0.564608287	1.34E-14		AT3G51010.1			hypothetical protein
Sapur.006G228000.1	292.8593251	-0.429151729	0.054316337	-7.90097	2.77E-15	7.18E-15	black	-0.57508781	3.35E-15	GO:0008176,GO:0006400	AT5G24840.1		tRNA (guanine-N-7) methyltransferase	tRNA (guanine-N(7))-methyltransferase
Sapur.011G041900.1	2388.2405	-0.305176175	0.038743498	-7.87684	3.36E-15	8.70E-15	black	-0.529867529	9.61E-13		AT5G46020.1			heat- and acid-stable phosphoprotein
Sapur.005G202400.1	28.11910125	-0.741628399	0.094350086	-7.86039	3.83E-15	9.90E-15	black	-0.495894209	4.01E-11					NA
Sapur.018G107200.1	4686.783031	-0.385443947	0.049138883	-7.84397	4.37E-15	1.13E-14	black	-0.561086036	2.12E-14		AT3G13580.3		Ribosomal protein L30/L7 family protein	60S ribosomal protein L7
Sapur.001G121600.1	162.3162217	-0.422223538	0.053880249	-7.83633	4.64E-15	1.20E-14	black	-0.546727636	1.29E-13		AT3G59840.1			NA
Sapur.003G117400.1	502.1605147	-0.385635743	0.049338248	-7.81616	5.45E-15	1.40E-14	black	-0.547128631	1.22E-13		AT5G47890.1		NADH-ubiquinone oxidoreductase B8 subunit, putative	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2
Sapur.016G230100.1	46.00978955	0.607360861	0.077718416	7.81489	5.50E-15	1.42E-14	black	0.543796884	1.84E-13	GO:0016787	AT5G55260.1	PPX-2,PPX2	protein phosphatase X 2	serine/threonine-protein phosphatase
Sapur.004G060300.1	2130.818888	-0.410973984	0.052639416	-7.80734	5.84E-15	1.50E-14	black	-0.556017531	4.05E-14		AT2G36620.1	RPL24A	ribosomal protein L24	60S ribosomal protein L24
Sapur.002G194500.1	887.2167659	-0.300988776	0.038692094	-7.77908	7.31E-15	1.87E-14	black	-0.554843766	4.69E-14	GO:0016020	AT4G27990.1	ATYLMG1-2,YLMG1-2	YGGT family protein	YGGT family protein
Sapur.008G080600.1	656.0717908	-0.289169969	0.037228477	-7.76744	8.01E-15	2.05E-14	black	-0.522116227	2.34E-12	GO:0019843,GO:0006412,GO:0005840,GO:0003735	AT3G17170.1	RFC3	Translation elongation factor EF1B/ribosomal protein S6 family protein	30S ribosomal protein S6
Sapur.012G098400.1	978.1070809	-0.505676335	0.065115779	-7.7658	8.11E-15	2.08E-14	black	-0.545049163	1.58E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G00100.1	ATRPS13A.PFL2.RPS13.RPS1	ribosomal protein S13A	40S ribosomal protein S13
Sapur.003G117800.1	955.3519464	-0.519561681	0.066925737	-7.76326	8.28E-15	2.12E-14	black	-0.540830164	2.63E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G09590.1		Translation protein SH3-like family protein	60S ribosomal protein L21
Sapur.008G059100.1	1326.353398	-0.557463369	0.071832316	-7.76062	8.45E-15	2.16E-14	black	-0.511444471	7.65E-12		AT4G14270.1			polyadenylate-binding protein interacting protein, putative
Sapur.002G041000.2	6.24224265	-0.901332536	0.116236661	-7.75429	8.88E-15	2.27E-14	black	-0.483693804	1.39E-10	GO:0006412	AT3G63190.1	AtcpRRF.cpRRF.HFP108.RRF	ribosome recycling factor, chloroplast precursor	ribosome recycling factor
Sapur.006G000100.1	60.56363443	-0.564013481	0.072796616	-7.7478	9.35E-15	2.39E-14	black	-0.503021009	1.90E-11		AT3G52155.1		Phosphoglycerate mutase family protein	NA
Sapur.003G082900.1	206.4085138	-0.342520128	0.044244933	-7.74145	9.83E-15	2.51E-14	black	-0.523356096	2.03E-12	GO:0016787	AT4G11980.1	ATNUDT14.ATNUDX14.NUI	nudix hydrolase homolog 14	nudix hydrolase
Sapur.018G010100.1	105.4457847	-0.371855264	0.048047385	-7.73934	9.99E-15	2.55E-14	black	-0.577819881	2.31E-15		AT5G10745.1			transmembrane protein, putative
Sapur.009G108400.1	129.5032478	-0.52748812	0.068286851	-7.72459	1.12E-14	2.86E-14	black	-0.534941094	5.31E-13		AT2G20940.1		Protein of unknown function (DUF1279)	transmembrane protein, putative
Sapur.002G155900.1	257.110614	-0.390383927	0.05057068	-7.71957	1.17E-14	2.97E-14	black	-0.534759817	5.42E-13	GO:0006396	AT5G27720.1	emb1644	Small nuclear ribonucleoprotein family protein	U6 snRNA-associated-like-Smprotein LSm4, putative
Sapur.016G128700.1	1179.372835	-0.308473057	0.039973545	-7.71693	1.19E-14	3.04E-14	black	-0.589708415	4.44E-16	GO:0006412,GO:0005840,GO:0003735	AT3G55280.2	RPL23AB	ribosomal protein L23AB	60S ribosomal protein L23a
Sapur.007G048200.1	82.0157325	0.542134963	0.070304143	7.71128	1.25E-14	3.17E-14	black	0.54833654	1.06E-13		AT4G37440.1			hypothetical protein
Sapur.010G156400.1	3758.52619	-0.446356252	0.058015977	-7.69368	1.43E-14	3.63E-14	black	-0.577835014	2.31E-15	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G74270.1		Ribosomal protein L35Ae family protein	60S ribosomal protein L35a
Sapur.001G138400.1	1833.754021	0.514109174	0.066875024	7.687611	1.50E-14	3.81E-14	black	0.509975012	8.98E-12	GO:0046872,GO:0030001,GO:0000166	AT5G44790.1	HMA7,RAN1	copper-exporting ATPase / responsive-to-antagonist 1 / copper-transporting ATPase (RAN1)	copper-transporting ATPase P-type protein, putative
Sapur.010G172700.1	2006.843232	-0.402958669	0.052676615	-7.64967	2.01E-14	5.10E-14	black	-0.534147944	5.83E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G02960.1		Ribosomal protein S12/S23 family protein	ribosomal protein S23 component of cytosolic 80S ribosome and 40S small subunit
Sapur.007G074400.1	213.9636807	-0.553377965	0.072778146	-7.60363	2.88E-14	7.24E-14	black	-0.531804417	7.67E-13		AT4G39470.1		Tetratricopeptide repeat (TPR)-like superfamily protein	lumen common family protein, putative
Sapur.001G134300.1	242.0769604	-0.520442085	0.06852104	-7.59536	3.07E-14	7.72E-14	black	-0.601379268	8.20E-17		AT1G53903.1		Protein of unknown function (DUF581)	DUF581 family protein
Sapur.003G008700.1	1906.497018	-0.571115564	0.075257603	-7.58881	3.23E-14	8.11E-14	black	-0.51189711	7.28E-12	GO:0051536,GO:0009055	AT1G60950.1	ATFD2,FED A	2Fe-2S ferredoxin-like superfamily protein	ferredoxin I
Sapur.018G044100.1	46.9833861	-0.582509678	0.076878082	-7.57706	3.53E-14	8.87E-14	black	-0.528191028	1.17E-12		AT4G21065.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.002G049600.1	198.0477651	-0.331433935	0.043801226	-7.56677	3.83E-14	9.59E-14	black	-0.51461439	5.40E-12	GO:0016020	AT5G36120.1	atylmg3,CCB3,YLMG3	cofactor assembly, complex C (B6F)	integral membrane protein, putative
Sapur.014G039600.1	1740.903006	-0.503921821	0.066740023	-7.55052	4.34E-14	1.08E-13	black	-0.544853814	1.62E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G10950.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L37a
Sapur.011G045100.1	288.9279991	0.410106124	0.054525426	7.521374	5.42E-14	1.35E-13	black	0.541816811	2.34E-13	GO:0003676	AT3G15010.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 1 in heterogeneous nuclear ribonucleoprotein A subfamily protein
Sapur.012G107100.1	1250.858133	-0.544855681	0.072798772	-7.48441	7.19E-14	1.79E-13	black	-0.568467868	8.10E-15		AT2G36620.1	RPL24A	ribosomal protein L24	60S ribosomal protein L24
Sapur.006G157200.1	1113.687826	-0.469758267	0.062847926	-7.47452	7.75E-14	1.92E-13	black	-0.556601196	3.76E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G61110.1	ARS27A,RS27A	ribosomal protein S27	40S ribosomal protein S27
Sapur.016G160400.1	2371.766575	0.312729152	0.041870725	7.468921	8.09E-14	2.01E-13	black	0.547691114	1.14E-13		AT5G19400.1	SMG7	Telomerase activating protein Est1	telomerase-binding protein EST1A
Sapur.002G027500.1	2177.487394	-0.475946515	0.063914078	-7.44666	9.57E-14	2.37E-13	black	-0.516888287	4.20E-12	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G27090.1		Ribosomal protein L14	60S ribosomal protein L14, putative
Sapur.15WG122000.1	1222.021872	-0.461390603	0.062175926	-7.42073	1.16E-13	2.87E-13	black	-0.527837564	1.22E-12	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G26880.1		Ribosomal protein L34e superfamily protein	60S ribosomal protein L34
Sapur.019G070100.1	288.2749082	-0.366355948	0.049491726	-7.40237	1.34E-13	3.29E-13	black	-0.505702446	1.42E-11		AT2G21195.1			hypothetical protein
Sapur.018G107900.1	1515.258414	0.373443987	0.050569201	7.384811	1.53E-13	3.75E-13	black	0.497771736	3.30E-11	GO:0005515,GO:0006468,GO:0004672	AT3G23750.1		Leucine-rich repeat protein kinase family protein	receptor-like kinase Rhg4
Sapur.002G099400.1	168.7032983	-0.375035477	0.050872165	-7.37212	1.68E-13	4.12E-13	black	-0.513062062	6.41E-12		AT1G47200.1	WPP2	WPP domain protein 2	WPP domain protein
Sapur.008G121300.1	878.3877931	-0.563459952	0.076700934	-7.34619	2.04E-13	5.00E-13	black	-0.502672676	1.97E-11	GO:0006412,GO:0005840,GO:0003735	AT5G18380.3		Ribosomal protein S5 domain 2-like superfamily protein	40S ribosomal protein S16
Sapur.008G032100.1	2547.519986	-0.447782808	0.060954592	-7.34617	2.04E-13	5.00E-13	black	-0.553269096	5.72E-14	GO:0005525	AT1G07920.1		GTP binding Elongation factor Tu family protein	elongation factor 1-alpha
Sapur.012G025600.1	729.6704914	-0.521629402	0.071054234	-7.34129	2.12E-13	5.18E-13	black	-0.568146239	8.45E-15		AT3G46560.1	emb2474,TIM9	Tim10/DDP family zinc finger protein	import inner membrane translocase subunit Tim9
Sapur.002G110100.1	852.0642946	-0.383138191	0.052281542	-7.32836	2.33E-13	5.69E-13	black	-0.528130589	1.18E-12	GO:0006457,GO:0005737	AT3G60210.1		GroES-like family protein	chaperonin 10 kDa subunit
Sapur.008G171700.1	90.44429409	-0.498766104	0.068188317	-7.31454	2.58E-13	6.30E-13	black	-0.502211984	2.07E-11		AT5G18920.1		Cox19-like CHCH family protein	Cox19-like CHCH family protein, putative
Sapur.003G119300.1	2556.988727	-0.436381175	0.059675564	-7.31256	2.62E-13	6.39E-13	black	-0.54996409	8.63E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G61110.1	ARS27A,RS27A	ribosomal protein S27	40S ribosomal protein S27
Sapur.003G107700.1	39.13860844	0.693639045	0.094937154	7.306297	2.75E-13	6.69E-13	black	0.523325459	2.04E-12					NA
Sapur.012G011400.1	504.2189248	-0.308074479	0.042333777	-7.27727	3.41E-13	8.27E-13	black	-0.552833955	6.04E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G53070.1		Ribosomal protein L9/RNase H1	ribosomal protein L9
Sapur.014G057000.1	290.0228694	-0.347618641	0.047819847	-7.26934	3.61E-13	8.76E-13	black	-0.518091073	3.67E-12	GO:0034227,GO:0005737	AT3G61113.1		Ubiquitin related modifier 1	ubiquitin-related modifier-like protein
Sapur.009G080500.1	1144.93205	0.43561054	0.060046456	7.254559	4.03E-13	9.76E-13	black	0.500190695	2.56E-11	GO:0006914	AT3G19190.1	ATATG2,ATG2	autophagy 2	autophagy-related protein
Sapur.T017400.1	6.355623851	0.96168046	0.13260878	7.252012	4.11E-13	9.94E-13	black	0.525106288	1.66E-12	GO:0006468,GO:0005524,GO:0004672	AT1G29720.1		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.010G111100.1	2657.79652	-0.456735033	0.062989873	-7.25093	4.14E-13	1.00E-12	black	-0.551687526	6.97E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G06680.1		Ribosomal L29e protein family	NA
Sapur.014G099500.1	193.6557714	-0.563619146	0.078280163	-7.20003	6.02E-13	1.45E-12	black	-0.512983514	6.46E-12	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT5G49300.1	GATA16	GATA transcription factor 16	GATA transcription factor, putative
Sapur.002G198700.1	235.5785506	-0.328663373	0.045675411	-7.19563	6.22E-13	1.50E-12	black	-0.505368511	1.48E-11		AT1G04130.1		Tetratricopeptide repeat (TPR)-like superfamily protein	heat shock protein 70 (HSP70)-interacting protein, putative
Sapur.007G004200.1	23.4407953	-0.567364681	0.078984098	-7.18328	6.81E-13	1.64E-12	black	-0.481407659	1.74E-10					NA
Sapur.002G044700.1	2332.656957	-0.442842622	0.061807317	-7.16489	7.78E-13	1.87E-12	black	-0.498930259	2.92E-11	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G32060.3		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	40S ribosomal protein S12
Sapur.005G075000.1	94.73705584	-0.559205875	0.078118809	-7.1584	8.16E-13	1.96E-12	black	-0.482192135	1.61E-10	GO:0006511	AT3G21860.1	ASK10,SK10	SKP1-like 10	Skp1 family, dimerization domain protein
Sapur.016G132600.1	486.5568258	-0.481243589	0.067324166	-7.14816	8.80E-13	2.11E-12	black	-0.548738715	1.00E-13		AT2G28900.1	ATOEP16-1.ATOEP16-L.OEP	outer plastid envelope protein 16-1	amino acid selective channel protein
Sapur.006G175200.1	1553.519027	-0.415617557	0.058242587	-7.13597	9.61E-13	2.30E-12	black	-0.544813083	1.63E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G02610.1		Ribosomal L29 family protein	60S ribosomal protein L35
Sapur.003G021700.1	523.6533822	-0.341488742	0.047856238	-7.13572	9.63E-13	2.30E-12	black	-0.518553912	3.49E-12	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G13882.1		Ribosomal L34	ribosomal protein L34
Sapur.008G124500.1	222.5268057	-0.331102007	0.046426453	-7.13175	9.91E-13	2.37E-12	black	-0.498305635	3.12E-11		AT4G14870.1		secE/sec61-gamma protein transport protein	SecE/Sec61-gamma subunit of protein translocation complex protein
Sapur.014G143200.1	22.92864779	-0.847891639	0.120038289	-7.06351	1.62E-12	3.86E-12	black	-0.487910053	9.08E-11	GO:0006412,GO:0005840,GO:0005622,GO:0003735,GO:0008097	AT5G39740.2	OLI7,RPL5B	ribosomal protein L5 B	NA
Sapur.009G123900.1	4346.970241	-0.373704746	0.052979586	-7.05375	1.74E-12	4.13E-12	black	-0.540460132	2.75E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G77940.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L30
Sapur.003G008300.1	882.774684	-0.380598596	0.053977778	-7.05102	1.78E-12	4.21E-12	black	-0.549490719	9.15E-14	GO:0006397	AT1G03330.1		Small nuclear ribonucleoprotein family protein	snRNP core Sm Sm-X5-like protein
Sapur.019G064500.1	145.1361591	-0.343251376	0.048709287	-7.04694	1.83E-12	4.33E-12	black	-0.475716143	3.05E-10		AT4G10330.1		glycine-rich protein	transmembrane protein, putative
Sapur.009G029400.1	215.6390635	-0.449016213	0.06373499	-7.04505	1.85E-12	4.39E-12	black	-0.550177102	8.41E-14		AT5G52370.1			hypothetical protein
Sapur.012G071500.1	795.6587021	-0.278000917	0.039539431	-7.03098	2.05E-12	4.85E-12	black	-0.510124156	8.83E-12	GO:0004017,GO:0019205,GO:0006139,GO:0005524	AT5G63400.1	ADK1	adenylate kinase 1	adenylate kinase
Sapur.007G032400.1	5206.242078	-0.332836853	0.047390898	-7.02322	2.17E-12	5.13E-12	black	-0.523401712	2.02E-12		AT2G27530.2	PGY1	Ribosomal protein L1p/L10e family	60S ribosomal protein L10a
Sapur.005G196800.1	1871.194808	-0.351662458	0.050136393	-7.01412	2.31E-12	5.47E-12	black	-0.561784812	1.94E-14	GO:0008168,GO:0008152,GO:0006694	AT1G20330.1	CVP1,FRL1,SMT2	sterol methyltransferase 2	sterol 24-C-methyltransferase
Sapur.007G010600.1	4816.49906	-0.351203464	0.050159852	-7.00168	2.53E-12	5.96E-12	black	-0.534735284	5.44E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G36130.1		Ribosomal protein L2 family	60S ribosomal protein L2
Sapur.001G173800.1	2336.54458	-0.483369165	0.069252662	-6.97979	2.96E-12	6.96E-12	black	-0.467971555	6.41E-10	GO:0016020,GO:0009765	AT1G15820.1	CP24,LHCB6	light harvesting complex photosystem II subunit 6	light harvesting chlorophyll A-B-binding protein
Sapur.010G086100.1	2929.063434	0.437098963	0.062664913	6.975179	3.05E-12	7.19E-12	black	0.487846853	9.14E-11	GO:0005524,GO:0046488,GO:0016307	AT1G71010.1	FAB1C	FORMS APLOID AND BINUCLEATE CELLS 1C	1-phosphatidylinositol-3-phosphate 5-kinase fab1
Sapur.002G116000.1	158.5988162	-0.388203211	0.055723971	-6.96654	3.25E-12	7.63E-12	black	-0.488910436	8.21E-11		AT3G15351.1			hypothetical protein
Sapur.004G032700.1	6.876495227	-1.016979016	0.146110183	-6.96036	3.39E-12	7.97E-12	black	-0.489632321	7.63E-11		AT5G46110.4	APE2,TPT	Glucose-6-phosphate/phosphate translocator-related	triose phosphate/phosphate translocator
Sapur.011G071500.1	575.920084	0.422961227	0.060798205	6.956805	3.48E-12	8.17E-12	black	0.496717879	3.68E-11	GO:0016020,GO:0006075,GO:0003843,GO:0000148	AT3G14570.1	ATGSL04,atgsl4,gsl04	glucan synthase-like 4	callose synthase
Sapur.014G037600.1	1723.249443	-0.309164949	0.044496092	-6.94814	3.70E-12	8.67E-12	black	-0.529590936	9.93E-13	GO:0006241,GO:0006228,GO:0006183,GO:0006165,GO:0004550	AT4G09320.1	NDPK1	Nucleoside diphosphate kinase family protein	nucleoside diphosphate kinase
Sapur.018G113200.1	1086.761294	-0.50027098	0.072063174	-6.94212	3.86E-12	9.04E-12	black	-0.488886265	8.23E-11	GO:0006412,GO:0005840,GO:0003735	AT2G37190.1		Ribosomal protein L11 family protein	60S ribosomal protein L12
Sapur.002G040000.1	3047.570346	-0.349163938	0.050338956	-6.93626	4.03E-12	9.42E-12	black	-0.476442147	2.84E-10	GO:0006412,GO:0005840,GO:0005622,GO:0003735,GO:0003723	AT1G34030.1		Ribosomal protein S13/S18 family	40S ribosomal protein S18
Sapur.003G068600.1	596.52509	-0.339592059	0.049076943	-6.91958	4.53E-12	1.06E-11	black	-0.503296798	1.84E-11	GO:0006351,GO:0003899,GO:0003677	AT1G61700.1		RNA polymerases N / 8 kDa subunit	DNA-directed RNA polymerase I, II
Sapur.006G102100.1	4734.967934	0.380214454	0.055230292	6.884165	5.81E-12	1.35E-11	black	0.486721166	1.02E-10	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT2G36910.1	ABCB1,ATPGP1,PGP1	ATP binding cassette subfamily B1	ABC transporter family B protein, group MDR/PGP protein PpABCB26 protein
Sapur.009G122800.1	552.9786872	-0.233954516	0.034091935	-6.86246	6.77E-12	1.57E-11	black	-0.508856446	1.01E-11	GO:0055114,GO:0016491	AT5G17770.1	ATCBR,CBR,CBR1	NADH:cytochrome B5 reductase 1	NADH-cytochrome b5 reductase
Sapur.016G289400.1	2856.823243	0.272695914	0.039739028	6.862169	6.78E-12	1.57E-11	black	0.504567631	1.61E-11	GO:0005975,GO:0004553	AT1G32860.1		Glycosyl hydrolase superfamily protein	1%2C3-beta-D-glucanase GH17-33
Sapur.014G102000.1	79.36428593	-0.643750354	0.094155772	-6.83708	8.08E-12	1.87E-11	black	-0.459568627	1.41E-09		AT4G02370.1		Protein of unknown function, DUF538	transmembrane protein, putative
Sapur.017G015800.1	2126.110855	-0.505385751	0.074090156	-6.82123	9.03E-12	2.09E-11	black	-0.539332265	3.15E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G59540.1		Ribosomal L38e protein family	NA
Sapur.001G182700.1	2649.169786	-0.213997251	0.031379361	-6.81968	9.12E-12	2.11E-11	black	-0.473969065	3.61E-10		AT5G49910.1	cpHsc70-2.CPHSC70-2EAT S	chloroplast heat shock protein 70-2	NA
Sapur.003G079500.1	1598.475525	-0.435738157	0.06394489	-6.81428	9.47E-12	2.19E-11	black	-0.501727834	2.17E-11	GO:0006412,GO:0005840,GO:0003735	AT1G07770.2	RPS15A	ribosomal protein S15A	40S ribosomal protein S15a
Sapur.009G106500.1	1380.681229	-0.263007438	0.038606224	-6.81257	9.59E-12	2.21E-11	black	-0.54408021	1.78E-13	GO:0019773,GO:0006511,GO:0004175,GO:0051603,GO:0005839,GO:0004298	AT5G66140.1	PAD2	proteasome alpha subunit D2	proteasome subunit alpha type-7 protein
Sapur.001G151100.1	565.1194081	-0.505370751	0.074219519	-6.80914	9.82E-12	2.27E-11	black	-0.499562312	2.73E-11	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G16080.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L37, putative
Sapur.009G085000.1	262.5107908	-0.576326422	0.084725537	-6.80228	1.03E-11	2.37E-11	black	-0.471190775	4.72E-10		AT2G15890.1	MEE14	maternal effect embryo arrest 14	maternal effect embryo arrest 14-2 protein, putative
Sapur.016G049000.1	4724.801881	-0.303463781	0.044811188	-6.77205	1.27E-11	2.92E-11	black	-0.501075136	2.33E-11	GO:0006412,GO:0005840,GO:0003735,GO:0003723	AT2G41840.1		Ribosomal protein S5 family protein	40S ribosomal protein S2
Sapur.017G115800.1	2233.872082	-0.32627632	0.048216473	-6.76691	1.32E-11	3.02E-11	black	-0.506248866	1.34E-11		AT1G17880.1	ATBTF3,BTF3	basic transcription factor 3	BTF3-like transcription factor
Sapur.011G048600.1	216.2884066	-0.297944943	0.044200423	-6.74077	1.58E-11	3.61E-11	black	-0.467803167	6.52E-10					NA
Sapur.002G011200.1	1641.539502	-0.331987896	0.049302681	-6.73367	1.65E-11	3.78E-11	black	-0.545407645	1.51E-13	GO:0008168,GO:0008152,GO:0006694	AT1G20330.1	CVP1,FRL1,SMT2	sterol methyltransferase 2	sterol 24-C-methyltransferase
Sapur.016G077300.1	1027.003092	-0.36789076	0.054779471	-6.71585	1.87E-11	4.27E-11	black	-0.496180349	3.89E-11	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G49010.1	ATBBC1,BBC1,RSU2	breast basic conserved 1	60S ribosomal protein L13
Sapur.007G097800.1	838.642135	0.372659507	0.055601004	6.702388	2.05E-11	4.67E-11	black	0.517694229	3.84E-12	GO:0016773,GO:0048015,GO:0046854,GO:0006661,GO:0004430	AT5G64070.1	PI-4KBETA1,PI4KBETA1	phosphatidylinositol 4-OH kinase beta1	phosphatidylinositol 4-kinase, putative
Sapur.019G027900.1	717.3403387	0.268453779	0.040092933	6.695788	2.15E-11	4.89E-11	black	0.487713544	9.27E-11	GO:0005634	AT1G08620.1	PKDM7D	Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein	transcription factor jumonji family protein
Sapur.008G056900.1	10.44586191	-0.886622576	0.13330368	-6.65115	2.91E-11	6.59E-11	black	-0.477364226	2.59E-10	GO:0019867	AT5G05520.1		Outer membrane OMP85 family protein	sorting and assembly machinery component-like protein
Sapur.009G093900.1	2079.276741	-0.422016858	0.063605013	-6.63496	3.25E-11	7.34E-11	black	-0.490380139	7.07E-11		AT4G39200.1		Ribosomal protein S25 family protein	40S ribosomal protein S25, putative
Sapur.001G183200.1	101.4959353	-0.434824862	0.065764393	-6.61186	3.80E-11	8.57E-11	black	-0.479662318	2.07E-10	GO:0009113,GO:0004637	AT1G09830.1		Glycinamide ribonucleotide (GAR) synthetase	phosphoribosylamine-glycine ligase
Sapur.001G012300.1	726.9998982	-0.661050277	0.100206061	-6.59691	4.20E-11	9.46E-11	black	-0.414718755	6.66E-08	GO:0005515,GO:0055114,GO:0046872,GO:0016702	AT3G45140.1	ATLOX2,LOX2	lipoxygenase 2	lipoxygenase
Sapur.010G186800.1	409.6473684	-0.341695386	0.052125382	-6.55526	5.55E-11	1.25E-10	black	-0.517970288	3.72E-12		AT3G52230.1			E24 ASN protein, putative
Sapur.007G078600.1	92.51686431	0.703658522	0.107761193	6.529795	6.59E-11	1.47E-10	black	0.44605207	4.78E-09	GO:0006468,GO:0004672,GO:0004674	AT5G58950.1		Protein kinase superfamily protein	tyrosine kinase family protein
Sapur.004G085300.1	28.3278125	0.482470886	0.074303069	6.493283	8.40E-11	1.87E-10	black	0.497864733	3.26E-11		AT1G67140.3	SWEETIE	HEAT repeat-containing protein	NA
Sapur.010G043400.1	1578.938116	-0.34962575	0.053940871	-6.48165	9.07E-11	2.02E-10	black	-0.514636763	5.39E-12	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G33450.1		Ribosomal L28 family	50S ribosomal protein L28

Sapur.012G098200.1	2665.219353	-0.339597179	0.052396168	-6.48134	9.09E-11	2.02E-10	black	-0.450711091	3.16E-09	GO:0006412,GO:0005840,GO:0003735	AT5G62300.2		Ribosomal protein S10p/S20e family protein	40S ribosomal protein S20
Sapur.018G044000.1	671.4274676	-0.186182707	0.02880293	-6.46402	1.02E-10	2.27E-10	black	-0.472825897	4.03E-10	GO:0006450	AT4G32915.1			aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C
Sapur.008G060800.1	1060.776238	-0.418980811	0.064851455	-6.46062	1.04E-10	2.32E-10	black	-0.514756435	5.32E-12	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G43460.1		Ribosomal L38e protein family	60S ribosomal protein L38
Sapur.003G044500.1	296.3469712	0.311223984	0.048215711	6.454825	1.08E-10	2.41E-10	black	0.485245818	1.19E-10	GO:0046872,GO:0030001,GO:0000166	AT5G44790.1	HMA7,RAN1	copper-exporting ATPase / responsive-to-antagonist 1 / copper-transporting ATPase (RAN1)	copper-transporting ATPase P-type protein, putative
Sapur.019G060600.1	2792.482809	-0.375397062	0.058175647	-6.45282	1.10E-10	2.44E-10	black	-0.489405144	7.81E-11	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G40510.1		Ribosomal protein S26e family protein	40S ribosomal protein S26
Sapur.004G137600.1	482.4016087	0.288964064	0.044797855	6.4504	1.12E-10	2.48E-10	black	0.455154645	2.11E-09	GO:0006468,GO:0005524,GO:0004672	AT4G35230.1	BSK1	BR-signaling kinase 1	kinase family protein
Sapur.009G040200.1	280.2980408	-0.234069835	0.036321448	-6.4444	1.16E-10	2.57E-10	black	-0.487514635	9.46E-11		AT3G20890.1		RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein, putative
Sapur.002G053700.1	637.7162081	-0.450350563	0.06999204	-6.43431	1.24E-10	2.75E-10	black	-0.484713103	1.25E-10		AT1G76860.1		Small nuclear ribonucleoprotein family protein	U6 snRNA-associated-like-Smprotein LsM3
Sapur.006G062500.1	62.9458512	-0.578470508	0.090185675	-6.41422	1.42E-10	3.13E-10	black	-0.469592546	5.50E-10		AT2G19080.1		metaxin-related	outer membrane import complex protein metaxin, putative
Sapur.002G171400.1	386.4575808	0.197909152	0.031041169	6.375699	1.82E-10	4.01E-10	black	0.444675852	5.40E-09		AT3G07790.1		DGCR14-related	nuclear protein Es2
Sapur.002G200400.1	461.1446193	-0.369014118	0.05793488	-6.36946	1.90E-10	4.17E-10	black	-0.523980109	1.89E-12	GO:0006886,GO:0005741	AT5G43970.1	ATTOM22-V.TOM22-V.TON	translocase of outer membrane 22-V	import receptor subunit Tom22
Sapur.019G074700.1	1088.972565	-0.265849934	0.04174677	-6.36816	1.91E-10	4.21E-10	black	-0.477598043	2.54E-10	GO:0005515,GO:0006414,GO:0003746	AT1G09640.1		Translation elongation factor EF1B, gamma chain	elongation factor 1-gamma 1
Sapur.016G265500.1	256.6633125	-0.449623235	0.07075389	-6.35475	2.09E-10	4.58E-10	black	-0.472857418	4.02E-10		AT4G27380.1			plant/M4I22-190 protein, putative
Sapur.008G041200.1	312.7989603	-0.399024254	0.062820853	-6.35178	2.13E-10	4.67E-10	black	-0.488546991	8.52E-11		AT3G12587.1		Oligosaccaryltransferase	dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 4B
Sapur.016G155600.1	790.8760906	-0.265238644	0.041930681	-6.32565	2.52E-10	5.51E-10	black	-0.474750761	3.35E-10	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G19740.1		Ribosomal protein L31e family protein	60S ribosomal protein L31
Sapur.004G102700.1	649.7485373	-0.288482649	0.045710289	-6.31111	2.77E-10	6.05E-10	black	-0.461625638	1.16E-09	GO:0051082,GO:0016272,GO:0006457	AT1G29990.1	PFD6	prefoldin 6	prefoldin subunit
Sapur.006G171700.1	2415.84733	-0.299418881	0.047548813	-6.29708	3.03E-10	6.61E-10	black	-0.451200246	3.02E-09	GO:0019843,GO:0005622,GO:0003723	AT5G39850.1		Ribosomal protein S4	NA
Sapur.013G007200.1	112.201717	-0.422736189	0.067204055	-6.29034	3.17E-10	6.90E-10	black	-0.496250813	3.86E-11		AT5G26800.1			IGR motif protein
Sapur.010G203300.1	94.91470387	-0.289852663	0.046228936	-6.26994	3.61E-10	7.85E-10	black	-0.427775932	2.30E-08	GO:0043565,GO:0008270,GO:0006355,GO:0003700,GO:0005515	AT1G51600.2	GATA28,TIFY2A,ZML2	ZIM-LIKE 2	GATA transcription factor
Sapur.005G016500.1	40.48442313	-0.534540345	0.085470564	-6.25409	4.00E-10	8.68E-10	black	-0.441045175	7.41E-09	GO:0004857				NA
Sapur.009G004000.1	35.29908205	-0.839773565	0.134495355	-6.24389	4.27E-10	9.25E-10	black	-0.427068295	2.43E-08					NA
Sapur.016G296200.1	423.5351247	-0.389531428	0.062443926	-6.2381	4.43E-10	9.60E-10	black	-0.500741648	2.41E-11	GO:0006351,GO:0003899,GO:0003677	AT5G41010.1	NRPB12,NRPD12,NRPE12	DNA directed RNA polymerase, 7 kDa subunit	DNA-directed RNA polymerase I, II
Sapur.001G105900.1	1799.622097	-0.14709757	0.02359845	-6.23336	4.57E-10	9.89E-10	black	-0.44966817	3.46E-09	GO:0005525	AT1G04170.1	EIF2 GAMMA	eukaryotic translation initiation factor 2 gamma subunit	eukaryotic translation initiation factor 2 gamma subunit
Sapur.007G076400.1	151.0172214	-0.379188788	0.061128323	-6.20316	5.53E-10	1.19E-09	black	-0.437968593	9.68E-09	GO:0005975,GO:0004134	AT5G64860.1	DPE1	disproportionating enzyme	4-alpha-glucanotransferase/amyloplastic protein
Sapur.008G121000.2	7.055871981	-0.901609445	0.145487769	-6.19715	5.75E-10	1.24E-09	black	-0.534331932	5.71E-13		AT5G19300.1			RNA methyltransferase, putative
Sapur.012G109500.1	1022.371667	-0.45618861	0.073762772	-6.18454	6.23E-10	1.34E-09	black	-0.466977453	7.05E-10	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G53740.4		Ribosomal protein L36e family protein	60S ribosomal protein L36
Sapur.001G139400.1	255.8875765	-0.224069751	0.036346543	-6.16482	7.06E-10	1.52E-09	black	-0.481333122	1.76E-10	GO:0005777	AT3G03490.1	AtPEX19-1,PEX19-1	peroxin 19-1	peroxisomal biogenesis factor
Sapur.008G050200.1	2778.015822	-0.299145463	0.048558972	-6.16046	7.25E-10	1.56E-09	black	-0.455738034	2.00E-09	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G74270.1		Ribosomal protein L35Ae family protein	60S ribosomal protein L35a
Sapur.010G042200.1	1726.522362	-0.339337234	0.055215477	-6.14569	7.96E-10	1.71E-09	black	-0.42857001	2.15E-08	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G27090.1		Ribosomal protein L14	60S ribosomal protein L14, putative
Sapur.014G116700.3	1.461053542	-1.542612759	0.252683033	-6.10493	1.03E-09	2.19E-09	black	-0.519350964	3.19E-12	GO:0008270,GO:0004553,GO:0015923,GO:0006013,GO:0005975,GO:0004559	AT5G13980.2		Glycosyl hydrolase family 38 protein	glycoside hydrolase family 38 protein
Sapur.016G258500.1	68.5675419	-0.70316829	0.115420298	-6.09224	1.11E-09	2.37E-09	black	-0.405426709	1.38E-07					hypothetical protein
Sapur.012G103200.1	68.20260234	-0.588971252	0.096704449	-6.09043	1.13E-09	2.40E-09	black	-0.447829257	4.08E-09		AT1G06010.1			transmembrane protein, putative
Sapur.009G039700.1	53.11097942	-0.549490438	0.090283483	-6.08628	1.16E-09	2.46E-09	black	-0.435987024	1.15E-08	GO:0055114,GO:0016491,GO:0051536,GO:0020037	AT5G04590.1	SIR	sulfite reductase	sulfite reductase [ferredoxin] protein
Sapur.15WG128800.1	1235.603107	-0.351228068	0.057848644	-6.0715	1.27E-09	2.69E-09	black	-0.460949725	1.24E-09	GO:0006412,GO:0005840,GO:0003735	AT2G47110.2	UBQ6	ubiquitin 6	NA
Sapur.001G046500.1	280.5749642	0.219650461	0.036240577	6.060899	1.35E-09	2.87E-09	black	0.462696856	1.05E-09		AT5G53150.1		DNAJ heat shock N-terminal domain-containing protein	chaperone protein DnaJ
Sapur.019G030800.1	557.0540148	-0.312885321	0.051641267	-6.05882	1.37E-09	2.91E-09	black	-0.470630092	4.98E-10	GO:0016491	AT3G06050.1	ATPRXIIF,PRXIIF	peroxiredoxin IIF	peroxiredoxin-2F protein
Sapur.006G129500.1	1071.449615	-0.359848195	0.05956859	-6.04091	1.53E-09	3.24E-09	black	-0.458123004	1.61E-09	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G43170.5	ARP1,emb2207,RP1,RPL3A	ribosomal protein 1	NA
Sapur.008G114400.1	1750.98908	-0.202317785	0.033569571	-6.02682	1.67E-09	3.54E-09	black	-0.458129588	1.61E-09	GO:0005515	AT2G46290.1		Transducin/WD40 repeat-like superfamily protein	eukaryotic translation initiation factor 3 subunit I
Sapur.016G120600.1	4045.900602	-0.198106775	0.032879659	-6.02521	1.69E-09	3.57E-09	black	-0.436106894	1.14E-08	GO:0006414,GO:0005853,GO:0003746	AT5G12110.1		Glutathione S-transferase, C-terminal-like;Translation elongation factor EF1B/ribosomal protein S6	elongation factor 1-beta
Sapur.006G181500.1	512.7042149	0.297944562	0.049546734	6.013405	1.82E-09	3.84E-09	black	0.433509894	1.42E-08		AT2G06040.1			Rad7, putative
Sapur.002G071700.1	1659.087886	0.298696591	0.049720299	6.007538	1.88E-09	3.97E-09	black	0.465893694	7.81E-10		AT1G77800.2		PHD finger family protein	PHD finger protein
Sapur.018G087900.1	1957.282155	0.315684333	0.052565847	6.005503	1.91E-09	4.02E-09	black	0.438433652	9.30E-09	GO:0008289	AT5G35180.2		Protein of unknown function (DUF1336)	plant/T25C13-60 protein
Sapur.002G046000.1	2633.39277	-0.348343817	0.058490354	-5.95558	2.59E-09	5.44E-09	black	-0.475791105	3.02E-10	GO:0006412,GO:0005840,GO:0003735	AT2G34480.1		Ribosomal protein L18ae/LX family protein	60S ribosomal protein L18a
Sapur.005G204100.2	12.25676176	-0.659883821	0.111130667	-5.93791	2.89E-09	6.05E-09	black	-0.138923563	0.082701575		AT1G76405.2			outer envelope pore protein 21B
Sapur.010G045300.1	6926.907436	-0.348847562	0.058948219	-5.91786	3.26E-09	6.82E-09	black	-0.497913137	3.25E-11	GO:0006412,GO:0005840,GO:0003735	AT3G04400.1	emb2171	Ribosomal protein L14p/L23e family protein	60S ribosomal protein L23
Sapur.006G074100.1	111.3272052	-0.296425826	0.050101404	-5.91652	3.29E-09	6.87E-09	black	-0.464383943	9.00E-10		AT3G53850.1		Uncharacterised protein family (UPF0497)	CASP-like protein Os09g0249400
Sapur.002G009200.1	198.1954108	-0.271903017	0.04609248	-5.89908	3.66E-09	7.63E-09	black	-0.46137701	1.19E-09		AT1G20430.1			transmembrane protein, putative
Sapur.018G037800.1	4279.529981	-0.227653557	0.038627232	-5.8936	3.78E-09	7.88E-09	black	-0.503346393	1.83E-11	GO:0003723	AT5G35530.1		Ribosomal protein S3 family protein	40S ribosomal protein S3
Sapur.005G115900.1	96.53741356	-0.568155008	0.096677139	-5.87683	4.18E-09	8.71E-09	black	-0.417086197	5.51E-08	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G10360.1	EMB3010,RPS6B	Ribosomal protein S6e	40S ribosomal protein S6
Sapur.012G012700.1	69.07660751	-0.32186856	0.055075615	-5.84412	5.09E-09	1.06E-08	black	-0.460945265	1.24E-09	GO:0008270,GO:0006351,GO:0003676	AT4G07950.1		DNA-directed RNA polymerase, subunit M, archaeal	DNA-directed RNA polymerase subunit
Sapur.006G198800.1	2562.470646	0.33733289	0.05777368	5.838868	5.26E-09	1.09E-08	black	0.428789709	2.11E-08		AT5G11560.1		catalytics	pqq-dh domain protein
Sapur.006G161300.1	229.4295711	-0.195075114	0.033500335	-5.82308	5.78E-09	1.20E-08	black	-0.414552494	6.75E-08	GO:0016592,GO:0006357,GO:0001104	AT5G03500.2		Mediator complex, subunit Med7	mediator of RNA polymerase II transcription subunit 7, putative
Sapur.016G188200.1	3087.21268	-0.300444073	0.051831565	-5.79655	6.77E-09	1.40E-08	black	-0.479865697	2.03E-10	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G10360.1	EMB3010,RPS6B	Ribosomal protein S6e	40S ribosomal protein S6
Sapur.010G050500.1	3414.895491	-0.334834063	0.057880827	-5.78489	7.26E-09	1.50E-08	black	-0.459806598	1.38E-09	GO:0006412,GO:0005840,GO:0003735,GO:0015934	AT1G67430.1		Ribosomal protein L22p/L17e family protein	60S ribosomal protein L17
Sapur.016G135200.1	58.29913952	-0.321028446	0.055732792	-5.76014	8.40E-09	1.73E-08	black	-0.457503311	1.70E-09		AT1G76440.2		HSP20-like chaperones superfamily protein	small heat shock protein
Sapur.007G066600.1	525.6175745	-0.202650556	0.035242289	-5.75021	8.91E-09	1.83E-08	black	-0.441377488	7.20E-09		AT5G23140.1	CLPP2,NCLPP7	nuclear-encoded CLP protease P7	ATP-dependent Clp protease proteolytic subunit
Sapur.001G113100.1	95.04592185	0.436756164	0.076004169	5.746476	9.11E-09	1.87E-08	black	0.459224075	1.45E-09					NA
Sapur.15WG076700.1	853.0278374	-0.402696651	0.070112553	-5.74357	9.27E-09	1.90E-08	black	-0.466163567	7.61E-10		AT5G08040.1	TOM5	mitochondrial import receptor subunit TOM5 homolog	import receptor subunit TOM5-like protein
Sapur.008G009300.1	789.8163773	0.213602936	0.037207597	5.740842	9.42E-09	1.93E-08	black	0.422185094	3.64E-08	GO:0006468,GO:0004672	AT5G04870.1	ATCPK1,CPK1	calcium dependent protein kinase 1	calcium/calmodulin-dependent kinase
Sapur.016G273300.1	82.14987859	-0.475768944	0.083390755	-5.7053	1.16E-08	2.37E-08	black	-0.444009439	5.72E-09	GO:0003676	AT5G54580.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif, a.k.a. RRM%2C RBD protein
Sapur.006G219900.1	1063.33668	-0.402703022	0.070716244	-5.69463	1.24E-08	2.52E-08	black	-0.426079889	2.64E-08		AT2G24940.1	AtMAPR2,MAPR2	membrane-associated progesterone binding protein 2	membrane steroid-binding protein
Sapur.006G035700.1	394.888149	0.28168395	0.049746853	5.662347	1.49E-08	3.04E-08	black	0.436968962	1.05E-08	GO:0005515	AT2G41520.1		Heat shock protein DnaJ with tetratricopeptide repeat	heat shock protein DnaJ with TPR protein, putative
Sapur.003G003400.1	35.89853179	0.455412444	0.080458471	5.660217	1.51E-08	3.07E-08	black	0.432683594	1.52E-08		AT4G24290.2		MAC/Perforin domain-containing protein	membrane-attack complex/perforin
Sapur.018G060200.2	5.348177525	0.826484431	0.146190512	5.653475	1.57E-08	3.19E-08	black	0.535690959	4.86E-13	GO:0055085,GO:0016021	AT1G67300.1		Major facilitator superfamily protein	plastidic glucose transporter, putative
Sapur.003G077800.1	325.1030305	0.764181616	0.135253684	5.649987	1.60E-08	3.26E-08	black	0.366579732	2.34E-06	GO:0004575,GO:0004564	AT1G12240.1	ATBETAFRUCT4,VAC-INV	Glycosyl hydrolases family 32 protein	acid vacuolar invertase
Sapur.009G117300.1	144.9349701	-0.464069576	0.08232789	-5.63685	1.73E-08	3.51E-08	black	-0.46561364	8.01E-10		AT2G27775.1			hypothetical protein
Sapur.013G018600.1	266.1402292	-0.244511829	0.043402659	-5.63357	1.77E-08	3.58E-08	black	-0.406720534	1.25E-07	GO:0005515,GO:0006508,GO:0004252	AT5G27660.1		Trypsin family protein with PDZ domain	trypsin-like serine protease
Sapur.012G024300.1	1120.225169	-0.323785804	0.057502674	-5.6308	1.79E-08	3.63E-08	black	-0.457750544	1.67E-09		AT1G17880.1	ATBTF3,BTF3	basic transcription factor 3	transcription factor-BTF3-like protein
Sapur.001G013000.1	652.8920731	0.218344583	0.039284072	5.558095	2.73E-08	5.49E-08	black	0.401293914	1.90E-07		AT1G73730.1	AtEIL3,ATSLIM,EIL3,SLIM1	ETHYLENE-INSENSITIVE3-like 3	ethylene insensitive (EIN3/EIL)-like transcription regulator
Sapur.019G054000.1	537.636053	-0.285823854	0.051634453	-5.53553	3.10E-08	6.23E-08	black	-0.460792039	1.26E-09		AT1G65290.1	mtACP2	mitochondrial acyl carrier protein 2	NA
Sapur.011G111000.1	336.2375355	-0.462575157	0.083906242	-5.513	3.53E-08	7.06E-08	black	-0.468514453	6.09E-10		AT1G61570.1	TIM13	translocase of the inner mitochondrial membrane 13	import inner membrane translocase subunit Tim13, putative
Sapur.006G039300.1	70.60046146	-0.424784605	0.077283769	-5.49643	3.88E-08	7.75E-08	black	-0.391999457	3.83E-07		AT2G41750.1		DTW domain-containing protein	DTW domain protein
Sapur.018G088000.1	646.0185168	-0.233076703	0.042447903	-5.49089	4.00E-08	7.99E-08	black	-0.388259447	5.05E-07	GO:0019843,GO:0006412,GO:0005840,GO:0003735	AT3G18760.1		Translation elongation factor EF1B/ribosomal protein S6 family protein	ribosomal protein S6
Sapur.001G091800.1	716.2546853	0.235283941	0.042966612	5.475971	4.35E-08	8.68E-08	black	0.419130592	4.67E-08		AT4G11860.1		Protein of unknown function (DUF544)	FAM63A protein
Sapur.009G006200.1	224.2944126	-0.367526083	0.067372918	-5.4551	4.89E-08	9.75E-08	black	-0.430549594	1.82E-08		AT4G27490.1		3\'-5\'-exoribonuclease family protein	exosome complex exonuclease
Sapur.014G119400.1	1512.771457	-0.154961454	0.028616688	-5.41507	6.13E-08	1.21E-07	black	-0.400266459	2.06E-07	GO:0005515,GO:0005852,GO:0005737,GO:0003743	AT1G10840.1	TIF3H1	translation initiation factor 3 subunit H1	eukaryotic translation initiation factor 3 subunit H
Sapur.006G199600.2	13.73287606	-0.571228176	0.105543757	-5.41224	6.22E-08	1.23E-07	black	-0.445179843	5.16E-09	GO:0005852,GO:0005737,GO:0003743	AT5G25757.1		RNA polymerase I-associated factor PAF67	eukaryotic translation initiation factor 3 subunit L
Sapur.008G094800.1	954.5021958	0.223157636	0.041257911	5.408845	6.34E-08	1.26E-07	black	0.414200866	6.94E-08		AT1G25540.1	PFT1	phytochrome and flowering time regulatory protein (PFT1)	mediator complex subunit 25 von willebrand factor type A protein
Sapur.016G287500.1	2212.517034	0.310015887	0.057404566	5.400544	6.64E-08	1.31E-07	black	0.425200117	2.84E-08		AT2G35630.1	GEM1,MOR1	ARM repeat superfamily protein	microtubule organization protein
Sapur.014G083300.1	865.5395623	0.287594586	0.053470192	5.378596	7.51E-08	1.48E-07	black	0.407665093	1.16E-07	GO:0016192,GO:0006886	AT4G00800.1		transducin family protein / WD-40 repeat family protein	transducin family protein/WD-40 repeat protein
Sapur.012G085600.1	3060.973881	-0.278131679	0.051792851	-5.37008	7.87E-08	1.55E-07	black	-0.462496098	1.07E-09	GO:0006412,GO:0005840,GO:0003735	AT2G47110.2	UBQ6	ubiquitin 6	ubiquitin-40S ribosomal protein S27a
Sapur.005G017200.1	694.6985863	-0.437087692	0.081510076	-5.36238	8.21E-08	1.62E-07	black	-0.552062228	6.65E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G05590.1	RPL18	ribosomal protein L18	60S ribosomal protein L18
Sapur.010G144600.1	1247.646719	-0.174157469	0.032570944	-5.34702	8.94E-08	1.76E-07	black	-0.391953262	3.84E-07	GO:0003676,GO:0005850,GO:0003743,GO:0003723	AT2G40290.1		Eukaryotic translation initiation factor 2 subunit 1	eukaryotic translation initiation factor 2 alpha subunit
Sapur.003G124800.1	1038.078159	-0.217613867	0.040886716	-5.32236	1.02E-07	2.01E-07	black	-0.387072752	5.50E-07	GO:0006457,GO:0003755,GO:0000413	AT5G13120.1	ATCYP20-2,CYP20-2	cyclophilin 20-2	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.014G017300.1	806.1194029	-0.247650192	0.046736368	-5.29888	1.17E-07	2.28E-07	black	-0.385762457	6.05E-07		AT1G45230.1		Protein of unknown function (DUF3223)	DCL protein
Sapur.016G163600.1	1567.749924	-0.205263507	0.039231834	-5.23207	1.68E-07	3.26E-07	black	-0.411362945	8.70E-08	GO:0046907	AT2G30060.1		Pleckstrin homology (PH) domain superfamily protein	Ran-binding protein 2, Ran-binding domain protein
Sapur.013G081200.1	503.161399	-0.196950736	0.037711886	-5.22251	1.77E-07	3.43E-07	black	-0.383135453	7.32E-07		AT2G40600.1		appr-1-p processing enzyme family protein	appr-1-P processing enzyme family protein
Sapur.012G064100.1	1436.075008	-0.312604851	0.060009359	-5.20927	1.90E-07	3.68E-07	black	-0.422800764	3.46E-08	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G29390.1		Ribosomal protein S30 family protein	40S ribosomal protein S30
Sapur.001G173100.1	1054.797357	-0.416602839	0.080046888	-5.20449	1.95E-07	3.78E-07	black	-0.381029053	8.52E-07	GO:0005515	AT2G30860.1	ATGSTF7.ATGSTF9.GLUTTR.	glutathione S-transferase PHI 9	glutathione S-transferase
Sapur.005G152800.1	1285.501265	-0.334720194	0.064468066	-5.19203	2.08E-07	4.03E-07	black	-0.422262347	3.62E-08	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G43170.2	ARP1,emb2207,RP1,RPL3A	ribosomal protein 1	60S ribosomal protein L3
Sapur.009G066200.1	1928.186245	0.296930737	0.05753185	5.161154	2.45E-07	4.74E-07	black	0.410109019	9.60E-08	GO:0005515,GO:0008144,GO:0016773	AT1G50030.1	TOR	target of rapamycin	Serine/Threonine-kinase TOR
Sapur.019G018300.1	144.3056415	0.330202434	0.064070734	5.153717	2.55E-07	4.93E-07	black	0.427061676	2.44E-08	GO:0005515,GO:0006468,GO:0004672	AT3G14840.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.004G161900.1	87.33276837	-0.280438413	0.054499614	-5.1457	2.67E-07	5.14E-07	black	-0.388736495	4.87E-07	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G45020.1		Ribosomal L18p/L5e family protein	ribosomal protein L18
Sapur.016G130700.3	96.27871932	0.400971766	0.078105204	5.133739	2.84E-07	5.47E-07	black	0.410396047	9.39E-08		AT3G46450.2		SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	SEC14 cytosolic factor
Sapur.010G127900.1	523.8761169	-0.229765723	0.044758819	-5.13342	2.85E-07	5.48E-07	black	-0.394703508	3.13E-07		AT1G26750.1			hypothetical protein
Sapur.019G095500.1	740.1856047	-0.293109516	0.057255987	-5.11928	3.07E-07	5.90E-07	black	-0.390570214	4.26E-07	GO:0009231,GO:0004746	AT2G20690.1		lumazine-binding family protein	NA
Sapur.009G043900.1	1149.185085	-0.203864673	0.039863396	-5.11408	3.15E-07	6.05E-07	black	-0.434715798	1.28E-08	GO:0050662,GO:0003824	AT5G19440.1		NAD(P)-binding Rossmann-fold superfamily protein	cinnamyl-alcohol dehydrogenase-like protein
Sapur.014G040400.1	5559.872057	-0.244788276	0.047954464	-5.1046	3.31E-07	6.36E-07	black	-0.429381465	2.01E-08	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G23740.1	RPS11-BETA	ribosomal protein S11-beta	40S ribosomal protein S11
Sapur.005G166900.1	3564.011189	-0.261710152	0.051323628	-5.09921	3.41E-07	6.54E-07	black	-0.411119314	8.87E-08	GO:0006412,GO:0005840,GO:0005622,GO:0003735,GO:0003723	AT1G22780.1	PFL,PFL1,RPS18A	Ribosomal protein S13/S18 family	40S ribosomal protein S18
Sapur.005G034300.1	504.8451454	-0.579202519	0.113706511	-5.09384	3.51E-07	6.72E-07	black	-0.370545362	1.78E-06					hypothetical protein
Sapur.009G128200.1	647.5318287	-0.293956898	0.057752371	-5.08995	3.58E-07	6.86E-07	black	-0.400164973	2.07E-07	GO:0051536,GO:0009055	AT2G27510.1	ATFD3,FD3	ferredoxin 3	ferredoxin-3 protein
Sapur.005G164100.1	199.6018877	-0.334811425	0.066468132	-5.03717	4.72E-07	8.99E-07	black	-0.367929347	2.13E-06		AT3G52420.1	ATOEP7,OEP7	outer envelope membrane protein 7	transmembrane protein, putative
Sapur.016G210200.1	397.3928431	-0.261849147	0.05200709	-5.03487	4.78E-07	9.10E-07	black	-0.403171366	1.65E-07		AT5G14290.1		Mitochondrial ribosomal protein L37	ribosomal protein L37
Sapur.011G078500.1	648.425842	-0.208856011	0.041501736	-5.03246	4.84E-07	9.21E-07	black	-0.423431818	3.29E-08		AT2G33845.1		Nucleic acid-binding, OB-fold-like protein	OB fold SoSSB-OBF: A subfamily protein, putative
Sapur.016G215900.1	3312.28234	-0.303047504	0.060378177	-5.01916	5.19E-07	9.86E-07	black	-0.437454786	1.01E-08	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G15000.1		Ribosomal L27e protein family	60S ribosomal protein L27
Sapur.005G017300.1	640.0846187	-0.213297545	0.042585095	-5.00874	5.48E-07	1.04E-06	black	-0.439144074	8.74E-09	GO:0003723	AT1G09150.1		pseudouridine synthase and archaeosine transglycosylase (PUA) domain-containing protein	pseudouridine synthase and archaeosine transglycosylase domain protein
Sapur.011G109600.1	4353.46448	-0.280138104	0.056147185	-4.98935	6.06E-07	1.15E-06	black	-0.438946119	8.89E-09	GO:0019843,GO:0006412,GO:0005840,GO:0003735	AT1G33140.1	PGY2	Ribosomal protein L6 family	60S ribosomal protein L9
Sapur.006G222800.1	83.67841555	0.383471435	0.077464828	4.950265	7.41E-07	1.40E-06	black	0.410076115	9.63E-08		AT1G62930.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.006G170400.1	197.0258649	-0.199202265	0.040405152	-4.93012	8.22E-07	1.55E-06	black	-0.362212923	3.14E-06	GO:0003676	AT5G06210.1		RNA binding (RRM/RBD/RNP motifs) family protein	RNA-binding protein 42 (RBM42)-like RNA recognition motif protein
Sapur.016G124100.2	5.076950714	-0.59490484	0.120769336	-4.92596	8.39E-07	1.58E-06	black	-0.365902064	2.45E-06					LIN37 protein
Sapur.009G115800.1	1977.42857	-0.39848056	0.081059984	-4.91587	8.84E-07	1.66E-06	black	-0.358880927	3.92E-06		AT3G44590.1		60S acidic ribosomal protein family	60S acidic ribosomal protein P2
Sapur.005G161800.1	110.2399083	-0.256611587	0.052223428	-4.91373	8.94E-07	1.68E-06	black	-0.383841545	6.96E-07		AT4G39235.1			NA
Sapur.008G013600.1	573.8847785	-0.394620169	0.080474958	-4.90364	9.41E-07	1.77E-06	black	-0.370083952	1.84E-06	GO:0006526,GO:0005524,GO:0004055	AT4G24830.1		arginosuccinate synthase family	argininosuccinate synthase
Sapur.006G057100.1	396.7462967	-0.220922928	0.045131906	-4.89505	9.83E-07	1.84E-06	black	-0.396044008	2.83E-07		AT5G40080.1		Mitochondrial ribosomal protein L27	ribosomal protein L27
Sapur.007G023700.2	1.863749474	-1.042971384	0.213172529	-4.89262	9.95E-07	1.87E-06	black	-0.567533569	9.16E-15		AT5G66770.1		GRAS family transcription factor	GRAS family transcription factor
Sapur.013G028300.1	2030.498227	-0.290674543	0.05999437	-4.84503	1.27E-06	2.36E-06	black	-0.400504053	2.02E-07		AT4G25740.1		RNA binding Plectin/S10 domain-containing protein	plectin/S10 domain protein
Sapur.013G014100.1	808.0851583	-0.321585204	0.066725704	-4.81951	1.44E-06	2.67E-06	black	-0.394316532	3.22E-07	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G05560.2		Ribosomal L22e protein family	60S ribosomal protein L22, putative
Sapur.019G070900.3	78.1979157	0.349905647	0.072973238	4.794986	1.63E-06	3.02E-06	black	0.40267291	1.71E-07		AT1G33780.1		Protein of unknown function (DUF179)	electron transporter, putative
Sapur.016G225900.1	3423.538544	-0.290653324	0.060924271	-4.77073	1.84E-06	3.40E-06	black	-0.408957887	1.05E-07	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G18100.1		Ribosomal protein L32e	60S ribosomal protein L32, putative
Sapur.T187400.1	55.20419024	0.23008632	0.04843759	4.75016	2.03E-06	3.75E-06	black	0.364709493	2.65E-06		AT1G59650.1	CW14	Protein of unknown function (DUF1336)	NA
Sapur.013G093700.1	110.8949189	-0.285435347	0.060213257	-4.74041	2.13E-06	3.93E-06	black	-0.369090649	1.97E-06		AT1G14060.1		GCK domain-containing protein	GCK domain protein
Sapur.004G170900.1	1206.988767	-0.157865101	0.033553189	-4.70492	2.54E-06	4.67E-06	black	-0.37198883	1.61E-06	GO:0016020	AT2G38550.1		Transmembrane proteins 14C	non-green plastid inner envelope membrane protein, putative
Sapur.009G086700.1	421.3007552	-0.300904692	0.063995644	-4.70196	2.58E-06	4.73E-06	black	-0.410689141	9.17E-08		AT1G49410.1	TOM6	translocase of the outer mitochondrial membrane 6	import receptor subunit TOM6-like protein
Sapur.005G187800.1	1032.110466	0.249461545	0.053255886	4.684206	2.81E-06	5.15E-06	black	0.338830101	1.42E-05		AT1G05150.1		Calcium-binding tetratricopeptide family protein	calcium-binding EF hand protein
Sapur.011G124900.1	661.8044255	0.218068188	0.047071194	4.632731	3.61E-06	6.58E-06	black	0.362344175	3.11E-06		AT5G56240.1			hypothetical protein
Sapur.006G065300.1	570.5505168	-0.215018736	0.04664011	-4.61017	4.02E-06	7.32E-06	black	-0.417066236	5.52E-08	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G18880.1		Nucleic acid-binding, OB-fold-like protein	30S ribosomal protein S17
Sapur.009G046900.1	123.1994402	-0.297480791	0.065006856	-4.57614	4.74E-06	8.59E-06	black	-0.332132753	2.14E-05					NA
Sapur.010G198600.1	2022.977001	-0.31620099	0.069169949	-4.57136	4.85E-06	8.78E-06	black	-0.385562596	6.14E-07	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G03850.1		Nucleic acid-binding, OB-fold-like protein	40S ribosomal protein S28
Sapur.15WG072700.1	244.986318	-0.286264684	0.062693627	-4.56609	4.97E-06	9.00E-06	black	-0.357459856	4.31E-06	GO:0003676	AT5G61030.1	GR-RBP3	glycine-rich RNA-binding protein 3	RNA recognition motif 2 in RNA-binding protein 28 (RBM28)-like protein
Sapur.003G077800.2	131.8291941	0.428545497	0.093968222	4.560536	5.10E-06	9.23E-06	black	0.356404865	4.62E-06		AT1G12240.1	ATBETAFRUCT4,VAC-INV	Glycosyl hydrolases family 32 protein	acid vacuolar invertase
Sapur.006G171600.1	2109.307271	-0.258441776	0.05718287	-4.51957	6.20E-06	1.12E-05	black	-0.390139935	4.40E-07	GO:0019843,GO:0005622,GO:0003723	AT5G39850.1		Ribosomal protein S4	NA
Sapur.005G195300.1	49.27851423	-0.438578539	0.097698169	-4.48912	7.15E-06	1.28E-05	black	-0.310624211	7.51E-05					NA
Sapur.011G104000.1	91.74854239	-0.319735278	0.071353723	-4.48099	7.43E-06	1.33E-05	black	-0.349635574	7.18E-06		AT3G18510.1			transmembrane protein, putative
Sapur.008G161900.1	70.80595973	-0.291540373	0.065277599	-4.46616	7.96E-06	1.43E-05	black	-0.313651417	6.33E-05		AT4G15820.1			hypothetical protein
Sapur.005G037700.1	1016.778246	0.16257746	0.036463942	4.458582	8.25E-06	1.48E-05	black	0.368832762	2.00E-06	GO:0008270,GO:0003676,GO:0004527	AT1G54490.1	AIN1,ATXRN4,EIN5,XRN4	exoribonuclease 4	5'-3' exoribonuclease
Sapur.014G114300.3	5.324368353	0.537159934	0.120692093	4.450664	8.56E-06	1.53E-05	black	0.377069679	1.13E-06	GO:0008152,GO:0003824	AT5G36880.2	ACS	acetyl-CoA synthetase	acetyl-CoA synthetase
Sapur.016G059100.1	765.3055341	-0.231044451	0.052030957	-4.44052	8.97E-06	1.60E-05	black	-0.327391099	2.85E-05	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G64140.1	RPS28	ribosomal protein S28	40S ribosomal protein S28
Sapur.005G021000.1	22.60449272	-0.509545492	0.115058179	-4.42859	9.49E-06	1.69E-05	black	-0.318054685	4.92E-05					hypothetical protein
Sapur.003G020300.2	83.39726742	-0.35088029	0.079692111	-4.40295	1.07E-05	1.90E-05	black	-0.320537448	4.26E-05	GO:0005515,GO:0042393,GO:0006355	AT2G02470.1	AL6	alfin-like 6	PHD finger ALFIN-like protein
Sapur.006G102000.1	820.0715931	-0.137132849	0.031498465	-4.35364	1.34E-05	2.37E-05	black	-0.364168183	2.75E-06		AT2G43630.1			transmembrane protein, putative
Sapur.006G207300.2	228.1655277	-0.367666389	0.084930434	-4.32903	1.50E-05	2.64E-05	black	-0.325079501	3.27E-05	GO:0005525	AT5G55190.1	ATRAN3,RAN3	RAN GTPase 3	GTP-binding nuclear protein Ran/TC4 protein
Sapur.010G133200.1	1180.096377	0.216292411	0.050873364	4.251585	2.12E-05	3.71E-05	black	0.355396497	4.93E-06	GO:0005524,GO:0003676,GO:0004386	AT5G13010.1	EMB3011	RNA helicase family protein	ATP-dependent RNA helicase, putative
Sapur.T063700.1	1352.387346	-0.411955754	0.097954226	-4.20559	2.60E-05	4.53E-05	black	-0.37952062	9.48E-07	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G59540.1		Ribosomal L38e protein family	60S ribosomal protein L38
Sapur.018G096900.1	53.41108505	-0.380036689	0.091208336	-4.16669	3.09E-05	5.35E-05	black	-0.314923229	5.89E-05					NA
Sapur.013G091200.1	3867.499798	-0.261202117	0.062699072	-4.16596	3.10E-05	5.37E-05	black	-0.376217113	1.20E-06	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G40590.1		Ribosomal protein S26e family protein	40S ribosomal protein S26
Sapur.016G293100.1	4884.374491	-0.266762171	0.064191887	-4.1557	3.24E-05	5.61E-05	black	-0.367311227	2.22E-06	GO:0019843,GO:0006412,GO:0005840,GO:0003735	AT4G10450.1		Ribosomal protein L6 family	60S ribosomal protein L9
Sapur.002G053100.2	3.563601973	-0.644560944	0.155130669	-4.15495	3.25E-05	5.63E-05	black	-0.483133612	1.47E-10					hypothetical protein
Sapur.019G060700.1	98.45564379	-0.293812614	0.070769243	-4.1517	3.30E-05	5.71E-05	black	-0.30205035	0.000120734	GO:0005737,GO:0003879,GO:0000287,GO:0000105	AT1G09795.1	ATATP-PRT2.ATP-PRT2.HISN	ATP phosphoribosyl transferase 2	ATP phosphoribosyltransferase
Sapur.15WG023200.1	3280.170523	-0.18274419	0.044397005	-4.11614	3.85E-05	6.63E-05	black	-0.316828791	5.28E-05	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G16780.1		Ribosomal protein L19e family protein	ribosomal protein L19
Sapur.016G292600.1	3055.671111	-0.234786775	0.057491714	-4.08384	4.43E-05	7.60E-05	black	-0.340122485	1.31E-05	GO:0019843,GO:0006412,GO:0005840,GO:0003735	AT1G33140.1	PGY2	Ribosomal protein L6 family	60S ribosomal protein L9
Sapur.016G222000.1	233.7630448	-0.214785237	0.052681132	-4.07708	4.56E-05	7.82E-05	black	-0.320759391	4.21E-05		AT5G14710.1			proteasome assembly chaperone 3-domain protein
Sapur.016G182700.1	1897.15829	-0.267474131	0.06576347	-4.06721	4.76E-05	8.15E-05	black	-0.353422774	5.62E-06	GO:0006412,GO:0005840,GO:0003735	AT5G18380.1		Ribosomal protein S5 domain 2-like superfamily protein	40S ribosomal protein S16
Sapur.005G001900.1	44.64956145	-0.253795783	0.062914037	-4.03401	5.48E-05	9.36E-05	black	-0.304064956	0.000108144					NA
Sapur.019G102900.1	239.0196708	-0.423895897	0.105293069	-4.02587	5.68E-05	9.68E-05	black	-0.279505028	0.000392426		AT4G28240.1		Wound-responsive family protein	DUF3774 domain protein
Sapur.005G194300.1	386.7249127	-0.215869293	0.05373937	-4.01697	5.90E-05	0.000100452	black	-0.350837261	6.64E-06	GO:0005515	AT5G42150.1		Glutathione S-transferase family protein	prostaglandin E synthase
Sapur.016G155500.1	1299.887673	-0.126957402	0.031780634	-3.9948	6.47E-05	0.00011005	black	-0.332979219	2.03E-05		AT2G03870.2		Small nuclear ribonucleoprotein family protein	U6 snRNA-associated-like-Smprotein LSm7
Sapur.016G161900.1	224.4053412	-0.22295844	0.056036785	-3.97879	6.93E-05	0.000117485	black	-0.333714873	1.95E-05		AT3G07910.1			reactive oxygen species modulator 1
Sapur.012G067500.1	144.4794843	-0.223536233	0.056715731	-3.94134	8.10E-05	0.000136846	black	-0.32179214	3.96E-05		AT5G63150.1			DUF1713 domain protein
Sapur.001G046400.2	149.5538752	0.299706402	0.076483817	3.91856	8.91E-05	0.000150027	black	0.330635947	2.34E-05	GO:0005515	AT1G27340.1		Galactose oxidase/kelch repeat superfamily protein	F-box only protein
Sapur.011G113600.1	1179.34922	0.274683256	0.071241458	3.855666	0.000115415	0.000193307	black	0.325026884	3.28E-05		AT2G35630.1	GEM1,MOR1	ARM repeat superfamily protein	microtubule organization protein
Sapur.013G087900.1	637.6322089	-0.115370741	0.030282272	-3.80984	0.000139054	0.000231785	black	-0.327146701	2.89E-05	GO:0005515	AT5G36230.1		ARM repeat superfamily protein	translation initiation factor
Sapur.006G108300.1	1492.846839	-0.252453431	0.066615953	-3.78968	0.000150839	0.000250847	black	-0.334097691	1.90E-05	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G02960.1		Ribosomal protein S12/S23 family protein	NA
Sapur.013G102800.1	421.1980226	-0.179551685	0.048082499	-3.73424	0.000188281	0.000311174	black	-0.299257944	0.00014046	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G20230.1		Ribosomal L18p/L5e family protein	50S ribosomal protein L18
Sapur.011G062000.3	0.87166412	-1.093824064	0.293970284	-3.72087	0.000198541	0.000327604	black	-0.435216849	1.23E-08	GO:0016021	AT1G78620.1		Protein of unknown function DUF92, transmembrane	integral membrane family protein
Sapur.15WG134700.1	360.2346426	-0.154262614	0.041524527	-3.71498	0.000203223	0.000335031	black	-0.294014849	0.000185852		AT1G31160.1	HINT 2	HISTIDINE TRIAD NUCLEOTIDE-BINDING 2	histidine triad nucleotide-binding protein
Sapur.004G140000.1	1435.706036	-0.31424038	0.084842139	-3.70382	0.000212373	0.000349541	black	-0.268261982	0.000681451		AT3G44590.1		60S acidic ribosomal protein family	60S acidic ribosomal protein P2
Sapur.001G097900.2	177.3329275	-0.311680381	0.084177915	-3.70264	0.000213369	0.000351145	black	-0.297072073	0.000157957		AT1G62780.1			subtilisin-like protease, putative
Sapur.003G028000.1	136.0574721	-0.170944038	0.046397714	-3.68432	0.000229314	0.000376524	black	-0.34196427	1.17E-05		AT1G15230.1			hypothetical protein
Sapur.005G073200.1	1632.613047	-0.157106571	0.043104809	-3.64476	0.000267644	0.000437225	black	-0.347871183	8.04E-06	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G14320.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L44
Sapur.010G016800.1	320.8673245	-0.196873555	0.054032364	-3.64362	0.000268827	0.000439071	black	-0.312725054	6.67E-05	GO:0006412,GO:0005840,GO:0003735	AT5G46160.1		Ribosomal protein L14p/L23e family protein	50S ribosomal protein L14
Sapur.007G121200.1	1582.391348	-0.222737989	0.061781409	-3.60526	0.000311842	0.000507347	black	-0.311926125	6.98E-05	GO:0016020	AT1G03860.3	ATPHB2,PHB2	prohibitin 2	prohibitin, putative
Sapur.003G153300.1	185.0154303	-0.187051642	0.052866259	-3.5382	0.000402858	0.000650814	black	-0.349042694	7.45E-06		AT3G07910.1			reactive oxygen species modulator 1
Sapur.002G180600.2	231.9419935	-0.293673944	0.083971569	-3.4973	0.000469989	0.000756287	black	-0.286058926	0.000281385	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G29390.1		Ribosomal protein S30 family protein	40S ribosomal protein S30
Sapur.013G010000.2	2.148357951	-0.693378056	0.199371857	-3.47781	0.000505522	0.000811712	black	-0.469991676	5.29E-10	GO:0003723,GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G07090.1		Ribosomal protein S4 (RPS4A) family protein	40S ribosomal protein S4
Sapur.008G054600.1	495.4385829	-0.166658178	0.048030755	-3.46982	0.000520803	0.000835477	black	-0.27538272	0.000481748	GO:0005515,GO:0042393,GO:0006355	AT5G05610.1	AL1	alfin-like 1	PHD finger protein
Sapur.002G033100.1	3321.135306	-0.197199087	0.0571516	-3.45046	0.00055964	0.000895955	black	-0.33518524	1.78E-05	GO:0006412,GO:0005840,GO:0003735	AT5G09500.1		Ribosomal protein S19 family protein	40S ribosomal protein S15
Sapur.005G073300.3	6.681804363	-0.440084354	0.128112565	-3.43514	0.000592252	0.00094647	black	-0.289015628	0.000241531		AT5G23140.1	CLPP2,NCLPP7	nuclear-encoded CLP protease P7	ATP-dependent Clp protease proteolytic subunit
Sapur.006G062900.1	940.82912	-0.177648415	0.051715714	-3.4351	0.000592345	0.000946573	black	-0.314291406	6.11E-05	GO:0030150,GO:0005742	AT5G41685.1		Mitochondrial outer membrane translocase complex, subunit Tom7	import receptor subunit TOM7-1
Sapur.009G070500.1	958.98861	-0.241241501	0.070743222	-3.4101	0.000649389	0.001035329	black	-0.28301864	0.000328664	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G44010.1		Ribosomal protein S14p/S29e family protein	40S ribosomal protein S29
Sapur.016G193300.1	458.6533759	-0.126343114	0.038257612	-3.30243	0.000958507	0.001508885	black	-0.254238188	0.001313092		AT5G49210.1			plant/K21P3-8 protein, putative
Sapur.014G101900.1	780.2870881	-0.214203808	0.06496683	-3.29713	0.000976798	0.001536507	black	-0.320457433	4.28E-05	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G05590.1	RPL18	ribosomal protein L18	60S ribosomal protein L18
Sapur.010G015000.1	586.3661979	-0.220645993	0.067795592	-3.25458	0.001135613	0.001778711	black	-0.31425224	6.12E-05	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G06320.1		Ribosomal protein L33 family protein	50S ribosomal protein L33
Sapur.019G063100.1	297.0423243	-0.125190201	0.039303346	-3.18523	0.00144639	0.00224929	black	-0.239898462	0.002476344	GO:0006413,GO:0003743,GO:0003723	AT2G40780.1		Nucleic acid-binding, OB-fold-like protein	RNA-binding protein EIF1AD, putative
Sapur.008G005600.1	73.07556546	-0.207322957	0.065322633	-3.17383	0.001504416	0.00233645	black	-0.268414827	0.000676463		AT1G10865.1			cytochrome C oxidase assembly protein
Sapur.016G178800.1	196.0245535	-0.202190817	0.065098791	-3.10591	0.001896961	0.002924537	black	-0.257841509	0.001113203		AT2G15000.2			hypothetical protein
Sapur.002G096700.1	327.2920333	-0.206348858	0.066901711	-3.08436	0.002039916	0.003139662	black	-0.263778944	0.000843686	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G43980.1		Ribosomal protein S14p/S29e family protein	40S ribosomal protein S29
Sapur.005G056600.1	39.85211671	-0.281249026	0.091649904	-3.06873	0.002149691	0.003303544	black	-0.229250329	0.003875644		AT5G10320.1			hypothetical protein
Sapur.018G018500.1	797.0930406	-0.2309757	0.075610546	-3.05481	0.002252047	0.003456985	black	-0.245239187	0.001963505	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G31985.1		Ribosomal protein L39 family protein	NA
Sapur.002G200700.1	474.3284781	-0.235774762	0.077443973	-3.04446	0.002331016	0.003573562	black	-0.230952033	0.003612617	GO:0006412,GO:0005840,GO:0003735	AT3G04400.1	emb2171	Ribosomal protein L14p/L23e family protein	60S ribosomal protein L23
Sapur.010G140800.1	1305.846771	-0.208564938	0.068532636	-3.04329	0.002340039	0.003586895	black	-0.308780909	8.33E-05	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G43460.1		Ribosomal L38e protein family	60S ribosomal protein L38
Sapur.014G009000.1	1042.229461	-0.202799593	0.0677136	-2.99496	0.002744799	0.004185986	black	-0.323341598	3.62E-05	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G44010.1		Ribosomal protein S14p/S29e family protein	NA
Sapur.005G193000.1	227.8980688	-0.161183763	0.054736198	-2.94474	0.003232283	0.00490028	black	-0.2326378	0.003368016		AT4G24175.1			kinesin heavy chain isolog protein, putative
Sapur.003G040600.1	2901.037537	-0.13489511	0.04656587	-2.89687	0.003769101	0.005681825	black	-0.257376722	0.001137319	GO:0006412,GO:0005840,GO:0005622,GO:0003735,GO:0015935	AT3G04770.2	RPSAb	40s ribosomal protein SA B	40S ribosomal protein Sa protein
Sapur.003G025100.1	970.9311942	-0.201242379	0.07010738	-2.87049	0.00409839	0.006162491	black	-0.265625432	0.000772989	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G16080.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L37, putative
Sapur.010G091000.2	1.087972304	-0.757139304	0.267736998	-2.82792	0.004685124	0.007014431	black	-0.721354354	1.65E-26	GO:0005515	AT1G49540.1	ELP2	elongator protein 2	elongator complex protein
Sapur.013G019700.1	1.813359113	-0.685117195	0.245429711	-2.7915	0.005246425	0.007815525	black	-0.250440808	0.001558797					hypothetical protein
Sapur.003G088200.1	2863.64318	-0.15008633	0.053946586	-2.78213	0.005400367	0.008034716	black	-0.230026829	0.003753557		AT2G36620.1	RPL24A	ribosomal protein L24	60S ribosomal protein L24
Sapur.009G007300.1	233.4083166	-0.105473717	0.037957864	-2.77871	0.005457601	0.008115124	black	-0.256271275	0.00119661		AT2G28370.1		Uncharacterised protein family (UPF0497)	CASP-like plant protein
Sapur.016G279900.1	820.3664279	-0.117191331	0.043332359	-2.70448	0.006841219	0.010082727	black	-0.303650961	0.000110626	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G34520.1	RPS14	mitochondrial ribosomal protein S14	ribosomal protein S14
Sapur.006G072900.1	6035.090348	-0.127096839	0.047191175	-2.69323	0.007076276	0.010418945	black	-0.261690129	0.00093079		AT1G70600.1		Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L27a
Sapur.003G019200.2	2307.402496	-0.211051883	0.081364039	-2.59392	0.009488831	0.013807021	black	-0.22974092	0.003798102	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G19730.3		Ribosomal L28e protein family	60S ribosomal protein L28
Sapur.005G168900.1	169.3716605	0.182433687	0.070651883	2.582149	0.009818719	0.014268831	black	0.237021457	0.002800316		AT1G03080.1		kinase interacting (KIP1-like) family protein	kinase interacting-like protein
Sapur.017G000900.1	2219.211415	-0.091858314	0.035974081	-2.55346	0.010665905	0.015452457	black	-0.247185344	0.00180206	GO:0009349,GO:0009231	AT2G44050.1	COS1	6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase	6%2C7-dimethyl-8-ribityllumazine synthase
Sapur.005G051400.2	6.709616303	-0.283258182	0.114574512	-2.47226	0.013426118	0.019247341	black	-0.444324996	5.56E-09	GO:0006355,GO:0003713,GO:0003677	AT5G09250.1	KIWI	ssDNA-binding transcriptional regulator	RNA polymerase II transcriptional coactivator KIWI protein, putative
Sapur.005G039500.1	649.8622297	-0.111583382	0.047057929	-2.37119	0.01773082	0.025101839	black	-0.167751699	0.035726095	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G34670.1		Ribosomal protein S3Ae	40S ribosomal protein S3a
Sapur.006G031100.1	302.0997937	-0.085365168	0.036108014	-2.36416	0.018070943	0.02556038	black	-0.223801817	0.004837638	GO:0055114,GO:0006561,GO:0004735	AT5G14800.1	AT-P5C1,AT-P5R,EMB2772,I	pyrroline-5- carboxylate (P5C) reductase	pyrroline-5-carboxylate reductase
Sapur.004G112200.1	535.0583448	-0.139166089	0.060375735	-2.305	0.021166556	0.029764569	black	-0.263632845	0.000849526		AT1G49410.1	TOM6	translocase of the outer mitochondrial membrane 6	import receptor subunit TOM6-like protein
Sapur.017G114400.1	164.2004753	-0.205102837	0.092625092	-2.21433	0.026805851	0.037326402	black	-0.156941096	0.049653894		AT1G74520.1	ATHVA22A,HVA22A	HVA22 homologue A	TB2/DP1, HVA22 family protein
Sapur.15WG005600.1	3916.609127	-0.131456127	0.060171929	-2.18468	0.028912661	0.040121564	black	-0.231927846	0.003469148	GO:0006412,GO:0005840,GO:0003735	AT3G52590.1	EMB2167.ERD16.HAP4.UBC	ubiquitin extension protein 1	ubiquitin-60S ribosomal L40 fusion protein
Sapur.013G142200.1	6633.300175	-0.09721456	0.045877762	-2.11899	0.034091237	0.046945357	black	-0.280269707	0.000377645	GO:0006412,GO:0005840,GO:0003735	AT1G26910.1	RPL10B	Ribosomal protein L16p/L10e family protein	60S ribosomal protein L10
Sapur.016G281700.1	1344.292089	-0.084012154	0.041097981	-2.04419	0.040934607	0.05589197	black	-0.188251511	0.018221528		AT3G20390.1		endoribonuclease L-PSP family protein	perchloric acid soluble translation inhibitor protein
Sapur.012G011700.1	87.41016122	-0.173031406	0.085290544	-2.02873	0.042485892	0.057895364	black	-0.168034005	0.035411923		AT5G53045.1			transcription factor Pcc1
Sapur.001G155500.1	320.3524492	-0.13307125	0.066642397	-1.9968	0.045847384	0.062235024	black	-0.213653918	0.007214449					hypothetical protein
Sapur.004G162400.1	389.954176	-0.136609915	0.068752698	-1.98698	0.04692513	0.06362749	black	-0.181107705	0.023210987		AT4G29735.1			transmembrane protein, putative
Sapur.002G040800.1	225.6060518	-0.083720646	0.04257168	-1.96658	0.049231564	0.066588342	black	-0.177175987	0.026428193		AT3G63170.1		Chalcone-flavanone isomerase family protein	chalcone-flavanone isomerase
Sapur.005G108200.1	1502.736061	-0.080299946	0.041382716	-1.94042	0.052328387	0.070589325	black	-0.17728906	0.026330598		AT3G57870.1	AHUS5.ATSCE1.EMB1637.S(	sumo conjugation enzyme 1	SUMO E2 conjugating enzyme SCE1
Sapur.008G003900.1	1557.769235	-0.091024997	0.050360141	-1.80748	0.070687322	0.093899609	black	-0.177344145	0.026283165	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G23390.1		Zinc-binding ribosomal protein family protein	60S ribosomal protein L44
Sapur.009G053500.1	616.1600229	0.125015528	0.073953696	1.690457	0.090940597	0.118997044	black	0.081590256	0.309701642	GO:0006457,GO:0005737	AT1G14980.1	CPN10	chaperonin 10	10 kDa chaperonin
Sapur.019G073500.2	0.909962942	-0.42417058	0.277031755	-1.53113	0.125738204	0.161627104	black	-0.238453765	0.002634522	GO:0008616,GO:0008479,GO:0006400				NA
Sapur.004G051300.1	2745.631764	-0.071289278	0.046581556	-1.53042	0.125913155	0.161833121	black	-0.19319711	0.015338196		AT4G25740.1		RNA binding Plectin/S10 domain-containing protein	plectin/S10 domain protein
Sapur.005G061000.1	499.2217902	0.083263605	0.054576308	1.525636	0.127100431	0.163276612	black	0.077486963	0.334744472	GO:0005515	AT2G35605.1		SWIB/MDM2 domain superfamily protein	SWIB/MDM2 domain protein
Sapur.014G138000.1	379.7167402	0.069592773	0.047249057	1.472892	0.140780075	0.179843963	black	0.074390488	0.354474399		AT2G04340.1			hypothetical protein
Sapur.016G227200.1	306.9524965	0.068860602	0.051119312	1.347057	0.177962034	0.223620543	black	0.037308714	0.642717413		AT5G55125.2		Ribosomal protein L31	ribosomal protein L31
Sapur.003G115400.1	158.4865491	-0.08701353	0.064921207	-1.34029	0.180149654	0.22619755	black	-0.151379698	0.058418232		AT4G20150.1			complex I subunit
Sapur.014G050100.1	1202.283742	-0.086905081	0.065023969	-1.33651	0.181383156	0.227642641	black	-0.144819196	0.070353063	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G60770.1		Ribosomal protein S13/S15	40S ribosomal protein S13
Sapur.010G094300.1	215.8915941	-0.08719328	0.065580115	-1.32957	0.183660357	0.230247239	black	-0.137315641	0.086355461	GO:0006950	AT1G68300.1		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.006G205900.1	350.0226772	-0.057049359	0.043632089	-1.30751	0.191039819	0.238873804	black	-0.180970196	0.023317546	GO:0008080	AT5G11340.1		Acyl-CoA N-acyltransferases (NAT) superfamily protein	N-acetyltransferase NAT13
Sapur.008G139300.1	714.7480261	-0.055762873	0.044861485	-1.243	0.21386745	0.26544026	black	-0.144888635	0.070217083	GO:0006413,GO:0005737,GO:0003743,GO:0003723	AT5G35620.1	EIF(ISO)4E,EIF4E2,eIFiso4E,L	Eukaryotic initiation factor 4E protein	eukaryotic translation initiation factor iso4E
Sapur.002G138500.1	8105.753808	-0.060413476	0.049066845	-1.23125	0.218229968	0.270499492	black	-0.177614054	0.026051807		AT5G24510.1		60S acidic ribosomal protein family	60S acidic ribosomal protein P1
Sapur.014G083200.1	1134.879423	-0.079892779	0.065789048	-1.21438	0.224603374	0.277889121	black	-0.141516768	0.07707113		AT5G24510.1		60S acidic ribosomal protein family	60S acidic ribosomal protein P1
Sapur.002G120200.1	1485.441744	0.072307139	0.060685568	1.191505	0.23345552	0.287904391	black	0.067080324	0.403865149	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G60770.1		Ribosomal protein S13/S15	40S ribosomal protein S13
Sapur.013G073100.1	96.44094307	-0.067107032	0.061030139	-1.09957	0.271518651	0.331030959	black	-0.451600514	2.91E-09	GO:0004527,GO:0003676	AT1G75660.1	AtXRN3,XRN3	5\'-3\' exoribonuclease 3	5'-3' exoribonuclease
Sapur.004G130500.1	988.9819738	-0.04400194	0.04454412	-0.98783	0.323236771	0.388570238	black	-0.105375711	0.189027053	GO:0019773,GO:0006511,GO:0004175,GO:0051603,GO:0005839,GO:0004298	AT5G66140.1	PAD2	proteasome alpha subunit D2	proteasome subunit alpha type-7 protein
Sapur.002G070800.1	403.517282	-0.051608161	0.056876764	-0.90737	0.364212175	0.432898392	black	-0.14945521	0.061732721	GO:0006412,GO:0005840,GO:0005622,GO:0003735,GO:0003723	AT1G77750.1		Ribosomal protein S13/S18 family	NA
Sapur.003G023000.2	1.556543404	-0.203107747	0.228052138	-0.89062	0.373133178	0.442389622	black	-0.49643898	3.79E-11		AT1G55080.1	MED9		hypothetical protein
Sapur.016G190900.1	113.1673651	-0.046904345	0.05804195	-0.80811	0.419026617	0.490862771	black	-0.075377446	0.348108279		AT5G55125.1		Ribosomal protein L31	ribosomal protein L31
Sapur.018G057500.1	787.660229	-0.025121798	0.034993445	-0.7179	0.472818888	0.547166267	black	-0.066678387	0.406694105		AT3G24506.1			hypothetical protein

Sapur.016G092900.2	0.938006937	0.177020228	0.264394868	0.66953	0.503157614	0.578048384	black	0.450091242	3.34E-09		AT2G37840.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.010G150400.1	1535.056315	-0.020969524	0.034467194	-0.60839	0.542928302	0.618496561	black	-0.061595467	0.44346831	GO:0005515	AT2G39990.1	AteIF3f,EIF2,eIF3F	eukaryotic translation initiation factor 2	eukaryotic translation initiation factor 3 subunit F
Sapur.011G072000.1	2232.532247	-0.027798565	0.053176403	-0.52276	0.601140388	0.675343654	black	-0.123154491	0.124380073	GO:0019843,GO:0005622,GO:0003723	AT5G39850.1		Ribosomal protein S4	40S ribosomal protein S9
Sapur.016G224900.1	1176.123665	-0.018632797	0.037597365	-0.49559	0.62018523	0.693558961	black	-0.10637725	0.184833887	GO:0003677	AT1G29850.1		double-stranded DNA-binding family protein	double-stranded DNA-binding protein
Sapur.012G081400.2	5.362888845	-0.073269098	0.148846683	-0.49225	0.622545857	0.695681376	black	-0.457978938	1.63E-09		AT4G25080.3	CHLM	magnesium-protoporphyrin IX methyltransferase	Mg-protoporphyrin IX methyltransferase
Sapur.004G102800.2	252.3960176	0.03468463	0.070559942	0.491563	0.623028576	0.696056179	black	0.017994247	0.823003469	GO:0006412,GO:0005840,GO:0003735	AT3G52580.1		Ribosomal protein S11 family protein	40S ribosomal protein S14
Sapur.009G021600.1	390.1797058	-0.027756091	0.056552355	-0.4908	0.623565473	0.696538365	black	-0.077674271	0.333573913		AT1G47278.2			histone-lysine N-methyltransferase ATX2, putative
Sapur.009G127500.1	630.0346907	0.020746083	0.045558276	0.455375	0.648839738	0.720899137	black	-0.009721369	0.90381945		AT2G27730.1		copper ion binding	F1F0-ATPase inhibitor protein, putative
Sapur.011G082100.1	146.0014297	-0.025952013	0.077231166	-0.33603	0.736848006	0.801635175	black	-0.068111903	0.396658175	GO:0016531,GO:0006825,GO:0005758,GO:0005507	AT3G15352.1	ATCOX17,COX17	cytochrome c oxidase 17	cytochrome C oxidase copper chaperone
Sapur.011G082900.2	0.168013728	-0.156914504	0.601818058	-0.26073	0.794297549	0.851479001	black	-0.32267435	3.76E-05	GO:0003723	AT1G53120.1		RNA-binding S4 domain-containing protein	RNA-binding S4 domain protein
Sapur.017G028300.1	124.0940256	0.015171437	0.060135113	0.252289	0.800817567	0.857048933	black	-0.020742293	0.796521869	GO:0005680,GO:0004842	AT3G05870.1	APC11	anaphase-promoting complex/cyclosome 11	anaphase-promoting complex subunit 11 RING-H2 finger protein
Sapur.010G010900.1	31.79963009	-0.021502264	0.101023199	-0.21284	0.831448012	0.881134017	black	-0.537275931	4.03E-13	GO:0016021	AT2G42770.1		Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	peroxisomal membrane protein, putative
Sapur.007G065100.2	0.449658237	0.066400046	0.359443168	0.18473	0.853440575	0.899340266	black	0.421375881	3.89E-08	GO:0006468,GO:0005524,GO:0004672	AT3G13530.1	MAP3KE1,MAPKKK7	mitogen-activated protein kinase kinase kinase 7	MAP3K epsilon kinase
Sapur.016G208600.1	392.2853166	-0.005405213	0.038977262	-0.13868	0.889706146	0.925961832	black	-0.02651544	0.741671592	GO:0006412,GO:0005840,GO:0003735	AT3G01790.1		Ribosomal protein L13 family protein	50S ribosomal protein L13
Sapur.005G038200.1	2763.760579	0.006850139	0.053127168	0.128939	0.897406293	0.931104424	black	-0.04627911	0.564919217	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G28060.1		Ribosomal protein S24e family protein	40S ribosomal protein S24
Sapur.011G077200.2	0.054607761	-0.179215633	1.53985739	-0.11638	0.907347767	0.938985316	black	-0.610849444	1.98E-17		AT1G31660.1			bystin, putative
Sapur.008G110400.2	2.928481777	0.009486712	0.171113592	0.055441	0.955787118	0.971024517	black	-0.338606277	1.44E-05	GO:0055114.GO:0051287.GO:0016620.GO:0046983.GO:0008652.GO:0005737.GO:000394	AT1G14810.1		semialdehyde dehydrogenase family protein	aspartate-semialdehyde dehydrogenase
Sapur.010G059100.5	0.043671962	0.085365484	1.690735716	0.05049	0.959731806	NA	black	0.7143987	8.21E-26	GO:0019901,GO:0006355,GO:0000079	AT4G19600.1	CYCT1;4	Cyclin family protein	cyclin T1
Sapur.009G038100.2	0.004112536	0.128661719	2.904823276	0.044292	0.964671295	NA	black	-0.218930761	0.005873258					NAD(P)H-quinone oxidoreductase chain, putative
Sapur.011G110100.2	0.011519773	0.091189602	2.904823276	0.031392	0.97495654	NA	black	-0.419889062	4.39E-08	GO:0016021,GO:0016020,GO:0022857	AT1G43650.1		nodulin MtN21 /EamA-like transporter family protein	60S ribosomal protein L9
Sapur.016G154200.2	20.11210769	5.089205813	0.204810254	24.84839	2.69E-136	4.65E-135	brown	0.104423736	0.193076692		AT5G13490.1	AAC2	ADP/ATP carrier 2	ADP%2CATP carrier protein
Sapur.013G028600.3	7.407332774	-3.872324023	0.174820794	-22.1502	1.04E-108	1.31E-107	brown	-0.3664656	2.35E-06	GO:0004871,GO:0000160	AT5G39340.1	AHP3,ATHP2	histidine-containing phosphotransmitter 3	histidine phosphotransfer protein
Sapur.011G036800.1	175.289554	0.894454241	0.040934567	21.85083	7.63E-106	9.38E-105	brown	-0.056250211	0.484092701		AT1G28240.1		Protein of unknown function (DUF616)	transmembrane protein, putative
Sapur.016G089100.4	26.13937444	-2.214361312	0.101785736	-21.7551	6.18E-105	7.50E-104	brown	-0.314136058	6.16E-05	GO:0006457	AT3G10060.1		FKBP-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase FKBP16-4
Sapur.008G118300.3	7.470513405	-2.257119349	0.127970299	-17.6378	1.26E-69	9.43E-69	brown	-0.081608864	0.309590942	GO:0055085,GO:0016020,GO:0006810,GO:0005215	AT1G60030.1	ATNAT7,NAT7	nucleobase-ascorbate transporter 7	nucleobase ascorbate transporter
Sapur.007G031600.1	12.45279231	-1.84743549	0.108283196	-17.0611	2.89E-65	2.02E-64	brown	-0.690976758	1.31E-23		AT5G66560.1		Phototropic-responsive NPH3 family protein	root phototropism protein
Sapur.005G089100.3	34.8936508	1.270844213	0.075625063	16.80454	2.26E-63	1.54E-62	brown	0.039535467	0.62299391		AT2G17840.1	ERD7	Senescence/dehydration-associated protein-related	senescence-associated protein
Sapur.004G119100.3	46.36407232	1.135572914	0.068112667	16.67198	2.10E-62	1.40E-61	brown	0.011123546	0.890028513		AT4G39140.3		RING/U-box superfamily protein	mandelonitrile lyase
Sapur.006G154400.5	27.09572236	1.32995315	0.080164075	16.59039	8.18E-62	5.43E-61	brown	0.007822713	0.92253856		AT5G35180.2		Protein of unknown function (DUF1336)	plant/T25C13-60 protein
Sapur.003G158500.3	6.10499613	-2.774736339	0.173277255	-16.0133	1.03E-57	6.42E-57	brown	-0.104663231	0.192052003		AT4G31980.1			transmembrane protein, putative
Sapur.003G164100.1	12.10405694	-3.881390518	0.251070783	-15.4593	6.53E-54	3.82E-53	brown	-0.493060176	5.37E-11		AT1G55230.1		Family of unknown function (DUF716)	proteinase inhibitor I4, serpin%2C putative
Sapur.019G005700.1	16.05234372	-2.47724064	0.161652993	-15.3244	5.25E-53	3.03E-52	brown	-0.128085574	0.109892892		AT2G02130.1	LCR68,PDF2.3	low-molecular-weight cysteine-rich 68	gamma-thionin family protein
Sapur.002G193300.4	6.468388113	-2.206653229	0.146774289	-15.0343	4.37E-51	2.44E-50	brown	-0.081608864	0.309590942		AT5G48545.1	HINT3	histidine triad nucleotide-binding 3	HIT family: HIT (histidine triad) family protein
Sapur.016G128500.5	62.98787652	0.911935161	0.062925457	14.49231	1.36E-47	7.12E-47	brown	-0.042566126	0.59657657	GO:0055085	AT5G59740.1		UDP-N-acetylglucosamine (UAA) transporter family	adenosine 3'-phospho 5'-phosphosulfate transporter
Sapur.15ZG052800.3	6.567211646	1.663903484	0.117723285	14.13402	2.34E-45	1.19E-44	brown	0.029442002	0.714336253	GO:0005515	AT5G07910.1		Leucine-rich repeat (LRR) family protein	LRR and ubiquitin-like domain protein
Sapur.004G019300.3	6.657795226	1.706347233	0.121723048	14.01828	1.21E-44	6.03E-44	brown	-0.025018857	0.755778587	GO:0046983	AT5G54680.1	bHLH105,ILR3	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	BHLH transcription factor
Sapur.018G042000.1	420.08832	-0.824039013	0.060127315	-13.7049	9.49E-43	4.58E-42	brown	-0.645834311	6.69E-20	GO:0046872	AT4G29190.1		Zinc finger C-x8-C-x5-C-x3-H type family protein	zinc finger CCCH domain protein
Sapur.014G115100.4	28.0652958	0.934147271	0.071439987	13.07597	4.52E-39	2.05E-38	brown	-0.081608864	0.309590942	GO:0046912	AT2G42790.1	CSY3	citrate synthase 3	citrate synthase 2, peroxisomal protein
Sapur.001G085800.2	54.73949164	-0.805395803	0.061978884	-12.9947	1.31E-38	5.88E-38	brown	-0.108114977	0.177720921	GO:0055114,GO:0016491,GO:0016209,GO:0006979,GO:0004602	AT1G63460.1	ATGPX8,GPX8	glutathione peroxidase 8	glutathione peroxidase
Sapur.018G006600.1	3.604903384	3.280229898	0.254103395	12.90904	4.00E-38	1.78E-37	brown	0.207459493	0.009130859	GO:0005515	AT3G25460.1		F-box and associated interaction domains-containing protein	NA
Sapur.005G185700.1	10.06184381	1.928085725	0.14959529	12.88868	5.21E-38	2.31E-37	brown	-0.081608864	0.309590942	GO:0030246,GO:0005975,GO:0004553	AT4G36360.1	BGAL3	beta-galactosidase 3	beta-galactosidase
Sapur.003G025900.2	43.02627582	0.724595709	0.057766022	12.54363	4.31E-36	1.84E-35	brown	-0.056621112	0.481210807		AT1G79830.2	GC5	golgin candidate 5	coiled-coil vesicle tethering protein, putative
Sapur.014G006500.2	18.64797595	-1.343676634	0.108190088	-12.4196	2.05E-35	8.62E-35	brown	-0.597010894	1.56E-16					NA
Sapur.012G081600.4	10.2326739	1.745450889	0.143507184	12.16281	4.90E-34	2.01E-33	brown	-0.081608864	0.309590942	GO:0003676	AT5G07290.1	AML4,ML4	MEI2-like 4	RNA recognition motif 1 in plant Mei2-like protein
Sapur.019G094600.3	12.67125867	-1.328703768	0.109296629	-12.1569	5.27E-34	2.16E-33	brown	-0.081608864	0.309590942		AT5G10460.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	HAD-family hydrolase IIA
Sapur.012G102900.4	11.18243534	-1.342779893	0.111320886	-12.0622	1.67E-33	6.78E-33	brown	-0.125984542	0.115895294		AT5G52030.2		TraB family protein	TraB family protein
Sapur.014G106200.1	56.43837115	1.673102669	0.13938853	12.00316	3.42E-33	1.38E-32	brown	0.078548531	0.32814497	GO:0071805,GO:0016020,GO:0015079	AT4G13420.1	ATHAK5,HAK5	high affinity K+ transporter 5	potassium transporter
Sapur.006G081800.3	7.210091227	-1.334196357	0.111538236	-11.9618	5.63E-33	2.26E-32	brown	-0.081608864	0.309590942		AT5G01470.2		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase family protein
Sapur.017G103100.3	4.849096319	-1.705409429	0.144021338	-11.8414	2.39E-32	9.46E-32	brown	-0.323841054	3.51E-05	GO:0006418,GO:0000166,GO:0005524,GO:0004812	AT5G16715.1	EMB2247	ATP binding;valine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases	valyl-tRNA synthetase
Sapur.016G105100.1	19.43679081	-0.738102558	0.062350099	-11.838	2.48E-32	9.84E-32	brown	-0.347170043	8.40E-06	GO:0033699,GO:0006281,GO:0003677	AT5G01310.1	APTX	APRATAXIN-like	transcription factor bHLH140
Sapur.010G003700.1	9.981794354	-2.221035689	0.188579705	-11.7777	5.09E-32	2.00E-31	brown	-0.394296514	3.23E-07	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G48350.1		Ribosomal L18p/L5e family protein	50S ribosomal protein L18
Sapur.008G055600.3	18.93729764	-1.038151253	0.088948886	-11.6713	1.79E-31	6.94E-31	brown	-0.188364638	0.018150656	GO:0005680	AT5G05560.1	EMB2771	E3 ubiquitin ligase, putative	anaphase-promoting complex subunit 1
Sapur.016G008100.3	2.666738827	-2.231096825	0.192361851	-11.5984	4.20E-31	1.62E-30	brown	-0.111472864	0.164551558		AT5G47530.1		Auxin-responsive family protein	auxin-induced in root cultures protein, putative
Sapur.009G004800.3	22.52130068	0.878558699	0.076745309	11.44772	2.41E-30	9.14E-30	brown	0.096186009	0.230778064		AT5G60760.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	2-phosphoglycerate kinase
Sapur.002G052400.2	1.205021318	3.652548882	0.331877995	11.0057	3.59E-28	1.30E-27	brown	0.15692963	0.049670772		AT2G21770.1	CESA09,CESA9	cellulose synthase A9	cellulose synthase A catalytic subunit 6 [UDP-forming] protein, putative
Sapur.010G004300.4	15.39924264	-1.055367116	0.095964687	-10.9975	3.93E-28	1.42E-27	brown	-0.081608864	0.309590942		AT3G16810.1	APUM24,PUM24	pumilio 24	pumilio domain protein
Sapur.T192500.1	9.564834821	-1.450590818	0.133566706	-10.8604	1.78E-27	6.35E-27	brown	-0.147918636	0.06448844		AT2G02130.1	LCR68,PDF2.3	low-molecular-weight cysteine-rich 68	NA
Sapur.15WG014600.1	9.036988177	-0.979086914	0.095222573	-10.2821	8.49E-25	2.84E-24	brown	-0.618309895	6.24E-18		AT5G53130.1	ATCNGC1,CNGC1	cyclic nucleotide gated channel 1	NA
Sapur.009G063200.3	2.728562232	1.847192529	0.179868708	10.26967	9.65E-25	3.23E-24	brown	0.003350686	0.966778834		AT4G37880.1		LisH/CRA/RING-U-box domains-containing protein	sporulation protein RMD5, putative
Sapur.15WG005700.1	16.14218136	-1.4583163	0.142331273	-10.2459	1.23E-24	4.11E-24	brown	-0.439083789	8.79E-09	GO:0005975	AT5G24400.1	EMB2024,PGL3	NagB/RpiA/CoA transferase-like superfamily protein	6-phosphogluconolactonase, putative
Sapur.15WG116800.1	2.545456599	-2.314802267	0.227998831	-10.1527	3.22E-24	1.06E-23	brown	-0.081608864	0.309590942	GO:0016597,GO:0008152	AT1G69040.2	ACR4	ACT domain repeat 4	ACT domain protein, putative
Sapur.002G073100.3	26.81799	0.733343714	0.072343045	10.13703	3.78E-24	1.25E-23	brown	0.089594416	0.26446936	GO:0006914	AT4G08540.1		DNA-directed RNA polymerase II protein	DNA-directed RNA polymerase II
Sapur.008G109700.4	26.08242929	-0.740940245	0.073780485	-10.0425	9.91E-24	3.22E-23	brown	-0.081608864	0.309590942		AT1G68070.1		Zinc finger, C3HC4 type (RING finger) family protein	cleavage and polyadenylation specifity factor, putative
Sapur.T096700.3	70.79858429	-0.609606421	0.060784935	-10.0289	1.14E-23	3.69E-23	brown	-0.195606618	0.014083643	GO:0043531	AT3G14470.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.007G102000.1	6.722745775	-3.743896304	0.374780179	-9.98958	1.69E-23	5.47E-23	brown	-0.373876042	1.41E-06					NA
Sapur.002G036900.16	10.38387366	-0.985510596	0.098883203	-9.96641	2.14E-23	6.89E-23	brown	-0.081608864	0.309590942		AT4G14720.1	PPD2,TIFY4B	TIFY domain/Divergent CCT motif family protein	jasmonate ZIM domain protein K.1, putative
Sapur.016G132400.2	13.27875354	-0.947437385	0.095879314	-9.88156	5.00E-23	1.60E-22	brown	-0.081608864	0.309590942	GO:0005525	AT1G07615.1		GTP-binding protein Obg/CgtA	NA
Sapur.008G002300.1	796.1795323	-0.639779564	0.066521135	-9.61769	6.73E-22	2.09E-21	brown	-0.526020898	1.50E-12	GO:0016829,GO:0006520	AT5G65720.1	ATNFS1.ATNIFS1.NFS1.NIFS	nitrogen fixation S (NIFS)-like 1	cysteine desulfurase
Sapur.017G113400.1	14.00826316	-1.083378471	0.113258891	-9.5655	1.12E-21	3.46E-21	brown	-0.495621484	4.12E-11	GO:0043531	AT3G14470.1		NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.017G003000.3	3.906718915	-1.917169784	0.207211401	-9.25224	2.20E-20	6.58E-20	brown	-0.173550013	0.02972609	GO:0008168,GO:0008152	AT2G43940.1	ATHOL3,HOL3	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	thiopurine S-methyltransferase
Sapur.016G284100.1	5.916749301	-0.982032258	0.10677759	-9.19699	3.68E-20	1.09E-19	brown	-0.134663372	0.092663579	GO:0043531	AT4G27220.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.002G192000.2	5.941338399	1.584194455	0.176359544	8.982754	2.64E-19	7.69E-19	brown	-0.115779006	0.148746091	GO:0006468,GO:0005524,GO:0004672	AT4G13020.1	MHK	Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.018G063900.1	11.66811148	-0.998714768	0.112908818	-8.84532	9.13E-19	2.62E-18	brown	-0.536454292	4.44E-13	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT3G28345.1		ABC transporter family protein	NA
Sapur.010G041300.1	14.39693761	-1.524425557	0.173284165	-8.79726	1.40E-18	4.00E-18	brown	-0.282633559	0.000335151		AT1G07090.1	LSH6	Protein of unknown function (DUF640)	G1-like protein, putative
Sapur.005G032900.1	1.857028037	-2.278136472	0.261648786	-8.70685	3.12E-18	8.84E-18	brown	-0.361452552	3.30E-06		AT5G27230.1		Frigida-like protein	NA
Sapur.013G113000.3	1.894526406	2.087008225	0.239792591	8.703389	3.22E-18	9.11E-18	brown	-0.047680036	0.553186213	GO:0043565,GO:0006355,GO:0003700	AT3G58120.1	ATBZIP61,BZIP61	Basic-leucine zipper (bZIP) transcription factor family protein	BZIP transcription factor
Sapur.017G049700.1	11.75978221	-1.144463928	0.132456493	-8.6403	5.61E-18	1.58E-17	brown	-0.49623775	3.87E-11	GO:0003676	AT4G13850.1	ATGRP2,GR-RBP2,GRP2	glycine-rich RNA-binding protein 2	eukaryotic RNA-binding protein RBM24 RNA recognition motif protein
Sapur.011G039000.3	3.080776283	-1.508182491	0.175869618	-8.57557	9.86E-18	2.75E-17	brown	-0.116616999	0.14580838	GO:0005515	AT1G28340.1	AtRLP4,RLP4	receptor like protein 4	receptor-like kinase
Sapur.003G032800.1	18.82984805	-0.864816635	0.102015698	-8.47729	2.31E-17	6.37E-17	brown	-0.220356044	0.00555146		AT1G48630.1	RACK1B_AT	receptor for activated C kinase 1B	NA
Sapur.006G161700.1	155.0898418	-0.82779485	0.097697377	-8.47305	2.39E-17	6.60E-17	brown	-0.478246706	2.38E-10	GO:0006412	AT2G37270.1	ATRPS5B,RPS5B	ribosomal protein 5B	40S ribosomal protein S5, putative
Sapur.016G302700.1	18.00947722	-0.681175233	0.080416491	-8.47059	2.44E-17	6.74E-17	brown	-0.529334886	1.02E-12	GO:0007017,GO:0005874	AT2G29550.1	TUB7	tubulin beta-7 chain	NA
Sapur.010G096500.1	2.427656534	-2.27426488	0.269265353	-8.44618	3.01E-17	8.28E-17	brown	-0.419212871	4.64E-08	GO:0005975,GO:0004553	AT1G68560.1	ATXYL1,TRG1,XYL1	alpha-xylosidase 1	alpha-xylosidase
Sapur.004G173300.2	1.111564778	2.684472285	0.319173791	8.410691	4.08E-17	1.12E-16	brown	0.056318038	0.483564995	GO:0003993	AT2G38600.1		HAD superfamily, subfamily IIIB acid phosphatase	acid phosphatase
Sapur.010G047700.1	14.06860295	1.383991888	0.165983826	8.338113	7.55E-17	2.05E-16	brown	0.064097679	0.425135042		AT1G04560.1		AWPM-19-like family protein	plasma membrane associated protein
Sapur.016G283600.1	5.300866094	-0.943971763	0.11395928	-8.28341	1.20E-16	3.23E-16	brown	-0.182700185	0.022007129	GO:0043531	AT4G27220.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.018G088700.1	3.859453283	-1.351597635	0.164236788	-8.22957	1.88E-16	5.04E-16	brown	-0.50529775	1.49E-11					NA
Sapur.001G067300.3	16.32546871	-0.835519278	0.101827016	-8.20528	2.30E-16	6.16E-16	brown	-0.051224376	0.524040785		AT4G24140.1		alpha/beta-Hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.019G012700.1	5.683481171	-1.37790409	0.168336687	-8.18541	2.71E-16	7.25E-16	brown	-0.423738939	3.21E-08	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.002G035700.3	3.996021359	-1.188748694	0.14590516	-8.14741	3.72E-16	9.89E-16	brown	-0.003909792	0.961239462	GO:0008168,GO:0008152	AT3G63410.1	APG1,E37,IEP37,VTE3	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	2-methyl-6-phytyl-1%2C4-benzoquinone methyltransferase
Sapur.016G299300.1	54.65435742	0.744408422	0.093266619	7.98151	1.45E-15	3.78E-15	brown	0.100063218	0.212433658		AT4G05320.2	UBQ10	polyubiquitin 10	NA
Sapur.004G063500.3	22.98099462	-1.126469366	0.141542408	-7.95853	1.74E-15	4.55E-15	brown	-0.102826508	0.200012351		AT1G66400.1	CML23	calmodulin like 23	NA
Sapur.001G058900.1	5.525906336	-1.536547202	0.193400716	-7.94489	1.94E-15	5.07E-15	brown	-0.462102778	1.11E-09	GO:0016021,GO:0005215	AT1G30840.2	ATPUP4,PUP4	purine permease 4	triose-phosphate transporter family protein
Sapur.006G157500.3	5.444713041	1.213610814	0.152921454	7.936171	2.09E-15	5.43E-15	brown	0.071253858	0.375185723		AT2G42040.1			WRC protein
Sapur.005G008300.1	33.9731799	-0.668666999	0.084368067	-7.92559	2.27E-15	5.91E-15	brown	0.078548531	0.32814497		AT1G09280.1			phospholipase/carboxylesterase family protein
Sapur.010G044000.1	1.495115859	-1.96847348	0.249380715	-7.89345	2.94E-15	7.63E-15	brown	-0.456311525	1.90E-09		AT2G33410.1		RNA-binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.002G109800.1	85.76663539	-0.471118231	0.060318585	-7.8105	5.70E-15	1.46E-14	brown	-0.480038332	1.99E-10		AT2G44600.1			hypothetical protein
Sapur.013G057300.1	70.931763	-1.041461131	0.13338971	-7.80766	5.83E-15	1.50E-14	brown	-0.383270005	7.25E-07					NA
Sapur.010G185500.1	2.988852776	-1.526362037	0.195613476	-7.80295	6.05E-15	1.55E-14	brown	-0.45239654	2.71E-09		AT5G02420.1			cyclin-dependent kinase inhibitor siamese protein, putative
Sapur.15WG062400.1	6.797733897	-1.26690026	0.163922106	-7.72867	1.09E-14	2.77E-14	brown	-0.390518775	4.27E-07		AT5G17900.1		microfibrillar-associated protein-related	NA
Sapur.012G106300.3	61.81120201	0.474012283	0.061686184	7.684254	1.54E-14	3.91E-14	brown	-0.121578455	0.129308907	GO:0007264,GO:0005525	AT5G52210.1	ATARLB1,ATGB1,GB1	GTP-binding protein 1	ADP-ribosylation factor(Arf)/Arf-like (Arl) small GTPase family protein
Sapur.013G002600.1	3.201233568	-1.351954178	0.176307839	-7.66815	1.75E-14	4.42E-14	brown	-0.439564995	8.43E-09	GO:0010468,GO:0005777	AT5G61190.1		putative endonuclease or glycosyl hydrolase with C2H2-type zinc finger domain	NA
Sapur.016G200500.5	9.558478793	-0.859949853	0.112442445	-7.64791	2.04E-14	5.16E-14	brown	-0.081608864	0.309590942		AT3G26990.1		ENTH/VHS family protein	regulation of nuclear pre-mRNA domain protein 1B
Sapur.010G047600.1	2.291384196	1.81052146	0.237330333	7.628698	2.37E-14	5.98E-14	brown	0.078580115	0.327949911	GO:0003676	AT2G21660.1	ATGRP7.CCR2.GR-RBP7.GRI	cold, circadian rhythm, and rna binding 2	NA
Sapur.007G052800.2	60.01142327	0.543907577	0.071589061	7.597635	3.02E-14	7.58E-14	brown	-0.103621445	0.196538298	GO:0006468,GO:0004672	AT5G66210.2	CPK28	calcium-dependent protein kinase 28	calcium-dependent kinase
Sapur.006G036200.1	169.2325066	-1.754076886	0.231113254	-7.58969	3.21E-14	8.06E-14	brown	-0.355690062	4.84E-06	GO:0005975,GO:0004553	AT3G57240.1	BG3	beta-1,3-glucanase 3	beta-1%2C3-glucanase
Sapur.003G049900.3	19.82259362	0.788020224	0.104221169	7.561038	4.00E-14	1.00E-13	brown	0.042928683	0.59345038		AT4G16845.1	VRN2	VEFS-Box of polycomb protein	polycomb protein embryonic flower, putative
Sapur.002G176200.2	8.227442685	-1.018819673	0.135130549	-7.53952	4.72E-14	1.18E-13	brown	-0.119128608	0.137266905					NA
Sapur.007G030700.2	1.006606141	-2.151956027	0.289875204	-7.42373	1.14E-13	2.81E-13	brown	-0.291371156	0.000213605		AT5G66600.4		Protein of unknown function, DUF547	electron transporter, putative
Sapur.006G119300.1	2.621767529	-1.502859962	0.203128072	-7.39858	1.38E-13	3.39E-13	brown	-0.488427105	8.62E-11	GO:0008270,GO:0005515	AT5G17600.1		RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.001G046200.3	36.09123886	-1.146976049	0.155278205	-7.38659	1.51E-13	3.70E-13	brown	-0.286599864	0.000273666	GO:0016020,GO:0009765	AT3G61470.1	LHCA2	photosystem I light harvesting complex gene 2	photosystem I light harvesting complex Lhca2/4, chlorophyll A/B-binding protein
Sapur.001G166200.3	2.172651428	-1.592850082	0.215841252	-7.37973	1.59E-13	3.90E-13	brown	-0.038830171	0.629213027	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G79850.1	CS17,PRPS17,RPS17	ribosomal protein S17	30S ribosomal protein S17
Sapur.007G003900.3	27.33011935	0.616041805	0.083647987	7.364694	1.78E-13	4.35E-13	brown	-0.034203333	0.670642572		AT5G67620.1			DUF4228 domain protein
Sapur.001G138900.1	1.01650146	-2.031164698	0.281359739	-7.2191	5.23E-13	1.26E-12	brown	-0.503938607	1.72E-11		AT4G12510.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/LTP family protein
Sapur.007G068000.1	1.53422956	-1.609752518	0.223569311	-7.20024	6.01E-13	1.45E-12	brown	-0.463792196	9.51E-10	GO:0006412,GO:0005840,GO:0003735	AT3G22300.1	RPS10	ribosomal protein S10	NA
Sapur.001G177300.5	8.711156788	-0.831805615	0.115851364	-7.17994	6.97E-13	1.68E-12	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.005G130000.1	25.20574992	-0.653688604	0.091443285	-7.14857	8.77E-13	2.10E-12	brown	-0.426186945	2.62E-08	GO:0005515	AT1G78100.1		F-box family protein	F-box plant protein
Sapur.002G005600.4	5.321781699	-0.947499377	0.133309938	-7.10749	1.18E-12	2.82E-12	brown	-0.157683657	0.048570943	GO:0003677	AT4G35550.1	ATWOX13,HB-4,WOX13	WUSCHEL related homeobox 13	HB1 homeodomain protein
Sapur.005G163000.5	9.771310414	-0.789538168	0.112166962	-7.03895	1.94E-12	4.59E-12	brown	-0.081608864	0.309590942		AT3G10260.3		Reticulon family protein	reticulon-like protein
Sapur.010G047900.1	5.743403438	-1.566075477	0.223514798	-7.00659	2.44E-12	5.76E-12	brown	-0.397745247	2.49E-07		AT4G13480.1	AtMYB79,MYB79	myb domain protein 79	MYB transcription factor
Sapur.006G061500.1	8.046327738	-0.950705121	0.135725846	-7.0046	2.48E-12	5.84E-12	brown	-0.452278204	2.74E-09	GO:0016020,GO:0005618,GO:0004252,GO:0006508	AT2G19170.1	SLP3	subtilisin-like serine protease 3	subtilisin-like serine protease
Sapur.017G120200.2	3.139027872	-1.27296759	0.181998768	-6.99437	2.66E-12	6.28E-12	brown	-0.45995434	1.36E-09		AT5G52760.1		Copper transport protein family	NA
Sapur.004G084300.1	3.830650357	-1.109014687	0.161390146	-6.87164	6.35E-12	1.48E-11	brown	-0.425451447	2.78E-08					NA
Sapur.010G007400.1	105.5994321	-0.596478265	0.086938392	-6.86093	6.84E-12	1.59E-11	brown	-0.459083941	1.47E-09					NA
Sapur.15WG018600.1	231.9491739	0.960460235	0.140649971	6.828727	8.57E-12	1.98E-11	brown	-0.041432704	0.606397174	GO:0005975,GO:0004553	AT5G24090.1	ATCHIA,CHIA	chitinase A	acidic chitinase
Sapur.017G002300.1	0.98176215	2.547783436	0.37442984	6.804435	1.01E-11	2.34E-11	brown	0.259125942	0.001048973		AT3G59850.1		Pectin lyase-like superfamily protein	endo-polygalacturonase
Sapur.010G118900.1	1.135705275	-2.063015361	0.304419128	-6.77689	1.23E-11	2.82E-11	brown	-0.386717544	5.65E-07		AT3G17340.1		ARM repeat superfamily protein	protein transporter, putative
Sapur.011G055800.5	1.609296964	-1.552565341	0.230340414	-6.74031	1.58E-11	3.62E-11	brown	-0.081608864	0.309590942		AT4G18390.2	TCP2	TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 2	TCP family transcription factor
Sapur.004G123800.4	22.21816775	0.771180411	0.114416461	6.740118	1.58E-11	3.62E-11	brown	-0.081608864	0.309590942	GO:0006355	AT5G45600.1	GAS41,TAF14B	YEATS family protein	NA
Sapur.006G151800.3	4.117083366	-1.048768112	0.157040821	-6.67832	2.42E-11	5.50E-11	brown	-0.107354602	0.18080809		AT5G58000.1		Reticulon family protein	reticulon protein
Sapur.005G138200.18	36.66772569	-0.394509324	0.059684466	-6.60992	3.85E-11	8.68E-11	brown	-0.020043286	0.803237189	GO:0006355,GO:0006289,GO:0000439	AT1G18340.1		basal transcription factor complex subunit-related	transcription factor tfb4
Sapur.010G045800.2	1.195581404	-1.756747096	0.267352803	-6.57089	5.00E-11	1.12E-10	brown	-0.131478704	0.100716042		AT1G04520.1	PDLP2	plasmodesmata-located protein 2	cysteine-rich repeat secretory protein
Sapur.004G162500.2	95.97375982	0.740093512	0.112708108	6.566462	5.15E-11	1.16E-10	brown	0.375062825	1.30E-06	GO:0006508,GO:0004185	AT3G45010.1	scpl48	serine carboxypeptidase-like 48	serine carboxypeptidase
Sapur.013G070700.3	2.280113945	-1.187817764	0.181984326	-6.52703	6.71E-11	1.50E-10	brown	-0.362708956	3.04E-06	GO:0006432,GO:0005524,GO:0003723,GO:0000287,GO:0004826	AT1G72550.1		tRNA synthetase beta subunit family protein	phenylalanyl-tRNA synthetase beta chain, putative
Sapur.002G158100.2	8.228856114	0.7182498	0.110059711	6.526001	6.75E-11	1.51E-10	brown	-0.003355642	0.966729723	GO:0006904,GO:0000145	AT4G02350.1	SEC15B	exocyst complex component sec15B	exocyst complex subunit Sec15-like protein
Sapur.003G073100.1	34.36990421	-0.424519863	0.065293454	-6.50172	7.94E-11	1.77E-10	brown	-0.487078636	9.88E-11		AT4G25170.1		Uncharacterised conserved protein (UCP012943)	hypothetical protein
Sapur.005G098300.2	2.254176081	-1.216357657	0.188642125	-6.44796	1.13E-10	2.51E-10	brown	-0.199960194	0.012042927	GO:0016491,GO:0008152	AT2G29150.1		NAD(P)-binding Rossmann-fold superfamily protein	tropinone reductase II
Sapur.012G033900.1	33.62707533	-0.646033863	0.100456544	-6.43098	1.27E-10	2.81E-10	brown	-0.392214848	3.77E-07	GO:0005515	AT1G18080.1	ATARCA.RACK1A.RACK1A_A	Transducin/WD40 repeat-like superfamily protein	guanine nucleotide-binding protein subunit beta-like protein
Sapur.005G007800.3	3.528660017	1.05649297	0.165708697	6.375604	1.82E-10	4.01E-10	brown	0.002391049	0.976290055	GO:0033926	AT1G56560.1		Plant neutral invertase family protein	neutral/alkaline invertase
Sapur.010G111900.8	7.452879818	0.780735177	0.123329012	6.330507	2.44E-10	5.35E-10	brown	-0.01862744	0.816882801	GO:0005515	AT5G49430.1		WD40/YVTN repeat-like-containing domain;Bromodomain	cytochrome cd1-nitrite reductase-like, carboxy-terminal heme protein d1, putative
Sapur.15ZG046200.1	2.304488435	-1.085180865	0.171660391	-6.32167	2.59E-10	5.66E-10	brown	-0.433293271	1.44E-08	GO:0006468,GO:0004672	AT3G02130.1	RPK2,TOAD2	receptor-like protein kinase 2	NA
Sapur.003G095800.1	4.570636832	-1.654922163	0.262302083	-6.30922	2.80E-10	6.12E-10	brown	-0.350164733	6.94E-06		AT1G63910.1	AtMYB103,MYB103	myb domain protein 103	NA
Sapur.019G018500.1	62.77347595	0.309681734	0.049660054	6.236033	4.49E-10	9.72E-10	brown	-0.081608864	0.309590942	GO:0005515,GO:0006468,GO:0004672	AT3G14840.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.T079500.1	10.24261456	0.995763612	0.160763856	6.193952	5.87E-10	1.26E-09	brown	0.356795153	4.50E-06	GO:0005509				NA
Sapur.T158800.3	0.360699327	-2.020025444	0.326927775	-6.17881	6.46E-10	1.39E-09	brown	-0.114902006	0.151868242		AT4G17790.1		SNARE associated Golgi protein family	NA
Sapur.014G020100.1	9.954113948	0.995946484	0.162911726	6.113412	9.75E-10	2.08E-09	brown	0.356512001	4.59E-06	GO:0005509				EF hand protein
Sapur.014G144300.2	2.649016015	-1.062466518	0.173880679	-6.11032	9.94E-10	2.12E-09	brown	-0.110935599	0.166608292	GO:0003723,GO:0032259,GO:0008168	AT3G25470.1		bacterial hemolysin-related	TlyA family rRNA methyltransferase/hemolysin protein, putative
Sapur.006G032500.2	1.312293765	-1.580588434	0.259656002	-6.08724	1.15E-09	2.45E-09	brown	0.078548531	0.32814497	GO:0006396,GO:0003723	AT3G57150.1	AtCBF5.AtNAP57.CBF5.NAP	homologue of NAP57	tRNA pseudouridine synthase
Sapur.016G092800.4	6.992798707	0.658879189	0.108391287	6.07871	1.21E-09	2.58E-09	brown	-0.163321145	0.040973418	GO:0030131,GO:0016192,GO:0006886,GO:0030117	AT1G60070.1		Adaptor protein complex AP-1, gamma subunit	AP-1 complex subunit gamma-2
Sapur.014G127700.4	4.758798858	-0.86607028	0.143038183	-6.05482	1.41E-09	2.98E-09	brown	-0.053754685	0.503721591		AT1G05060.1			hypothetical protein
Sapur.006G211500.2	68.07903587	-0.458726561	0.076219583	-6.01849	1.76E-09	3.72E-09	brown	-0.380481452	8.86E-07	GO:0045263,GO:0015986,GO:0015078	AT4G32260.1		ATPase, F0 complex, subunit B/B\', bacterial/chloroplast	ATP synthase subunit B' protein
Sapur.012G081400.1	84.96495508	-0.470287708	0.078155194	-6.01736	1.77E-09	3.75E-09	brown	-0.035956871	0.654815399		AT4G25080.2	CHLM	magnesium-protoporphyrin IX methyltransferase	Mg-protoporphyrin IX methyltransferase
Sapur.002G038100.2	5.057327942	-0.921214914	0.153213191	-6.01263	1.83E-09	3.85E-09	brown	0.046803126	0.560516638		AT3G04810.2	ATNEK2,NEK2	NIMA-related kinase 2	Serine/Threonine kinase domain protein
Sapur.019G003800.1	1.467926923	-1.274340868	0.217450384	-5.86038	4.62E-09	9.60E-09	brown	-0.440333878	7.89E-09	GO:0046872,GO:0000166,GO:0016887,GO:0016021,GO:0006812	AT5G23630.1	MIA,PDR2	phosphate deficiency response 2	cation-transporting ATPase, putative
Sapur.010G118000.3	3.172733672	0.87908561	0.150660169	5.834891	5.38E-09	1.12E-08	brown	-0.049116522	0.541279578	GO:0003824,GO:0006470,GO:0004722	AT1G48040.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.017G051800.1	39.65507551	-0.406144766	0.070041235	-5.79865	6.68E-09	1.38E-08	brown	-0.37931131	9.63E-07	GO:0005515	AT3G26810.1	AFB2	auxin signaling F-box 2	transport inhibitor response protein
Sapur.004G010800.3	5.041605679	-0.680448955	0.117451551	-5.79344	6.90E-09	1.42E-08	brown	-0.0065031	0.93557451		AT4G21790.1	ATTOM1,TOM1	tobamovirus multiplication 1	tobamovirus multiplication protein
Sapur.T168600.1	3.559086623	-0.820858214	0.14184112	-5.78717	7.16E-09	1.48E-08	brown	-0.393113096	3.53E-07		AT3G07930.3		DNA glycosylase superfamily protein	NA
Sapur.009G013000.1	106.1582257	-0.34598153	0.060053478	-5.76122	8.35E-09	1.72E-08	brown	-0.409431306	1.01E-07		AT2G27260.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.006G211100.8	30.19463445	-0.422779938	0.07344522	-5.7564	8.59E-09	1.77E-08	brown	-0.095731004	0.23300179		AT4G35530.1		phosphatidylinositolglycan-related	GPI-GlcNAc transferase complex, PIG-H component
Sapur.011G119800.1	1.102160265	-1.744208647	0.303358518	-5.74966	8.94E-09	1.84E-08	brown	-0.381529697	8.22E-07	GO:0055114,GO:0050660,GO:0016491	AT5G44400.1		FAD-binding Berberine family protein	reticuline oxidase
Sapur.004G050500.4	7.946468929	-0.604276756	0.10512554	-5.74814	9.02E-09	1.85E-08	brown	-0.081608864	0.309590942		AT5G62650.1		Tic22-like family protein	plant/MRG21-7 protein, putative
Sapur.003G159500.2	2.149169985	-1.304065312	0.227718032	-5.72667	1.02E-08	2.10E-08	brown	-0.387432336	5.36E-07		AT5G12900.1			NA
Sapur.006G207100.2	15.50619715	1.296303172	0.227203507	5.705472	1.16E-08	2.37E-08	brown	0.289312936	0.000237828		AT5G11420.1		Protein of unknown function, DUF642	plant/F18G18-200 protein
Sapur.018G045000.3	24.49550829	0.427488375	0.075003251	5.699598	1.20E-08	2.45E-08	brown	-0.066031628	0.411270694					hypothetical protein
Sapur.002G044900.1	36.54457682	0.507957504	0.089157165	5.697327	1.22E-08	2.48E-08	brown	0.351500566	6.36E-06					zeta toxin protein
Sapur.016G168700.1	1364.573745	0.512841518	0.090194341	5.685961	1.30E-08	2.65E-08	brown	0.420258727	4.26E-08	GO:0016884	AT5G64440.1	AtFAAH,FAAH	fatty acid amide hydrolase	glutamyl-tRNA(Gln) amidotransferase subunit A
Sapur.014G118600.1	11.99875512	-0.56630101	0.099630736	-5.684	1.32E-08	2.68E-08	brown	-0.373026269	1.50E-06		AT4G14200.1		Pentatricopeptide repeat (PPR) superfamily protein	salt-inducible protein, putative
Sapur.018G092600.1	0.876952818	-1.511221395	0.266297774	-5.67493	1.39E-08	2.82E-08	brown	-0.397063059	2.62E-07	GO:0031515,GO:0030488,GO:0016429	AT5G14600.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NA
Sapur.002G054700.1	167.7581802	-0.221517952	0.039247572	-5.64412	1.66E-08	3.37E-08	brown	-0.409560026	1.00E-07	GO:0005515	AT1G76920.1		F-box family protein	SKP1-interacting partner 15
Sapur.002G074600.1	1.546757151	-1.455552252	0.258850145	-5.62315	1.88E-08	3.80E-08	brown	-0.187943157	0.018415925	GO:0006633,GO:0005524,GO:0003989	AT1G36160.1	ACC1.AT-ACC1.EMB22.GK.P	acetyl-CoA carboxylase 1	acetyl-CoA carboxylase
Sapur.003G018000.3	1.392233209	1.336129364	0.238291652	5.607118	2.06E-08	4.16E-08	brown	-0.081608864	0.309590942		AT1G52080.1	AR791	actin binding protein family	CHUP1, putative
Sapur.006G153700.1	147.8720892	-0.825916649	0.148109744	-5.57638	2.46E-08	4.95E-08	brown	-0.409870399	9.78E-08	GO:0005975,GO:0004553	AT4G19810.1		Glycosyl hydrolase family protein with chitinase insertion domain	glycoside hydrolase family 18 protein
Sapur.T167600.4	2.855364922	-1.209827856	0.217135037	-5.57178	2.52E-08	5.08E-08	brown	-0.250407815	0.001561104		AT3G12340.1		FKBP-like peptidyl-prolyl cis-trans isomerase family protein	minichromosome maintenance protein
Sapur.T054700.1	2.886936284	-0.924579957	0.167034725	-5.53526	3.11E-08	6.24E-08	brown	-0.387833976	5.21E-07					NA
Sapur.009G012700.6	1.900014709	-1.119636526	0.204383283	-5.47812	4.30E-08	8.58E-08	brown	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004672	AT3G44200.1	ATNEK6,IBO1,NEK6	NIMA (never in mitosis, gene A)-related 6	Serine/Threonine-kinase, putative
Sapur.003G150200.1	4.179670795	-0.821614656	0.150648591	-5.45385	4.93E-08	9.81E-08	brown	-0.32122122	4.10E-05		AT5G09860.1	AtHPR1.AtTHO1.HPR1.THO	nuclear matrix protein-related	THO complex subunit 1 transcription elongation factor
Sapur.001G043300.3	19.89186394	-0.411587668	0.075692871	-5.4376	5.40E-08	1.07E-07	brown	-0.102505665	0.201427015	GO:0016020	AT4G13590.1		Uncharacterized protein family (UPF0016)	transmembrane protein TPARL protein, putative
Sapur.014G085600.4	31.54671986	-0.391899071	0.072331173	-5.41812	6.02E-08	1.19E-07	brown	-0.081608864	0.309590942		AT1G02270.1		Calcium-binding endonuclease/exonuclease/phosphatase family	carbon catabolite repressor protein, putative
Sapur.013G028800.2	16.99801393	-0.417005765	0.077084836	-5.4097	6.31E-08	1.25E-07	brown	-0.394269406	3.24E-07		AT5G27320.1	ATGID1C,GID1C	alpha/beta-Hydrolases superfamily protein	gibberellin receptor GID1, putative
Sapur.012G097400.1	32.7554697	1.229844936	0.22767602	5.401732	6.60E-08	1.31E-07	brown	0.25365021	0.001348661	GO:0004857	AT4G25250.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	pectinesterase/pectinesterase inhibitor, putative
Sapur.008G126300.2	0.72598102	-1.795175001	0.332528799	-5.39855	6.72E-08	1.33E-07	brown	-0.375111993	1.29E-06		AT4G14770.1	ATTCX2,TCX2	TESMIN/TSO1-like CXC 2	TSO1, putative
Sapur.007G030000.2	0.962583215	1.647281696	0.305561237	5.391003	7.01E-08	1.39E-07	brown	-0.036141691	0.653156004	GO:0008270	AT4G36860.1	DAR1	LIM domain-containing protein	zinc ion-binding protein, putative
Sapur.003G107200.3	0.469150756	1.850187057	0.343614951	5.384478	7.27E-08	1.44E-07	brown	-0.016661323	0.835922479	GO:0016021,GO:0005789	AT5G42000.1		ORMDL family protein	ORMDL family protein
Sapur.001G164800.2	1.045212623	-1.466538834	0.273643139	-5.35931	8.35E-08	1.65E-07	brown	-0.129501545	0.105986807		AT4G29100.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor, putative
Sapur.011G096100.2	14.28954323	-0.815084295	0.152812102	-5.3339	9.61E-08	1.89E-07	brown	-0.076723289	0.339544052	GO:0016491	AT4G27270.1		Quinone reductase family protein	quinone oxidoreductase, putative
Sapur.018G019500.1	6.714961526	-0.814531249	0.154664642	-5.26643	1.39E-07	2.72E-07	brown	-0.330212322	2.40E-05		AT5G25265.1			transmembrane protein, putative
Sapur.004G009000.1	2.742667398	-1.072995209	0.204212452	-5.25431	1.49E-07	2.90E-07	brown	-0.281217057	0.000360049	GO:0006468,GO:0004672	AT4G04720.1	CPK21	calcium-dependent protein kinase 21	calcium-dependent kinase
Sapur.006G123200.1	1.46927542	-1.285479158	0.244694752	-5.2534	1.49E-07	2.91E-07	brown	-0.350515913	6.78E-06	GO:0003723	AT4G29750.1		CRS1 / YhbY (CRM) domain-containing protein	CRS1/YhbY domain protein
Sapur.018G065700.1	2.603798171	-1.050023751	0.199977843	-5.2507	1.52E-07	2.96E-07	brown	-0.380249051	9.00E-07					NA
Sapur.016G162500.2	5.341181666	-0.740507385	0.141905149	-5.21833	1.81E-07	3.51E-07	brown	-0.348172561	7.88E-06		AT2G30000.1		PHF5-like protein	PHD finger-like domain protein 5A
Sapur.013G070700.1	1.754841505	-1.057508096	0.202980659	-5.2099	1.89E-07	3.67E-07	brown	-0.053853062	0.502939991	GO:0006432,GO:0005524,GO:0003723,GO:0000287,GO:0004826	AT1G72550.1		tRNA synthetase beta subunit family protein	phenylalanyl-tRNA synthetase beta chain, putative
Sapur.018G061300.2	5.690733545	-0.605334047	0.116864855	-5.17978	2.22E-07	4.30E-07	brown	-0.381664565	8.14E-07		AT5G19570.1			transmembrane protein, putative
Sapur.019G078200.1	1.385704334	1.91621854	0.370263222	5.175287	2.28E-07	4.41E-07	brown	0.010291096	0.898212268		AT4G03500.1		Ankyrin repeat family protein	ankyrin repeat protein
Sapur.016G246200.5	0.57717906	-1.73499567	0.336154188	-5.16131	2.45E-07	4.74E-07	brown	-0.089328523	0.265895437	GO:0005992,GO:0003824	AT1G78580.1	ATTPS1,TPS1	trehalose-6-phosphate synthase	trehalose-6-phosphate synthase
Sapur.016G014800.1	3.456076036	-0.831106669	0.161436559	-5.14819	2.63E-07	5.08E-07	brown	-0.347582868	8.19E-06		AT3G22160.1		VQ motif-containing protein	VQ motif protein
Sapur.006G075900.4	31.64330779	0.515982608	0.100311506	5.143803	2.69E-07	5.19E-07	brown	-0.073064326	0.363142303		AT5G02020.1			plant/T7H20-70 protein, putative
Sapur.T171600.1	2.015379227	-0.921958458	0.180067409	-5.12007	3.05E-07	5.87E-07	brown	-0.394932538	3.08E-07		AT1G06530.1		Tropomyosin-related	NA
Sapur.006G148100.1	14.93782319	0.547894395	0.107338246	5.104373	3.32E-07	6.37E-07	brown	0.320820746	4.19E-05					transmembrane protein, putative
Sapur.011G050900.5	2.823768359	-1.613708908	0.317629764	-5.08047	3.76E-07	7.20E-07	brown	-0.103853871	0.19553086		AT1G29750.2	RKF1	receptor-like kinase in flowers 1	receptor-like kinase, putative
Sapur.006G202000.1	0.896419069	-1.911427342	0.377089951	-5.06889	4.00E-07	7.65E-07	brown	-0.210892547	0.008019529		AT5G25590.1		Protein of unknown function (DUF630 and DUF632)	NA
Sapur.016G256300.1	6.611677712	-0.788425336	0.15570785	-5.06349	4.12E-07	7.86E-07	brown	-0.277067712	0.000443182	GO:0003824,GO:0006470,GO:0004722	AT3G15260.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.003G136700.1	2.352559822	-0.921717271	0.182614628	-5.04734	4.48E-07	8.54E-07	brown	-0.364190986	2.75E-06	GO:0006810,GO:0005643	AT1G80680.1	MOS3,NUP96,PRE,SAR3	SUPPRESSOR OF AUXIN RESISTANCE 3	nucleoporin, putative
Sapur.002G060700.4	5.29258026	-0.802719653	0.160160412	-5.01197	5.39E-07	1.02E-06	brown	-0.070805882	0.378203	GO:0005515	AT1G77250.1		RING/FYVE/PHD-type zinc finger family protein	PHD-finger protein
Sapur.016G136700.1	825.6099064	-0.206671523	0.041371789	-4.99547	5.87E-07	1.11E-06	brown	-0.360182059	3.60E-06	GO:0003824,GO:0006470,GO:0004722	AT2G29380.1	HAI3	highly ABA-induced PP2C gene 3	protein phosphatase 2C
Sapur.003G045200.3	0.81030093	-1.449116737	0.290924446	-4.98108	6.32E-07	1.20E-06	brown	-0.037830542	0.638072215	GO:0008168,GO:0006479	AT4G16570.1	ATPRMT7,PRMT7	protein arginine methyltransferase 7	arginine N-methyltransferase
Sapur.010G085900.3	2.995609009	-0.960377099	0.192849303	-4.97994	6.36E-07	1.20E-06	brown	-0.081608864	0.309590942		AT1G71000.1		Chaperone DnaJ-domain superfamily protein	heat shock protein-binding protein, putative
Sapur.016G167400.1	2.813423552	0.854833297	0.171766925	4.976705	6.47E-07	1.22E-06	brown	0.371630586	1.65E-06		AT2G02560.2	ATCAND1.CAND1.ETA2.HVE	cullin-associated and neddylation dissociated	NA
Sapur.010G163200.3	3.302268406	-0.845663176	0.170949232	-4.94687	7.54E-07	1.42E-06	brown	-0.322818674	3.73E-05	GO:0006418,GO:0005524,GO:0004812,GO:0000166	AT3G55400.1	OVA1	methionyl-tRNA synthetase / methionine--tRNA ligase / MetRS (cpMetRS)	methionyl-tRNA synthetase
Sapur.008G015700.1	5.258676282	-0.933159875	0.188795343	-4.94271	7.70E-07	1.45E-06	brown	-0.285584952	0.000288315		AT5G04700.1		Ankyrin repeat family protein	ankyrin repeat protein
Sapur.019G042400.1	0.78288651	-1.464549694	0.297399446	-4.92452	8.46E-07	1.59E-06	brown	-0.362080665	3.17E-06	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.15WG013500.1	4.329812597	1.266127642	0.258087243	4.905813	9.30E-07	1.75E-06	brown	0.333723451	1.94E-05	GO:0006468,GO:0005524,GO:0004672	AT1G66920.2		Protein kinase superfamily protein	NA
Sapur.008G063100.1	0.97493116	1.921410971	0.392887645	4.890485	1.01E-06	1.89E-06	brown	0.31349938	6.39E-05	GO:0005975,GO:0004553	AT1G65610.1	ATGH9A2,KOR2	Six-hairpin glycosidases superfamily protein	endo-1%2C4-beta-glucanase
Sapur.010G090700.1	1.994569299	-1.172286513	0.239845399	-4.88768	1.02E-06	1.91E-06	brown	-0.225961823	0.004433241		AT1G15080.1	ATLPP2,ATPAP2,LPP2	lipid phosphate phosphatase 2	lipid phosphate phosphatase
Sapur.T048000.2	0.743905908	-1.373197013	0.282877851	-4.85438	1.21E-06	2.25E-06	brown	-0.388457068	4.97E-07	GO:0055114,GO:0016491,GO:0006633,GO:0005506	AT1G02205.3	CER1	Fatty acid hydroxylase superfamily	sterol desaturase, putative
Sapur.017G057100.3	0.900173876	-1.40695293	0.289876341	-4.85363	1.21E-06	2.26E-06	brown	-0.150950439	0.059144556	GO:0006355,GO:0005739,GO:0003690	AT4G14605.1		Mitochondrial transcription termination factor family protein	transcription termination factor-like protein
Sapur.006G017500.5	6.425182717	0.546319627	0.113014651	4.83406	1.34E-06	2.49E-06	brown	-0.184060018	0.021022105		AT3G22260.1		Cysteine proteinases superfamily protein	OTU-like cysteine protease
Sapur.15WG044700.1	0.51922244	-2.420214376	0.501390715	-4.827	1.39E-06	2.58E-06	brown	-0.334153146	1.89E-05	GO:0006950,GO:0005516	AT1G73805.1		Calmodulin binding protein-like	calmodulin-binding protein
Sapur.006G103900.5	3.987160936	0.628305695	0.130764689	4.804857	1.55E-06	2.87E-06	brown	-0.081608864	0.309590942		AT2G37025.1	TRFL8	TRF-like 8	Myb-like DNA-binding domain protein
Sapur.019G090500.3	13.62869845	-0.545483211	0.114064285	-4.78224	1.73E-06	3.21E-06	brown	-0.131333931	0.101094824		AT1G05710.3		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor BHLH protein
Sapur.002G183300.1	347.5056982	-0.204547274	0.042798326	-4.77933	1.76E-06	3.26E-06	brown	-0.369696732	1.89E-06		AT5G13890.3		Family of unknown function (DUF716)	transmembrane protein, putative
Sapur.013G013700.2	565.0849632	-0.427317539	0.08966277	-4.76583	1.88E-06	3.48E-06	brown	-0.283905028	0.000314171		AT1G56220.1		Dormancy/auxin associated family protein	dormancy/auxin associated protein
Sapur.006G091800.1	0.524309656	-1.773618777	0.37218757	-4.76539	1.88E-06	3.48E-06	brown	-0.377164465	1.12E-06	GO:0055085,GO:0016021	AT5G01990.1		Auxin efflux carrier family protein	auxin efflux carrier family transporter
Sapur.005G000500.2	4.209243206	-0.959052682	0.20213593	-4.74459	2.09E-06	3.85E-06	brown	-0.230903743	0.003619854	GO:0006418.GO:0005737.GO:0005524.GO:0004812.GO:0000166.GO:0043039.GO:001687	AT5G26710.1		Glutamyl/glutaminyl-tRNA synthetase, class Ic	glutamyl-tRNA synthetase
Sapur.012G035200.1	0.796983525	1.669820446	0.353703413	4.720962	2.35E-06	4.32E-06	brown	0.095606828	0.233611275	GO:0016021,GO:0016020,GO:0022857	AT5G07050.1		nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4
Sapur.001G108900.3	2.211160108	0.843224331	0.17873686	4.717686	2.39E-06	4.39E-06	brown	-0.150946015	0.05915208	GO:0032502,GO:0006351,GO:0005634	AT4G37740.1	AtGRF2,GRF2	growth-regulating factor 2	growth-regulating factor, putative
Sapur.003G151300.1	108.2106235	0.202913082	0.043133512	4.704302	2.55E-06	4.68E-06	brown	0.29451021	0.000181041	GO:0005515	AT1G08315.1		ARM repeat superfamily protein	ubiquitin-protein ligase, putative
Sapur.006G070000.4	6.04252626	-0.608608767	0.12981145	-4.68841	2.75E-06	5.05E-06	brown	-0.085896783	0.284771806	GO:0010338,GO:0006351,GO:0005634	AT2G37630.1	AS1.ATMYB91.ATPHAN.MYB	myb-like HTH transcriptional regulator family protein	MYB-related transcription factor, putative
Sapur.006G217000.1	12.0372242	-0.462004362	0.099010751	-4.6662	3.07E-06	5.62E-06	brown	-0.2922129	0.000204376	GO:0016020,GO:0008375	AT2G37585.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	core-2/I-branching beta-1%2C6-N-acetylglucosaminyltransferase-like protein
Sapur.019G010800.1	0.676305462	-1.632942643	0.35070175	-4.65621	3.22E-06	5.89E-06	brown	-0.323352566	3.62E-05		AT5G14930.2	SAG101	senescence-associated gene 101	hypothetical protein
Sapur.001G135600.3	20.87906716	0.305032286	0.065548115	4.653563	3.26E-06	5.96E-06	brown	-0.057082019	0.477642493		AT1G17280.2	UBC34	ubiquitin-conjugating enzyme 34	ubiquitin-conjugating enzyme E2, putative
Sapur.001G136400.1	3.656728857	-0.927935487	0.199455088	-4.65235	3.28E-06	6.00E-06	brown	-0.244197493	0.002055221	GO:0046872,GO:0000166	AT1G17260.1	AHA10	autoinhibited H(+)-ATPase isoform 10	plasma membrane H+-ATPase
Sapur.010G096800.2	56.4113954	0.327735978	0.070639451	4.63956	3.49E-06	6.38E-06	brown	0.002227394	0.977912453	GO:0005515,GO:0043161,GO:0006289,GO:0003684	AT5G38470.1	RAD23D	Rad23 UV excision repair protein family	UV excision repair protein RAD23, putative
Sapur.004G084100.1	12.12926519	-0.488854733	0.105574541	-4.63042	3.65E-06	6.65E-06	brown	-0.264202205	0.000826975	GO:0005524,GO:0051082,GO:0006457	AT3G02530.1		TCP-1/cpn60 chaperonin family protein	NA
Sapur.003G056000.3	30.70118185	-0.32603715	0.070873825	-4.60025	4.22E-06	7.67E-06	brown	0.021762757	0.786745202	GO:0016021	AT1G32400.3	TOM2A	tobamovirus multiplication 2A	tetraspanin family protein
Sapur.008G161900.2	1.55107641	-1.038590071	0.225879925	-4.59797	4.27E-06	7.75E-06	brown	-0.320200015	4.35E-05		AT4G15820.1			hypothetical protein
Sapur.011G042600.2	10.17651377	0.635527624	0.138726847	4.581144	4.62E-06	8.39E-06	brown	0.078548531	0.32814497		AT4G18470.1	SNI1	negative regulator of systemic acquired resistance (SNI1)	SNI1
Sapur.006G114500.1	2.978029054	-0.88368729	0.193360844	-4.57015	4.87E-06	8.83E-06	brown	-0.308969721	8.24E-05	GO:0006355,GO:0003700	AT5G21960.1		Integrase-type DNA-binding superfamily protein	NA

Sapur.T033100.1	0.319757142	-1.789409224	0.397521968	-4.50141	6.75E-06	1.21E-05	brown	-0.20265116	0.010915634	GO:0006284	AT3G07930.3		DNA glycosylase superfamily protein	NA
Sapur.018G010500.1	0.886512302	-1.605869041	0.357439258	-4.4927	7.03E-06	1.26E-05	brown	-0.318382955	4.83E-05	GO:0006508,GO:0004190	AT5G10770.1		Eukaryotic aspartyl protease family protein	aspartic proteinase nepenthesin protein, putative
Sapur.002G042400.1	1.390989945	-1.071202794	0.23843342	-4.49267	7.03E-06	1.26E-05	brown	-0.322243654	3.86E-05	GO:0016020,GO:0015031	AT2G31530.1	EMB2289,SCY2	SecY protein transport family protein	preprotein translocase subunit SecY
Sapur.15WG080100.1	1.370747514	-1.249684559	0.279640582	-4.4689	7.86E-06	1.41E-05	brown	-0.270244333	0.000619317	GO:0016857,GO:0005975	AT5G61410.1	EMB2728,RPE	D-ribulose-5-phosphate-3-epimerase	ribulose-5-phosphate 3-epimerase
Sapur.T187700.2	8.422462812	0.546192221	0.122924536	4.443313	8.86E-06	1.58E-05	brown	-0.116624511	0.145782248					hypothetical protein
Sapur.012G002400.4	2.058842303	-1.213925641	0.273541051	-4.43782	9.09E-06	1.62E-05	brown	-0.248142713	0.001727159	GO:0000160,GO:0005515	AT5G24470.1	APRR5,PRR5	pseudo-response regulator 5	PRR response regulator
Sapur.009G093500.2	2.638594997	0.939984683	0.211861469	4.436789	9.13E-06	1.63E-05	brown	-0.170726222	0.032531367	GO:0016021	AT2G21600.1	ATRER1B,RER1B	endoplasmatic reticulum retrieval protein 1B	RER1A protein
Sapur.009G087600.4	3.080077098	-0.922788198	0.208728592	-4.421	9.82E-06	1.75E-05	brown	-0.225389586	0.00453731		AT3G18890.1		NAD(P)-binding Rossmann-fold superfamily protein	NAD-dependent epimerase/dehydratase family protein
Sapur.011G012200.4	2.544744014	-0.816227767	0.184644299	-4.42054	9.85E-06	1.75E-05	brown	-0.184124168	0.020976592		AT4G22290.1		Ubiquitin-specific protease family C19-related protein	ubiquitin thiolesterase, putative
Sapur.003G043800.1	7.942038444	-1.054347199	0.238600636	-4.41888	9.92E-06	1.77E-05	brown	-0.378499979	1.02E-06	GO:0006412,GO:0003735	AT1G70190.1		Ribosomal protein L7/L12, oligomerisation;Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like	50S ribosomal protein L7/L12, putative
Sapur.005G031200.3	3.520317682	0.82708223	0.18786499	4.402535	1.07E-05	1.90E-05	brown	0.129219897	0.106754943	GO:0055085,GO:0016021	AT1G08930.1	ERD6	Major facilitator superfamily protein	NA
Sapur.003G116600.3	0.478811497	-1.656883616	0.378031441	-4.38293	1.17E-05	2.08E-05	brown	-0.189630914	0.017373531	GO:0006221,GO:0003883	AT1G30820.1		CTP synthase family protein	CTP synthase
Sapur.003G058000.1	13.28778437	-0.417422196	0.095427641	-4.37423	1.22E-05	2.16E-05	brown	-0.283851548	0.000315028		AT1G32540.3	LOL1	lsd one like 1	zinc finger, LSD1 subclass protein
Sapur.002G022900.1	27.62691115	-0.656068756	0.150119842	-4.3703	1.24E-05	2.20E-05	brown	-0.309738958	7.90E-05	GO:0055114,GO:0050660,GO:0016491,GO:0019139,GO:0009690	AT1G75450.1	ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	cytokinin oxidase/dehydrogenase
Sapur.006G145900.1	35.93461331	-0.617078297	0.141236118	-4.36913	1.25E-05	2.21E-05	brown	-0.394807804	3.11E-07	GO:0016758,GO:0008152	AT5G54010.1		UDP-Glycosyltransferase superfamily protein	UDP rhamnose:anthocyanidin-3-glucoside rhamnosyltransferase, putative
Sapur.010G111900.7	3.223424185	0.755547297	0.173724732	4.349106	1.37E-05	2.42E-05	brown	-0.081608864	0.309590942	GO:0005515	AT5G49430.1		WD40/YVTN repeat-like-containing domain;Bromodomain	cytochrome cd1-nitrite reductase-like, carboxy-terminal heme protein d1, putative
Sapur.017G081500.1	1.3302372	-1.09216436	0.252188538	-4.33075	1.49E-05	2.62E-05	brown	-0.331275425	2.26E-05	GO:0006355,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AT3G02310.1	AGL4,SEP2	K-box region and MADS-box transcription factor family protein	MIKC MADS-box transcription factor SEPALLATA protein
Sapur.005G057600.1	10.43185954	-0.528956609	0.122159983	-4.33003	1.49E-05	2.63E-05	brown	-0.334507318	1.85E-05		AT5G22890.1		C2H2 and C2HC zinc fingers superfamily protein	NA
Sapur.005G052200.1	28.09507646	0.747625803	0.173308671	4.31384	1.60E-05	2.82E-05	brown	0.123807144	0.122381999	GO:0006629	AT3G52430.1	ATPAD4,PAD4	alpha/beta-Hydrolases superfamily protein	NA
Sapur.002G203900.3	2.47360193	-0.802709394	0.186164348	-4.31183	1.62E-05	2.85E-05	brown	-0.129433365	0.106172353	GO:0005975,GO:0004553	AT5G42720.1		Glycosyl hydrolase family 17 protein	glucan endo-1%2C3-beta-glucosidase, putative
Sapur.008G011700.3	7.717793757	-0.48405025	0.112441695	-4.3049	1.67E-05	2.94E-05	brown	-0.176176723	0.027304203	GO:0007034	AT5G04850.2	VPS60.2	SNF7 family protein	charged multivesicular body protein
Sapur.010G135600.4	19.14282922	-0.480816834	0.111995587	-4.29318	1.76E-05	3.09E-05	brown	-0.183074815	0.021731867		AT1G79380.1		Ca(2)-dependent phospholipid-binding protein (Copine) family	E3 ubiquitin-protein ligase RGLG1
Sapur.003G072100.5	1.037042421	-1.263250408	0.294293436	-4.29249	1.77E-05	3.10E-05	brown	-0.042508134	0.597077305	GO:0005089	AT1G31650.1	ATROPGEF14,ROPGEF14	RHO guanyl-nucleotide exchange factor 14	Rop guanine nucleotide exchange factor, putative
Sapur.017G100600.2	22.06474372	0.477585506	0.112054882	4.262068	2.03E-05	3.54E-05	brown	0.314639407	5.99E-05		AT3G14460.1		LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.002G123000.1	1.858222461	-1.197715965	0.282684249	-4.23694	2.27E-05	3.95E-05	brown	-0.180126826	0.023980333	GO:0005515,GO:0006950,GO:0006355	AT3G61050.1	NTMC2T4,NTMC2TYPE4	Calcium-dependent lipid-binding (CaLB domain) family protein	integral membrane single C2 domain protein
Sapur.004G114400.3	2.42164504	0.741406978	0.176340618	4.204403	2.62E-05	4.55E-05	brown	-0.063922497	0.426404114	GO:0048015,GO:0046854	AT1G49340.2	ATPI4K ALPHA	Phosphatidylinositol 3- and 4-kinase family protein	phosphatidylinositol 4-kinase
Sapur.018G003700.1	19.1484868	-0.470351992	0.111914113	-4.20279	2.64E-05	4.58E-05	brown	-0.315732719	5.62E-05		AT1G10330.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.014G036800.1	1.461631965	-1.33750387	0.31843738	-4.20021	2.67E-05	4.63E-05	brown	-0.283700925	0.000317454	GO:0043565,GO:0006355,GO:0003700				NA
Sapur.009G130000.3	3.972367469	-0.798009365	0.19040035	-4.19122	2.77E-05	4.82E-05	brown	-0.071910395	0.370790412	GO:0016567,GO:0004842,GO:0005515	AT5G42340.1	PUB15	Plant U-Box 15	E3 ubiquitin ligase PUB14, putative
Sapur.017G014800.1	3.587894307	-0.709063572	0.171273579	-4.13995	3.47E-05	6.00E-05	brown	-0.301534745	0.00012417		AT3G60470.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.004G048300.1	18.75616123	-0.394372353	0.09527154	-4.13946	3.48E-05	6.01E-05	brown	-0.297102321	0.000157701		AT2G25720.1			hypothetical protein
Sapur.010G107100.1	18.23783993	-0.629730549	0.153421027	-4.10459	4.05E-05	6.96E-05	brown	-0.319593646	4.50E-05	GO:0016758,GO:0008152	AT5G03490.1		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase, putative
Sapur.012G003100.1	67.77393962	-0.376552675	0.091740157	-4.10456	4.05E-05	6.96E-05	brown	-0.294882834	0.000177499		AT3G49470.1	NACA2	nascent polypeptide-associated complex subunit alpha-like protein 2	nascent polypeptide-associated complex subunit alpha-like protein, putative
Sapur.004G146000.2	0.772701327	-1.101932422	0.268679387	-4.10129	4.11E-05	7.06E-05	brown	-0.371000519	1.72E-06	GO:0008270,GO:0003676	AT3G43590.1		zinc knuckle (CCHC-type) family protein	NA
Sapur.003G050500.1	135.3247104	-0.969769352	0.237363974	-4.08558	4.40E-05	7.54E-05	brown	-0.316356685	5.43E-05	GO:0016747	AT5G02890.1		HXXXD-type acyl-transferase family protein	transferase family protein
Sapur.014G018900.2	1.261653896	-0.996659836	0.244762323	-4.07195	4.66E-05	7.99E-05	brown	-0.13774921	0.085357723		AT4G33350.1		Tic22-like family protein	Tic22 family import component
Sapur.011G036300.2	1.927274057	-0.770390191	0.190058779	-4.05343	5.05E-05	8.63E-05	brown	-0.189457446	0.017478252		AT2G33770.1	ATUBC24,PHO2,UBC24	phosphate 2	ubiquitin-conjugating enzyme
Sapur.001G108700.5	3.104246431	-0.568358876	0.140761621	-4.03774	5.40E-05	9.22E-05	brown	-0.037887817	0.637563208		AT4G19070.1		Putative membrane lipoprotein	cadmium-induced protein AS8, putative
Sapur.005G175300.5	15.96500688	0.353798859	0.0876688	4.03563	5.45E-05	9.30E-05	brown	-0.081608864	0.309590942		AT4G19540.1	INDL	IND1(iron-sulfur protein required for NADH dehydrogenase)-like	MRP-like protein (ATP/GTP-binding protein)
Sapur.001G118600.1	0.46858472	-1.550200619	0.38477996	-4.0288	5.61E-05	9.56E-05	brown	-0.363843331	2.81E-06		AT4G17800.1		Predicted AT-hook DNA-binding family protein	AT-hook motif nuclear localized protein, putative
Sapur.010G204900.1	1.101899809	-1.18861348	0.29663541	-4.00698	6.15E-05	0.000104679	brown	-0.237374836	0.002758557		AT1G16810.2			7-dehydrocholesterol reductase, putative
Sapur.008G029900.1	130.3711588	-0.313751953	0.078556181	-3.99398	6.50E-05	0.000110422	brown	-0.265834517	0.000765337		AT5G19290.1		alpha/beta-Hydrolases superfamily protein	esterase/lipase/thioesterase family protein
Sapur.009G059600.2	1.115386731	-1.18087966	0.297791034	-3.96546	7.33E-05	0.000124048	brown	-0.280523523	0.000372855	GO:0050662,GO:0003824	AT5G58490.1		NAD(P)-binding Rossmann-fold superfamily protein	cinnamoyl-CoA reductase
Sapur.002G079400.3	0.86955034	-1.273145542	0.321922623	-3.95482	7.66E-05	0.00012955	brown	-0.207135622	0.009242419		AT4G08980.2	FBW2	F-BOX WITH WD-40 2	F-box protein, putative
Sapur.018G007500.1	3.00355458	-0.689658599	0.174457154	-3.95317	7.71E-05	0.000130427	brown	-0.290754379	0.000220611	GO:0008270,GO:0003676	AT4G31580.2	RSZP22,SRZ-22,SRZ22	serine/arginine-rich 22	RNA recognition motif 1 in vertebrate serine/arginine-rich splicing factor
Sapur.003G145200.1	2.284950159	-0.704660664	0.179162911	-3.93307	8.39E-05	0.000141471	brown	-0.184219445	0.020909151		AT3G11450.1		DnaJ domain ;Myb-like DNA-binding domain	DnaJ family C protein
Sapur.002G102500.4	9.24055636	0.518576404	0.132193771	3.922851	8.75E-05	0.000147476	brown	-0.074532331	0.353555021		AT5G42900.1	COR27	cold regulated gene 27	transmembrane protein, putative
Sapur.016G104100.6	0.85270654	-1.053652957	0.268652964	-3.92199	8.78E-05	0.000147992	brown	-0.078265667	0.329895244	GO:0016021,GO:0004659	AT3G51820.1	ATG4,CHLG,G4	UbiA prenyltransferase family protein	bacteriochlorophyll synthase, putative
Sapur.016G079600.1	72.31057625	0.318870106	0.081497981	3.912614	9.13E-05	0.000153669	brown	0.258176053	0.001096136	GO:0005515	AT5G02790.1	GSTL3	Glutathione S-transferase family protein	glutathione S-transferase
Sapur.019G035100.1	0.874943372	-1.351663059	0.350358884	-3.85794	0.000114347	0.000191577	brown	-0.231295527	0.003561516	GO:0045454	AT3G03860.1	APRL5,ATAPRL5	APR-like 5	5'-adenylylsulfate reductase-like protein, putative
Sapur.006G143900.2	0.542394309	1.313965778	0.343071405	3.830007	0.00012814	0.000214067	brown	-0.006746778	0.933165918	GO:0003968	AT2G19910.1		RNA-dependent RNA polymerase family protein	NA
Sapur.T091600.5	32.94052023	0.25547032	0.067099879	3.807314	0.000140484	0.000234121	brown	-0.169951101	0.033339589		AT3G59480.1		pfkB-like carbohydrate kinase family protein	pfkB-type carbohydrate kinase family protein
Sapur.15WG013600.1	1.971832146	1.107588368	0.291403201	3.800879	0.000144184	0.000240141	brown	0.265436918	0.000779948		AT5G53110.1		RING/U-box superfamily protein	NA
Sapur.002G052200.1	3.616635121	-0.676020215	0.178154736	-3.79457	0.000147901	0.000246085	brown	-0.257379947	0.00113715	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G43170.8	ARP1,emb2207,RP1,RPL3A	ribosomal protein 1	60S ribosomal protein L3
Sapur.017G100900.1	25.98269838	0.3939058	0.103834564	3.79359	0.000148485	0.000247025	brown	0.214193814	0.007065715		AT3G14470.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.006G022900.1	0.513161102	-1.447354088	0.381823134	-3.79064	0.00015026	0.000249921	brown	-0.320084027	4.38E-05	GO:0016021	AT5G19750.1		Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	Mpv17/PMP22 family protein
Sapur.013G029600.1	1.45251863	-0.997525823	0.263287489	-3.78873	0.000151418	0.000251785	brown	-0.233158326	0.003295565		AT5G27240.1		DNAJ heat shock N-terminal domain-containing protein	DnaJ heat shock amino-terminal domain protein, putative
Sapur.016G290900.3	3.358900244	-0.551018882	0.145788939	-3.77957	0.000157102	0.000260974	brown	0.070566546	0.379821058	GO:0055085,GO:0016021,GO:0008324,GO:0006812	AT3G58810.1	ATMTP3.ATMTPA2.MTP3.M	metal tolerance protein A2	metal tolerance protein
Sapur.009G003800.1	19.06978473	-0.375304956	0.099335225	-3.77817	0.000157988	0.000262406	brown	-0.2616617	0.00093203		AT5G57620.1	AtMYB36,MYB36	myb domain protein 36	transcription factor MYBJ7
Sapur.007G087100.3	2.630770261	0.797844041	0.212688698	3.751229	0.00017597	0.000291409	brown	-0.110658643	0.167675968	GO:0006468,GO:0004672	AT4G33950.1	ATOST1.OST1.P44.SNRK2-6	Protein kinase superfamily protein	Serine/Threonine-kinase SAPK2
Sapur.002G159600.4	4.039808911	0.762798426	0.203761435	3.743586	0.000181413	0.000300152	brown	-0.127292237	0.112130118	GO:0016829,GO:0006099	AT2G47510.2	FUM1	fumarase 1	NA
Sapur.010G193700.2	0.855008656	1.304231387	0.348770602	3.739511	0.000184379	0.000304907	brown	-0.081608864	0.309590942	GO:0006310,GO:0006281,GO:0006260,GO:0005634,GO:0003677	AT4G18590.1		Nucleic acid-binding, OB-fold-like protein	replication protein A 14 kDa subunit A
Sapur.013G101400.1	18.79353124	-0.321892447	0.086378485	-3.72654	0.00019413	0.0003206	brown	-0.281907202	0.000347712		AT1G35430.1			NA
Sapur.006G161000.1	152.5821932	-0.600393276	0.161385521	-3.72024	0.000199032	0.000328367	brown	-0.248468021	0.001702361	GO:0005515	AT2G44130.1		Galactose oxidase/kelch repeat superfamily protein	F-box protein
Sapur.013G052800.1	1.378723747	-0.775115667	0.208398224	-3.7194	0.000199699	0.000329403	brown	0.002894256	0.971302128		AT5G30495.1		Fcf2 pre-rRNA processing protein	NA
Sapur.009G121800.5	2.621507843	-0.584748138	0.157506022	-3.71254	0.000205186	0.000338132	brown	0.006697046	0.933657435		AT5G20930.1	TSL	Protein kinase superfamily protein	tousled-like kinase
Sapur.001G117500.1	1811.354939	-0.406438532	0.110062913	-3.69278	0.000221813	0.00036466	brown	-0.237103481	0.002790573					NA
Sapur.013G142600.6	3.22096519	-0.664113639	0.179932636	-3.6909	0.000223461	0.000367205	brown	-0.276015799	0.000466909		AT5G01960.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.009G036200.4	1.461114282	0.8050036	0.218445499	3.685146	0.000228571	0.000375398	brown	0.078548531	0.32814497	GO:0016021,GO:0015693,GO:0015095	AT1G34470.1		Protein of unknown function (DUF803)	Non-imprinted in prader-willi/angelman syndrome region protein, putative
Sapur.15WG090000.1	190.5550015	0.153294729	0.041721366	3.67425	0.000238549	0.0003913	brown	0.260415172	0.000987934	GO:0016567,GO:0004842,GO:0005515	AT5G65200.1	ATPUB38,PUB38	plant U-box 38	U-box protein
Sapur.017G078000.1	2.255303148	-1.142530897	0.311822724	-3.66404	0.000248268	0.000406556	brown	-0.270754674	0.000604189	GO:0003676	AT2G21660.1	ATGRP7.CCR2.GR-RBP7.GRI	cold, circadian rhythm, and rna binding 2	NA
Sapur.008G034100.1	0.780153513	-1.311936795	0.35909372	-3.65347	0.000258724	0.000423113	brown	-0.194722734	0.014533032		AT5G13610.1		Protein of unknown function (DUF155)	plant/MSH12-7 protein
Sapur.001G104200.3	14.84785698	-0.288670208	0.079160783	-3.64663	0.0002657	0.000434157	brown	-0.14527568	0.069463057	GO:0003723,GO:0003676,GO:0045131,GO:0000398	AT5G51300.3		splicing factor-related	zinc finger protein, putative
Sapur.15WG108400.3	3.184038937	-0.624020671	0.171205441	-3.64486	0.000267532	0.000437064	brown	-0.115551012	0.149553048	GO:0008234,GO:0006508	AT3G48480.1		Cysteine proteinases superfamily protein	sentrin/sumo-specific protease, putative
Sapur.T053800.1	9.272459368	-0.456394813	0.125346489	-3.64107	0.000271512	0.000443303	brown	-0.182766287	0.021958343	GO:0005515,GO:0006468,GO:0004672	AT3G14840.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.013G100200.2	1.536315608	-0.874595898	0.241161451	-3.6266	0.000287179	0.000468189	brown	-0.285135641	0.00029503	GO:0006508,GO:0004176,GO:0030163,GO:0005524,GO:0004252	AT1G35340.1		ATP-dependent protease La (LON) domain protein	NA
Sapur.016G308600.3	6.147555429	0.465150132	0.128280268	3.626046	0.000287794	0.000469123	brown	-0.081608864	0.309590942		AT1G55690.3		Sec14p-like phosphatidylinositol transfer family protein	SEC14 cytosolic factor family protein
Sapur.001G148100.2	0.530222929	-1.344373299	0.371802145	-3.61583	0.000299387	0.000487563	brown	-0.318785034	4.72E-05	GO:0006355,GO:0005634,GO:0005524,GO:0032502,GO:0006351	AT3G13960.1	AtGRF5,GRF5	growth-regulating factor 5	QLQ protein
Sapur.016G139500.1	0.461348913	-1.707046087	0.47322998	-3.60722	0.000309492	0.000503672	brown	-0.2052388	0.009920296	GO:0051536,GO:0009228	AT2G29630.2	PY,THIC	thiaminC	thiamine biosynthesis protein ThiC
Sapur.002G064100.2	0.562538888	-1.213370349	0.336858662	-3.60202	0.000315759	0.000513517	brown	-0.26214677	0.000911072	GO:0005515	AT1G21700.1	ATSWI3C,CHB4,SWI3C	SWITCH/sucrose nonfermenting 3C	chromatin remodeling complex subunit
Sapur.006G182900.3	7.095974842	-0.502122615	0.139433002	-3.60117	0.000316782	0.000515157	brown	-0.1947537	0.014517079	GO:0016558,GO:0008270,GO:0007031,GO:0005779,GO:0005515	AT2G26350.1	ATPEX10,PEX10	peroxin 10	peroxisome biogenesis factor 10
Sapur.004G151200.1	1.277821933	-0.940567032	0.26131146	-3.59941	0.00031894	0.000518615	brown	-0.273371934	0.00053182	GO:0006355,GO:0005667,GO:0003700	AT5G22220.2	ATE2FB,E2F1,E2FB	E2F transcription factor 1	transcription factor E2F
Sapur.004G098000.2	1.074637376	-0.931245887	0.259112321	-3.59399	0.000325658	0.000529383	brown	-0.259673501	0.001022638	GO:0004045	AT5G38290.2		Peptidyl-tRNA hydrolase family protein	group IIB intron splicing facilitator CRS2
Sapur.003G005300.3	5.77541057	-0.625500332	0.174066204	-3.59346	0.000326313	0.000530395	brown	-0.069154573	0.389452387	GO:0003723	AT4G25880.1	APUM6,PUM6	pumilio 6	pumilio domain protein
Sapur.004G121900.2	17.7305993	-0.326987172	0.091129312	-3.58817	0.000333011	0.000540857	brown	-0.267175117	0.000717904	GO:0008270,GO:0003676	AT1G75560.1		zinc knuckle (CCHC-type) family protein	zinc knuckle protein
Sapur.005G101200.3	16.96953321	-0.494746069	0.137986986	-3.58545	0.000336492	0.000546322	brown	-0.099173288	0.216549061	GO:0003677	AT4G36740.1	ATHB40,HB-5,HB40	homeobox protein 40	homeobox leucine zipper protein ATHB-40
Sapur.007G006000.1	1.691472545	-1.191352114	0.332673964	-3.58114	0.000342098	0.000555234	brown	-0.245597401	0.001932836		AT3G49690.1	ATMYB84,MYB84,RAX3	myb domain protein 84	R2R3-Myb transcription factor MYB1.1
Sapur.008G085000.1	516.688175	-0.10883374	0.03049219	-3.56923	0.000358027	0.000580461	brown	-0.287736545	0.000258081		AT5G49400.1		zinc knuckle (CCHC-type) family protein	zinc knuckle protein
Sapur.001G062800.1	1.117228872	-1.01233648	0.284412937	-3.55939	0.000371718	0.000602125	brown	-0.21190621	0.007715182					NA
Sapur.016G283400.1	1.142133024	-0.792989423	0.223391144	-3.54978	0.000385553	0.000623742	brown	-0.284866382	0.000299123	GO:0005515	AT1G17170.1	ATGSTU24,GST,GSTU24	glutathione S-transferase TAU 24	tau class glutathione transferase GSTU8
Sapur.004G065600.1	287.998343	0.183544498	0.05214487	3.519896	0.000431717	0.000695974	brown	0.228874574	0.003935996		AT5G23530.1	AtCXE18,CXE18	carboxyesterase 18	neutral cholesterol ester hydrolase
Sapur.009G058900.1	2.34564911	-0.650526015	0.185328438	-3.51013	0.000447896	0.000721353	brown	-0.273940395	0.000517198	GO:0006468,GO:0004672	AT5G45840.2		Leucine-rich repeat protein kinase family protein	Serine/Threonine kinase domain protein
Sapur.005G166300.1	3.615039124	-0.564199328	0.160736788	-3.51008	0.000447968	0.000721435	brown	-0.217528093	0.006206102	GO:0008380,GO:0005681	AT1G03140.1		splicing factor Prp18 family protein	splicing factor Prp18 family protein
Sapur.009G020700.2	4.844941869	-0.412630524	0.11973165	-3.44629	0.000568331	0.000909428	brown	-0.267771193	0.000697696	GO:0005622,GO:0003779,GO:0030042,GO:0015629	AT5G59890.1	ADF4,ATADF4	actin depolymerizing factor 4	actin-depolymerizing factor
Sapur.008G046800.2	21.6324154	-0.400636213	0.116334397	-3.44383	0.00057353	0.000917526	brown	-0.261504847	0.000938901	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G74270.1		Ribosomal protein L35Ae family protein	60S ribosomal protein L35a
Sapur.010G135700.3	7.223205322	-0.360508822	0.106003397	-3.40092	0.000671601	0.001069246	brown	-0.178463968	0.02533464	GO:0005515,GO:0006355	AT1G79350.1	EMB1135	RING/FYVE/PHD zinc finger superfamily protein	strawberry notch-like protein
Sapur.005G190600.3	3.715589996	0.456059787	0.134901991	3.380675	0.00072308	0.001148773	brown	-0.081608864	0.309590942		AT2G28305.1	ATLOG1,LOG1	Putative lysine decarboxylase family protein	cytokinin riboside 5'-monophosphate phosphoribohydrolase
Sapur.009G032600.1	168.5810555	-0.227438208	0.06744936	-3.37198	0.000746286	0.001184446	brown	-0.272741073	0.000548492		AT2G29660.1		zinc finger (C2H2 type) family protein	zinc finger protein, putative
Sapur.016G080300.2	53.31223302	0.26486631	0.079129439	3.347254	0.000816165	0.001291694	brown	-0.01949924	0.808473797		AT3G09600.1		Homeodomain-like superfamily protein	MYB transcription factor
Sapur.002G080400.4	0.31536684	-1.304572692	0.390572811	-3.34015	0.000837324	0.001324296	brown	-0.081608864	0.309590942	GO:0006418,GO:0005524,GO:0004812,GO:0000166,GO:0006434,GO:0005737,GO:000482	AT1G11870.2	ATSRS,OVA7,SRS	Seryl-tRNA synthetase	seryl-tRNA synthetase/serine-tRNA ligase, putative
Sapur.005G057900.1	0.566381489	-1.987053121	0.596894281	-3.32899	0.000871626	0.001376374	brown	-0.251371661	0.001494967		AT1G34670.1	AtMYB93,MYB93	myb domain protein 93	Myb-like DNA-binding domain protein
Sapur.008G128700.1	0.83606707	-1.174763855	0.354358352	-3.31519	0.000915822	0.001443819	brown	-0.19916924	0.012393142		AT3G22910.1		ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	NA
Sapur.019G011900.1	4.656677847	-0.491370666	0.148252843	-3.31441	0.000918362	0.001447627	brown	-0.219092781	0.005835857	GO:0007165,GO:0005515,GO:0043531	AT5G36930.1		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.010G194100.1	33.4704998	-0.293855311	0.088670462	-3.31402	0.000919663	0.00144953	brown	-0.242532215	0.002209949		AT3G54290.1			hemerythrin HHE cation-binding domain protein
Sapur.010G019600.3	1.490474537	-0.692174535	0.209171866	-3.30912	0.000935901	0.001474281	brown	-0.115783338	0.148730788		AT5G37190.1	CIP4	COP1-interacting protein 4	hypothetical protein
Sapur.010G066000.1	0.936988362	-1.065435503	0.322184744	-3.30691	0.000943317	0.001485679	brown	-0.190132578	0.017073741		AT1G04200.1			dyggve-melchior-clausen syndrome protein
Sapur.009G018800.2	2.816250188	-0.628969186	0.190283892	-3.30543	0.000948324	0.001493209	brown	-0.241068983	0.002354551	GO:0031011	AT3G45830.1			nuclear factor kappa-B-binding-like protein, putative
Sapur.002G035800.6	1.262319719	-0.786082315	0.238205581	-3.30002	0.000966792	0.001521564	brown	-0.081608864	0.309590942	GO:0006457,GO:0003755,GO:0000413	AT3G63400.3		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.003G038200.1	5.275691909	0.50008606	0.151588151	3.298979	0.000970373	0.001526765	brown	0.256713652	0.001172552		AT1G72510.2		Protein of unknown function (DUF1677)	DUF1677 family protein
Sapur.016G108300.1	46.5518539	0.240176112	0.072863889	3.29623	0.00097919	0.001541197	brown	0.222833157	0.005029493		AT2G38310.1	PYL4,RCAR10	PYR1-like 4	abscisic acid receptor PYL4
Sapur.018G119000.5	14.44699778	-0.328645578	0.100308991	-3.27633	0.001051648	0.001651106	brown	-0.0181084	0.82189923		AT5G53530.1	VPS26A	vacuolar protein sorting 26A	vacuolar protein sorting-associated protein
Sapur.018G060300.1	303.9815549	-0.130450147	0.039858412	-3.27284	0.001064733	0.001670936	brown	-0.27646753	0.00045658	GO:0006468,GO:0004672,GO:0005524	AT4G28980.2	CAK1AT,CDKF;1	CDK-activating kinase 1AT	cyclin-dependent kinase
Sapur.019G088400.1	3.136733059	0.566786706	0.173435729	3.267993	0.001083131	0.001698842	brown	0.213483064	0.007262093	GO:0046983,GO:0008171	AT4G35160.1		O-methyltransferase family protein	orcinol O-methyltransferase, putative
Sapur.018G045200.1	1.442245337	-0.84216292	0.25784413	-3.26617	0.001090125	0.001709407	brown	-0.223863517	0.004825643		AT2G34357.1		ARM repeat superfamily protein	RRP12-like protein
Sapur.008G160800.1	7.116001799	-0.368290938	0.112898024	-3.26216	0.001105684	0.001732818	brown	-0.244226912	0.002052578		AT3G16720.1	ATL2,TL2	TOXICOS EN LEVADURA 2	RING-H2 finger protein ATL2
Sapur.019G011800.1	31.48028425	-0.207123641	0.063514532	-3.26104	0.001110031	0.001739383	brown	-0.212307514	0.007597554	GO:0055114,GO:0016491,GO:0008270	AT5G63620.1		GroES-like zinc-binding alcohol dehydrogenase family protein	NA
Sapur.006G057600.1	88.39828027	0.552347498	0.170118736	3.246835	0.001166959	0.001826339	brown	0.227865281	0.004102309	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	AT4G25810.1	XTH23,XTR6	xyloglucan endotransglycosylase 6	xyloglucan endotransglycosylase/hydrolase
Sapur.013G074000.2	23.80040176	0.510635207	0.157278698	3.24669	0.001167554	0.001827183	brown	0.410183041	9.55E-08					NA
Sapur.016G095300.3	0.345409678	-1.271960957	0.392189117	-3.24323	0.001181812	0.001848972	brown	-0.17944497	0.024527956		AT2G38010.1		Neutral/alkaline non-lysosomal ceramidase	neutral/alkaline nonlysosomal ceramidase
Sapur.014G025700.5	40.15239405	0.222858686	0.06881971	3.238297	0.001202454	0.001879754	brown	-0.094099345	0.24109972	GO:0055085,GO:0016020,GO:0006810,GO:0005215	AT2G26510.2	PDE135	Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.008G124700.1	0.939523506	-0.998129194	0.311083395	-3.20856	0.001334023	0.00207973	brown	-0.148366489	0.063675066		AT2G32090.1		Lactoylglutathione lyase / glyoxalase I family protein	lactoylglutathione lyase-like lyase
Sapur.009G076000.6	1.689610325	-0.641771468	0.200215877	-3.2054	0.001348761	0.002101716	brown	-0.260021413	0.001006222		AT2G01640.1			ribosome biogenesis protein SLX9
Sapur.008G163100.2	0.886536906	-1.139063761	0.355474543	-3.20435	0.001353693	0.002109102	brown	-0.188101716	0.018315741		AT4G15820.1			NA
Sapur.017G102200.4	0.44662427	-1.109387406	0.350324174	-3.16675	0.001541553	0.002392442	brown	-0.081608864	0.309590942	GO:0016742,GO:0009058	AT1G66520.1	pde194	formyltransferase, putative	methionyl-tRNA formyltransferase
Sapur.T079400.1	1.544119046	-0.608923827	0.192343798	-3.16581	0.00154652	0.002399813	brown	-0.181478963	0.022925381	GO:0005509	AT5G42380.1	CML37,CML39	calmodulin like 37	NA
Sapur.009G009800.4	27.80125354	0.242301873	0.076640562	3.161536	0.001569396	0.002434853	brown	-0.042149077	0.600181773	GO:0055114,GO:0016627,GO:0003995,GO:0050660,GO:0008152	AT3G45300.1	ATIVD,IVD,IVDH	isovaleryl-CoA-dehydrogenase	isovaleryl-CoA dehydrogenase
Sapur.004G173900.4	0.607278614	-0.99753426	0.315845138	-3.1583	0.001586912	0.00246105	brown	-0.081608864	0.309590942	GO:0006468,GO:0004672,GO:0005515	AT5G01950.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.016G113700.1	820.6585246	-0.099106096	0.031624558	-3.13383	0.001725388	0.00266923	brown	-0.261002294	0.000961231	GO:0016020,GO:0008375	AT5G22070.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	core-2/I-branching enzyme
Sapur.013G006600.1	0.432944109	-1.315797498	0.422030542	-3.11778	0.001822201	0.002813607	brown	-0.306005711	9.72E-05		AT1G09320.1		agenet domain-containing protein	agenet domain protein
Sapur.001G168800.2	0.472084415	-1.180869159	0.380310331	-3.10501	0.001902696	0.002933241	brown	-0.081608864	0.309590942		AT1G36050.2		Endoplasmic reticulum vesicle transporter protein	endoplasmic reticulum vesicle transporter protein
Sapur.008G029800.3	0.74339287	-1.19223566	0.387082229	-3.08006	0.002069604	0.003184169	brown	-0.249267172	0.001642813		AT5G49015.1		Expressed protein	hypothetical protein
Sapur.001G090800.5	6.293392917	-0.363374153	0.118372041	-3.06976	0.002142285	0.003292621	brown	-0.076434331	0.341371454		AT4G11790.1		Pleckstrin homology (PH) domain superfamily protein	RanBP1 domain protein
Sapur.006G175900.1	1.777790456	-1.155450711	0.376482811	-3.06907	0.002147289	0.003300007	brown	-0.218369897	0.006004386		AT2G39370.1			NA
Sapur.018G091700.1	1.90486318	-0.545343921	0.178021623	-3.06336	0.002188682	0.00336159	brown	-0.266507522	0.000741176	GO:0031515,GO:0030488,GO:0016429	AT5G14600.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NA
Sapur.018G030600.2	1.078960362	-0.797021326	0.261106913	-3.05247	0.002269655	0.003482883	brown	-0.222854205	0.005025253		AT5G25630.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.001G090900.4	1.197167138	-0.857412369	0.281527895	-3.04557	0.002322412	0.003560702	brown	-0.081608864	0.309590942	GO:0006351,GO:0003899,GO:0003677	AT1G63020.1	NRPD1.NRPD1A.POL IVA.SD	nuclear RNA polymerase D1A	DNA-directed RNA polymerase
Sapur.016G308400.2	0.360963192	-1.334800512	0.440493684	-3.03024	0.00244361	0.00373994	brown	-0.32173988	3.97E-05		AT5G56140.1		RNA-binding KH domain-containing protein	nucleic acid-binding protein, putative
Sapur.008G086000.7	0.271562106	-1.36416814	0.451138416	-3.02384	0.002495925	0.003816116	brown	-0.267355151	0.000711744		AT4G16146.1		cAMP-regulated phosphoprotein 19-related protein	negatively light-regulated protein, putative
Sapur.003G093600.1	10.40679261	-0.512380662	0.170422824	-3.00653	0.002642514	0.00403446	brown	-0.266721223	0.000733652		AT1G63800.1	UBC5	ubiquitin-conjugating enzyme 5	ubiquitin-conjugating enzyme E2
Sapur.007G068100.2	0.288031467	-1.659603234	0.552007747	-3.00649	0.002642867	0.004034627	brown	-0.238148579	0.002669084	GO:0046983,GO:0003677,GO:0006355,GO:0005634,GO:0003700	AT5G23260.2	ABS,AGL32,TT16	K-box region and MADS-box transcription factor family protein	MADS-box DNA-binding domain transcription factor
Sapur.001G107900.2	16.1228671	0.34968901	0.116448449	3.002951	0.002673753	0.004079894	brown	-0.10345754	0.197250991	GO:0008168	AT4G19120.1	ERD3	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.001G146600.3	37.16662207	-0.224113234	0.074646401	-3.00233	0.002679203	0.004088022	brown	-0.042157239	0.600111122	GO:0016020,GO:0008233,GO:0006465	AT1G52600.1		Peptidase S24/S26A/S26B/S26C family protein	microsomal signal peptidase subunit
Sapur.008G005500.4	1.176232341	-0.748194657	0.249528387	-2.99844	0.0027137	0.004140468	brown	-0.192326932	0.015814639	GO:0006418,GO:0005524,GO:0004812,GO:0000166	AT2G33840.1		Tyrosyl-tRNA synthetase, class Ib, bacterial/mitochondrial	tyrosyl-tRNA synthetase
Sapur.003G068200.5	2.428740233	0.819558532	0.27405546	2.990484	0.002785355	0.004245096	brown	0.246990994	0.001817621					hypothetical protein
Sapur.019G031600.1	56.98618307	-0.511384456	0.171473215	-2.9823	0.002860921	0.004356651	brown	-0.221637064	0.005275777	GO:0016788	AT5G33370.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.013G099700.2	0.662104112	-0.91428095	0.306702459	-2.981	0.00287306	0.004374129	brown	-0.163311325	0.04098573		AT1G51965.1	ABO5	ABA Overly-Sensitive 5	PPR containing plant protein
Sapur.T079600.1	0.743285034	-0.806223775	0.271232598	-2.97244	0.002954389	0.004494019	brown	-0.297553445	0.000153938	GO:0005509	AT5G42380.1	CML37,CML39	calmodulin like 37	NA
Sapur.018G081100.1	0.299765077	-1.475159145	0.500658849	-2.94644	0.003214592	0.004874577	brown	-0.372464992	1.56E-06		AT3G43630.1		Vacuolar iron transporter (VIT) family protein	NA
Sapur.010G069200.1	0.487384656	-0.958512337	0.326407317	-2.93655	0.003318823	0.005027372	brown	-0.121078947	0.130902001	GO:0008017,GO:0007010	AT1G68060.1	ATMAP70-1,MAP70-1	microtubule-associated proteins 70-1	microtubule-associated protein 70-2
Sapur.005G207100.1	301.8792105	0.30078412	0.102658309	2.929954	0.003390122	0.005131809	brown	0.196109783	0.013833284		AT1G76560.1	CP12-3	CP12 domain-containing protein 3	CP12 domain protein
Sapur.010G186600.2	0.617480659	-1.048777466	0.35913166	-2.92031	0.003496781	0.005285764	brown	-0.25030536	0.001568289		AT3G52210.3		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase domain protein
Sapur.001G057100.1	1.403329703	-0.696292703	0.239385445	-2.90867	0.003629725	0.005478961	brown	-0.194663658	0.014563509		AT5G47860.1		Protein of unknown function (DUF1350)	plant/MCA23-20 protein
Sapur.005G206900.1	462.0478339	-0.108674847	0.037394186	-2.9062	0.003658518	0.005520912	brown	-0.21876003	0.005912901	GO:0046872,GO:0005634,GO:0003723	AT5G42820.1	ATU2AF35B,U2AF35B	Zinc finger C-x8-C-x5-C-x3-H type family protein	splicing factor U2af small protein
Sapur.002G068900.4	10.73798358	0.303905088	0.105012315	2.893995	0.003803745	0.005732483	brown	0.20161687	0.01133743		AT4G08240.1			hypothetical protein
Sapur.006G203200.1	0.566092801	-1.390005437	0.484256063	-2.87039	0.004099613	0.00616405	brown	-0.171473904	0.031767566	GO:0008270,GO:0005515	AT5G25560.1		CHY-type/CTCHY-type/RING-type Zinc finger protein	RING finger and CHY zinc finger protein
Sapur.004G059200.1	0.369880238	-1.247494423	0.435748874	-2.86287	0.004198166	0.006308215	brown	-0.329075942	2.57E-05		AT1G66140.1	ZFP4	zinc finger protein 4	zinc finger protein, putative
Sapur.001G183900.3	0.734282994	-0.982401067	0.346235432	-2.83738	0.004548561	0.006817071	brown	-0.031334039	0.696852582		AT1G09660.1		RNA-binding KH domain-containing protein	KH domain plant protein
Sapur.001G178900.1	4.714586735	-0.792672921	0.280718943	-2.82372	0.004746919	0.007103733	brown	-0.219133065	0.005826591	GO:0003677	AT1G13260.1	EDF4,RAV1	related to ABI3/VP1 1	B3 DNA-binding domain protein
Sapur.T190200.1	1.902711134	-0.488668046	0.174307563	-2.80348	0.005055412	0.007545588	brown	-0.244133806	0.002060952	GO:0055114,GO:0016491,GO:0045454	AT3G54660.1	ATGR2,EMB2360,GR	glutathione reductase	glutathione reductase
Sapur.008G155500.6	11.57193578	-0.225585568	0.080500766	-2.80228	0.005074304	0.007572078	brown	-0.115729365	0.148921509		AT1G70180.2		Sterile alpha motif (SAM) domain-containing protein	SAM domain protein, putative
Sapur.012G028800.1	39.99313939	-0.291761272	0.104229086	-2.79923	0.00512245	0.007639787	brown	-0.207977624	0.008954861		AT1G73500.1	ATMKK9,MKK9	MAP kinase kinase 9	MAP kinase kinase
Sapur.002G022500.2	5.703407318	0.363177683	0.129799548	2.797989	0.005142189	0.00766819	brown	0.179436277	0.024535006	GO:0055114,GO:0016491,GO:0016209,GO:0045454,GO:0015035,GO:0006662	AT1G45145.1	ATH5,ATTRX5,LIV1,TRX5	thioredoxin H-type 5	thioredoxin H-type protein
Sapur.005G019300.1	0.470330412	-1.431882337	0.512156646	-2.79579	0.005177306	0.007717772	brown	-0.192983393	0.015454036	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G27700.1		Ribosomal protein S21e	40S ribosomal protein S21
Sapur.003G122600.1	3.096015357	0.656131451	0.236756819	2.771331	0.005582769	0.008289315	brown	0.180704104	0.02352494		AT5G13210.1		Uncharacterised conserved protein UCP015417, vWA	NA
Sapur.002G173300.5	2.087342952	0.494200195	0.17865632	2.766206	0.005671269	0.008416941	brown	-0.081608864	0.309590942	GO:0046872	AT1G04990.1		Zinc finger C-x8-C-x5-C-x3-H type family protein	zinc finger CCCH domain protein
Sapur.013G038100.2	0.866403558	-0.787867512	0.284895015	-2.76547	0.005684151	0.008434925	brown	-0.33222114	2.13E-05		AT5G28840.1	GME	GDP-D-mannose 3\',5\'-epimerase	GDP-D-mannose-3'%2C5'-epimerase
Sapur.008G136000.1	11.34941357	-0.348890547	0.126295494	-2.76249	0.005736161	0.008510959	brown	-0.207900215	0.008980963		AT2G31160.1	LSH3	Protein of unknown function (DUF640)	DUF640 family protein
Sapur.15WG029400.1	5.843650466	-0.394896545	0.143380191	-2.75419	0.005883728	0.008719739	brown	-0.232641103	0.003367552		AT3G17930.1			NA
Sapur.017G017800.2	0.671381583	-0.815445594	0.296550968	-2.74977	0.005963794	0.008834044	brown	0.077982483	0.331653479		AT1G30890.1		Integral membrane HRF1 family protein	integral membrane HRF1 family protein
Sapur.013G108400.1	0.496847263	-1.043285253	0.381013717	-2.73818	0.00617797	0.009138202	brown	-0.200831842	0.011667073	GO:0005515	AT1G71840.1		transducin family protein / WD-40 repeat family protein	angio-associated migratory cell protein, putative
Sapur.013G056700.1	0.903466996	-0.884433125	0.323443395	-2.73443	0.00624885	0.009239738	brown	-0.176326699	0.027171164	GO:0005515,GO:0003723	AT5G17930.1		MIF4G domain-containing protein / MA3 domain-containing protein	MIF4G domain protein
Sapur.003G071100.1	0.418398122	-1.83447461	0.672060697	-2.72963	0.006340614	0.009370396	brown	-0.25807085	0.001101477	GO:0006508,GO:0004190	AT2G35615.1		Eukaryotic aspartyl protease family protein	aspartic proteinase nepenthesin protein
Sapur.001G117400.1	1808.745402	-0.358241968	0.131883585	-2.71635	0.006600611	0.009740267	brown	-0.174984547	0.028381679					NA
Sapur.008G124400.5	0.601402078	0.954003628	0.351777411	2.711952	0.006688818	0.009864709	brown	-0.081608864	0.309590942		AT4G14880.1	ATCYS-3A.CYTACS1.OASA1.	O-acetylserine (thiol) lyase (OAS-TL) isoform A1	cysteine synthase
Sapur.002G021300.3	0.85352513	0.715492969	0.263935835	2.71086	0.006710905	0.009895077	brown	-0.081608864	0.309590942	GO:0033179,GO:0015991,GO:0015078	AT4G39080.1	VHA-A3	vacuolar proton ATPase A3	vacuolar proton ATPase a3
Sapur.014G002600.1	0.592021336	-0.97905988	0.361970066	-2.70481	0.006834368	0.010073528	brown	-0.228658647	0.003971058	GO:0043531	AT3G14460.1		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.016G297500.1	1.216408308	-0.698997241	0.259588156	-2.69272	0.007087256	0.010433718	brown	-0.196502548	0.013640571		AT5G23530.1	AtCXE18,CXE18	carboxyesterase 18	acetyl esterase, putative
Sapur.009G016200.1	0.233257603	1.514491713	0.566709827	2.672429	0.007530433	0.011061536	brown	0.08708668	0.278127621	GO:0055114,GO:0016491	AT4G25300.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	flavonol synthase/flavanone 3-hydroxylase, putative
Sapur.005G021200.3	2.722696485	-0.414112499	0.155074996	-2.6704	0.00757606	0.011127075	brown	-0.132440013	0.09822921	GO:0019901,GO:0006355,GO:0000079,GO:0070985,GO:0016538,GO:0006351	AT5G27620.1	CYCH;1	cyclin H;1	cyclin H-1
Sapur.001G165500.3	1.316511779	0.609970279	0.228637758	2.667846	0.007633929	0.011207092	brown	0.042956499	0.593210842	GO:0008270,GO:0003676,GO:0016787,GO:0005524,GO:0003677	AT5G51280.1		DEAD-box protein abstrakt, putative	DEAD-box ATP-dependent RNA helicase, putative
Sapur.001G171200.1	1.037734109	-0.770196035	0.291039451	-2.64636	0.008136246	0.011913852	brown	-0.188326033	0.018174815	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G33430.1	ATBAK1.ATSERK3.BAK1.ELG	BRI1-associated receptor kinase	somatic embryogenesis receptor kinase
Sapur.014G062000.2	1.992655572	0.600298969	0.227269716	2.64135	0.008257625	0.012082494	brown	-0.035492717	0.658990221	GO:0009298,GO:0005737,GO:0004615	AT2G45790.1	ATPMM,PMM	phosphomannomutase	NA
Sapur.017G112400.2	0.409009605	1.310384732	0.496698571	2.638189	0.00833501	0.012189252	brown	-0.087483663	0.275934373	GO:0043531	AT3G14470.1		NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.003G002300.1	1.088778476	-0.713418705	0.270604119	-2.63639	0.008379271	0.012248564	brown	-0.146755074	0.066641418	GO:0005515,GO:0006414,GO:0003746	AT1G09640.1		Translation elongation factor EF1B, gamma chain	elongation factor 1-gamma 1
Sapur.007G100400.3	2.628179541	-0.43828381	0.16708095	-2.62318	0.008711262	0.012715874	brown	-0.064664627	0.421042876		AT4G05440.1	EDA35	temperature sensing protein-related	cell division cycle-like protein
Sapur.010G129800.2	18.76397642	-0.249474939	0.095589144	-2.60987	0.009057747	0.013202412	brown	0.027839374	0.729263094	GO:0016020,GO:0008378,GO:0006486,GO:0030246	AT1G26810.1	GALT1	galactosyltransferase1	beta-1%2C3-galactosyltransferase
Sapur.T171300.1	6.931467057	-0.479151819	0.183626232	-2.60939	0.009070472	0.013219794	brown	-0.13059337	0.103050032	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	AT4G14130.1	XTH15,XTR7	xyloglucan endotransglucosylase/hydrolase 15	xyloglucan endotransglycosylase/hydrolase
Sapur.016G086100.1	11.5423089	0.280847996	0.108271201	2.593931	0.00948856	0.013807021	brown	0.198196413	0.012836111		AT5G03330.1		Cysteine proteinases superfamily protein	cysteine-type peptidase
Sapur.016G127200.1	0.961802808	-0.781197022	0.302143594	-2.58552	0.009723343	0.014135196	brown	-0.18781003	0.018500407	GO:0031011	AT3G45830.1			nuclear factor kappa-B-binding-like protein, putative
Sapur.014G006200.2	0.321172289	-1.471083874	0.569740191	-2.58203	0.009822224	0.014273297	brown	-0.476035392	2.95E-10	GO:0005515	AT4G07410.1		Transducin family protein / WD-40 repeat family protein	NA
Sapur.016G004400.4	3.324124289	-0.396347155	0.15425773	-2.56938	0.010187985	0.014785968	brown	-0.054811046	0.495362204	GO:0006468,GO:0004672,GO:0005524	AT5G47750.1	D6PKL2,PK5	D6 protein kinase like 2	Serine/Threonine kinase domain protein
Sapur.003G125700.1	1.765874441	-0.543916433	0.211844057	-2.56753	0.010242528	0.014863822	brown	-0.222067914	0.005185846		AT5G41020.1		myb family transcription factor	Myb-like DNA-binding domain protein
Sapur.004G078700.3	7.415905786	-0.31913135	0.124314485	-2.56713	0.010254439	0.014879801	brown	-0.115749337	0.148850914		AT5G15930.1	PAM1	plant adhesion molecule 1	plant adhesion molecule protein
Sapur.004G074700.4	1.930315789	-0.671106156	0.261925871	-2.5622	0.010401176	0.015084784	brown	-0.056877273	0.479225854	GO:0008270,GO:0006281,GO:0006351,GO:0006289,GO:0000439	AT1G05055.1	ATGTF2H2,GTF2H2	general transcription factor II H2	general transcription factor IIH subunit
Sapur.016G182100.1	8.661440694	0.322956743	0.12627941	2.557477	0.010543439	0.015284406	brown	-0.042702753	0.595397613	GO:0016758,GO:0008152	AT4G34131.1	UGT73B3	UDP-glucosyl transferase 73B3	UDP-glucose:glucosyltransferase
Sapur.014G138700.1	1.536269275	-0.558754873	0.219503101	-2.54554	0.010910751	0.015791273	brown	-0.108585588	0.175829782	GO:0008270,GO:0005622,GO:0005515	AT3G07650.3	COL9	CONSTANS-like 9	zinc finger constans-like protein
Sapur.016G174600.3	1.744044944	0.46645482	0.184088677	2.533859	0.011281399	0.016304173	brown	-0.071712452	0.372112234	GO:0007264,GO:0005525	AT3G49870.1	ARLA1C,ATARLA1C	ADP-ribosylation factor-like A1C	ADP-ribosylation factor-like protein
Sapur.017G019900.2	8.404172146	0.536483396	0.212339945	2.526531	0.011519531	0.016633791	brown	-0.07017963	0.382445746	GO:0016567,GO:0004842	AT2G31510.1	ARI7,ATARI7	IBR domain-containing protein	E3 ubiquitin-protein ligase ARI7, putative
Sapur.016G263200.1	0.452296329	-2.266981813	0.898280859	-2.52369	0.011613051	0.016764438	brown	-0.269781993	0.000633323		AT5G53742.1		Protein of unknown function (DUF1278)	prolamin-like protein
Sapur.014G037900.1	4.738137869	-0.715250024	0.283959386	-2.51885	0.011774007	0.01698419	brown	-0.247379984	0.001786597		AT1G02150.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.002G100600.1	0.691378495	0.779406308	0.312717884	2.492362	0.012689647	0.018234236	brown	-0.081608864	0.309590942		AT3G57870.1	AHUS5.ATSCE1.EMB1637.S	sumo conjugation enzyme 1	SUMO E2 conjugating enzyme SCE1
Sapur.012G068200.1	0.252922122	-1.352015596	0.543428014	-2.48794	0.012848587	0.0184522	brown	-0.404305372	1.51E-07		AT4G24790.1		AAA-type ATPase family protein	DNA polymerase III subunit gamma/tau
Sapur.014G068900.1	1.11484625	0.61989233	0.249219198	2.487338	0.012870313	0.018480994	brown	0.201457031	0.011403876		AT2G46080.1			NA
Sapur.15ZG052300.1	1.124837751	-0.59915448	0.242617667	-2.46954	0.01352862	0.019387563	brown	-0.174969611	0.028395406		AT2G27030.3	ACAM-2,CAM5	calmodulin 5	NA
Sapur.014G120100.2	13.68680104	0.338939352	0.137659749	2.462153	0.013810578	0.019772782	brown	0.021337749	0.790813093		AT1G60710.1	ATB2	NAD(P)-linked oxidoreductase superfamily protein	aldo/keto reductase family protein
Sapur.005G203900.4	0.373368734	-1.166159111	0.474063298	-2.45992	0.013896691	0.019889184	brown	-0.275496967	0.000479039	GO:0006457	AT1G20810.1		FKBP-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase FKBP18
Sapur.005G094000.1	0.275545482	-1.449414945	0.596084957	-2.43156	0.015034055	0.02145387	brown	-0.26322532	0.000866012	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT5G66320.1	GATA5	GATA transcription factor 5	GATA transcription factor, putative
Sapur.017G127800.1	0.567659774	1.102888227	0.45431288	2.427596	0.015199255	0.021671846	brown	0.140956031	0.078261642	GO:0004866	AT1G17860.1		Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor
Sapur.018G082200.2	2.135274269	-0.481779606	0.199117373	-2.41958	0.015538616	0.022136638	brown	-0.390208824	4.37E-07	GO:0043565,GO:0006355,GO:0003700	AT4G30935.1	ATWRKY32,WRKY32	WRKY DNA-binding protein 32	WRKY transcription factor, putative
Sapur.019G097100.1	1.37349745	-0.555914541	0.230341784	-2.41343	0.015803018	0.022492965	brown	-0.19374167	0.015046444		AT1G03670.1		ankyrin repeat family protein	NA
Sapur.017G042500.1	0.321882394	-1.432294219	0.593854149	-2.41186	0.01587129	0.022586251	brown	-0.20245612	0.010994101	GO:0007050,GO:0005634,GO:0004861	AT5G48820.1	ICK6,KRP3	inhibitor/interactor with cyclin-dependent kinase	cyclin-dependent kinase inhibitor
Sapur.012G057000.1	33.31464348	-0.171653728	0.071208499	-2.41058	0.015927213	0.022662908	brown	-0.189513965	0.017444072	GO:0003682,GO:0006351,GO:0005634,GO:0003677	AT3G48050.1		BAH domain ;TFIIS helical bundle-like domain	BAH and TFIIS domain protein
Sapur.006G205200.2	0.278185715	-1.328463478	0.552895417	-2.40274	0.016272789	0.023119818	brown	-0.298615225	0.000145407	GO:0055114,GO:0016491	AT1G52820.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.010G111300.3	0.829736096	0.698741829	0.29126291	2.399007	0.01643959	0.023342764	brown	0.047900702	0.55134894		AT3G06670.1		binding	NA
Sapur.006G140100.4	0.469818324	0.886718428	0.372111815	2.382935	0.017175207	0.024340251	brown	0.002063705	0.979535279	GO:0008152,GO:0003824,GO:0016114,GO:0008661	AT4G15560.1	CLA,CLA1,DEF,DXPS2,DXS	Deoxyxylulose-5-phosphate synthase	1-deoxy-D-xylulose-5-phosphate synthase
Sapur.005G032100.2	10.38501438	-0.236524523	0.099810842	-2.36973	0.017801187	0.025197143	brown	-0.186034796	0.01965947	GO:0016787,GO:0008152	AT5G27320.1	ATGID1C,GID1C	alpha/beta-Hydrolases superfamily protein	gibberellin receptor GID1, putative
Sapur.012G081300.1	0.492339885	-0.870227825	0.367234496	-2.36968	0.017803541	0.025199398	brown	-0.224344661	0.004733012	GO:0008270,GO:0004553,GO:0005975,GO:0004559,GO:0015923,GO:0006013	AT5G13980.1		Glycosyl hydrolase family 38 protein	glycoside hydrolase family 38 protein
Sapur.016G263000.1	0.559736298	-1.263353712	0.533585393	-2.36767	0.017900532	0.025332343	brown	-0.18172757	0.022735823		AT5G53742.1		Protein of unknown function (DUF1278)	prolamin-like protein
Sapur.010G071100.1	0.320938972	-1.257022561	0.537747985	-2.33757	0.019409662	0.027387166	brown	-0.254283264	0.001310401		AT1G66140.1	ZFP4	zinc finger protein 4	zinc finger protein, putative
Sapur.002G180700.1	848.9619477	-0.095769477	0.041062806	-2.33227	0.019686584	0.02776014	brown	-0.210131037	0.008255122	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G64940.1	CYP89A6	cytochrome P450, family 87, subfamily A, polypeptide 6	cytochrome P450 family protein
Sapur.15WG086000.1	0.599736302	0.816058195	0.350720012	2.326808	0.019975476	0.028150706	brown	0.193082609	0.015400164	GO:0055085,GO:0016021	AT1G74780.1		Nodulin-like / Major Facilitator Superfamily protein	nodulin-like protein
Sapur.018G022300.1	5.169807714	-0.351331276	0.151012066	-2.32651	0.019991291	0.028171792	brown	-0.126116841	0.115509955	GO:0009116	AT5G11160.1	APT5	adenine phosphoribosyltransferase 5	adenine phosphoribosyltransferase
Sapur.010G009300.1	1.072582857	-0.682080231	0.294139571	-2.3189	0.020400463	0.028721476	brown	-0.148286494	0.06381973		AT4G15830.1		ARM repeat superfamily protein	clasp amino-terminal protein
Sapur.016G286400.1	0.816288541	-0.775638075	0.334968106	-2.31556	0.020582415	0.028966545	brown	-0.145508401	0.069012857	GO:0006468,GO:0004672	AT4G21390.1	B120	S-locus lectin protein kinase family protein	NA
Sapur.019G008600.1	0.455657272	-0.943765753	0.408137282	-2.31237	0.02075712	0.02920496	brown	-0.121522762	0.129485788		AT2G02100.1	LCR69,PDF2.2	low-molecular-weight cysteine-rich 69	gamma-thionin, putative
Sapur.001G143700.2	0.634500042	0.802855968	0.348484593	2.303849	0.021231107	0.0298518	brown	0.178915	0.024960972		AT1G80280.1		alpha/beta-Hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.017G020100.9	24.77451702	0.166017901	0.072162068	2.300626	0.021412803	0.030099326	brown	-0.115107846	0.151131044	GO:0055085,GO:0016021	AT2G43330.1	ATINT1,INT1	inositol transporter 1	sugar porter (SP) family MFS transporter
Sapur.T079700.1	0.994876975	0.917127031	0.39955602	2.295365	0.021712197	0.03049555	brown	-0.045228308	0.573796931	GO:0005509				NA
Sapur.001G141600.9	14.10333483	-0.249854631	0.109245112	-2.2871	0.022189915	0.031122906	brown	-0.081608864	0.309590942		AT4G19160.2			transglutaminase family protein
Sapur.002G107300.3	1.392252749	-0.667703322	0.295161918	-2.26216	0.023687554	0.033136232	brown	-0.112353917	0.161219824	GO:0016567,GO:0004842	AT1G65430.1	ARI8,ATARI8	IBR domain-containing protein	ariadne-1 protein, putative
Sapur.010G040700.1	0.469472676	1.34347623	0.594187602	2.26103	0.023757375	0.033228376	brown	0.151010251	0.059042908	GO:0055085,GO:0016021	AT5G43360.1	ATPT4,PHT1;3,PHT3	phosphate transporter 1;3	inorganic phosphate transporter, putative
Sapur.005G184900.2	1.296551701	-0.569967777	0.258171866	-2.20771	0.02726472	0.037933424	brown	-0.100926505	0.208495218		AT1G04945.3		HIT-type Zinc finger family protein	NA
Sapur.010G050700.2	0.809656	0.663815496	0.303052768	2.190429	0.028493157	0.039570971	brown	-0.014962225	0.852453854	GO:0055114,GO:0047134	AT1G60420.1		DC1 domain-containing protein	protein disulfide isomerase (PDI)-like protein
Sapur.003G003800.3	8.842755494	-0.290772456	0.133330917	-2.18083	0.029195775	0.040495746	brown	-0.146812324	0.066534132	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G61580.1	ARP2,RPL3B	R-protein L3 B	60S ribosomal protein L3
Sapur.15WG087400.3	0.988906049	-0.618253595	0.283551857	-2.18039	0.029228575	0.04053954	brown	-0.049600786	0.537294403	GO:0046983	AT5G62610.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	BHLH transcription factor, putative
Sapur.15WG132800.2	0.36409258	0.87407504	0.404303049	2.16193	0.030623544	0.042370267	brown	0.207388044	0.009155368	GO:0005515	AT4G19880.1		Glutathione S-transferase family protein	glutathione S-transferase-like protein
Sapur.004G070100.3	3.010930698	-0.339765357	0.157882439	-2.15201	0.031396183	0.043389493	brown	-0.184387668	0.020790534	GO:0043565,GO:0006355,GO:0003700	AT2G03340.1	WRKY3	WRKY DNA-binding protein 3	WRKY transcription factor

Sapur.012G033700.1	0.338521019	-1.732756909	0.807234708	-2.14653	0.031830383	0.043963839	brown	-0.274288987	0.000508416		AT3G25170.1	RALFL26	ralf-like 26	rapid aLkalinization factor
Sapur.012G062900.3	1.601429829	0.503008018	0.234406043	2.145883	0.031882289	0.044030014	brown	0.176761573	0.026788529	GO:0005524,GO:0003676	AT5G63120.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.010G167500.1	12.39950554	-0.223092161	0.104632054	-2.13216	0.032993788	0.045508009	brown	-0.147003943	0.066176067	GO:0005975,GO:0004553	AT3G55260.1	ATHEX2,HEXO1	beta-hexosaminidase 1	beta-hexosaminidase
Sapur.010G196300.5	9.814301073	-0.225089983	0.105595446	-2.13163	0.033037616	0.04556276	brown	-0.081608864	0.309590942	GO:0007034	AT3G10640.1	VPS60.1	SNF7 family protein	charged multivesicular body protein
Sapur.008G005200.1	203.4461884	0.093119829	0.043735017	2.129182	0.033239169	0.045823529	brown	0.130976587	0.102034588		AT1G51660.1	ATMEK4,ATMKK4,MKK4	mitogen-activated protein kinase kinase 4	MAP kinase kinase
Sapur.006G083200.3	0.418359642	-1.030340078	0.484248932	-2.12771	0.033361344	0.045984292	brown	-0.119733809	0.135267041	GO:0006629,GO:0055114,GO:0016717	AT5G05580.1	FAD8	fatty acid desaturase 8	omega-3 fatty acid desaturase
Sapur.016G106200.1	11.0884154	-0.247010074	0.116287029	-2.12414	0.033658334	0.046374328	brown	-0.162322304	0.042241767	GO:0016787	AT1G28960.4	ATNUDT15.ATNUDX15.NUI	nudix hydrolase homolog 15	nudix hydrolase
Sapur.016G171300.1	0.216630512	1.476662141	0.695881931	2.122001	0.033837656	0.046611688	brown	0.084155697	0.294683913		AT2G14610.1	ATPR1,PR 1,PR1	pathogenesis-related gene 1	cysteine-rich secretory family protein
Sapur.016G003600.1	36.87408598	0.185005251	0.088329964	2.094479	0.036217336	0.04973643	brown	0.10865342	0.175558428					transmembrane protein, putative
Sapur.018G088800.2	0.608800149	-0.669647179	0.320754655	-2.08772	0.036822742	0.050517478	brown	-0.120997319	0.131163768					NA
Sapur.016G263400.1	0.383606346	-1.306687121	0.626444245	-2.08588	0.036989552	0.050735805	brown	-0.21295503	0.007411112		AT5G53742.1		Protein of unknown function (DUF1278)	NA
Sapur.013G027300.1	1.660931406	0.785431304	0.377236566	2.082066	0.037336472	0.051196785	brown	0.144878373	0.070237165		AT4G24310.1		Protein of unknown function (DUF679)	NA
Sapur.013G036700.7	5.218976498	-0.270178427	0.129980214	-2.07861	0.037653031	0.051609463	brown	-0.152967746	0.055794692		AT3G04830.2		Protein prenylyltransferase superfamily protein	O-linked GlcNAc transferase-like protein
Sapur.007G007500.1	0.383517136	-0.916320968	0.440988658	-2.07788	0.037720527	0.051691266	brown	-0.194050425	0.014883186	GO:0003676	AT5G09880.1		Splicing factor, CC1-like	splicing factor-like protein
Sapur.001G161100.1	13.08806346	0.382230805	0.185029639	2.065781	0.038849116	0.053156365	brown	0.145761591	0.068525759		AT5G56550.1	ATOXS3,OXS3	oxidative stress 3	hypothetical protein
Sapur.013G117500.1	0.636395387	-0.78068618	0.37807221	-2.06491	0.038931243	0.053262128	brown	-0.138123061	0.084504837	GO:0006468,GO:0005524,GO:0004672	AT1G53050.1		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.003G072200.1	2.043496622	-0.426191267	0.206923319	-2.05966	0.039431249	0.053912738	brown	-0.142937098	0.074120913	GO:0016161,GO:0000272	AT5G45300.1	BAM8,BMY2	beta-amylase 2	beta-amylase
Sapur.017G058200.3	0.739723108	-0.692104037	0.33866678	-2.04361	0.040991735	0.055963041	brown	-0.127196191	0.112403365	GO:0005515,GO:0003723	AT2G39260.1		binding;RNA binding	NA
Sapur.014G020200.1	0.608346536	-0.586915801	0.287871813	-2.03881	0.041469039	0.056586641	brown	-0.228889897	0.003933518	GO:0005509	AT5G42380.1	CML37,CML39	calmodulin like 37	EF hand protein
Sapur.016G165400.1	19.0051816	0.227882863	0.111793649	2.038424	0.041507542	0.056636843	brown	0.151043811	0.058985938	GO:0006468,GO:0005524,GO:0004672	AT5G58520.1		Protein kinase superfamily protein	tyrosine kinase family protein
Sapur.004G134100.1	0.657032776	-0.828445659	0.407092413	-2.03503	0.041847759	0.05707752	brown	-0.086357931	0.282184322	GO:0008536,GO:0006886	AT2G16950.2	ATTRN1,TRN1	transportin 1	transportin-1 protein
Sapur.009G032100.1	488.894001	-0.079991828	0.039332251	-2.03375	0.04197716	0.057239851	brown	-0.169544108	0.03377073	GO:0005515	AT1G07310.1		Calcium-dependent lipid-binding (CaLB domain) family protein	C2 domain-like protein
Sapur.017G118900.1	23.59981419	-0.216401458	0.106420956	-2.03345	0.042007304	0.057276232	brown	-0.187265033	0.018849771	GO:0043565,GO:0006355,GO:0003700	AT5G52830.1	ATWRKY27,WRKY27	WRKY DNA-binding protein 27	WRKY DNA-binding domain protein
Sapur.012G009300.2	2.005010101	-0.409476912	0.201627529	-2.03086	0.042269386	0.057616949	brown	-0.133460814	0.095641911	GO:0016021,GO:0015689,GO:0015098	AT4G27720.1		Major facilitator superfamily protein	MFS transporter
Sapur.014G000600.2	2.442731791	-0.351585946	0.173355277	-2.02812	0.042547624	0.057977098	brown	-0.054143267	0.500638042		AT3G13060.2	ECT5	evolutionarily conserved C-terminal region 5	YTH domain protein
Sapur.005G078600.2	0.678970818	-0.612571306	0.304868776	-2.00929	0.044505858	0.060525771	brown	-0.159224416	0.046386488	GO:0016021,GO:0006952	AT2G17480.1	ATMLO8,MLO8	Seven transmembrane MLO family protein	MLO-like protein
Sapur.016G042700.2	0.346621205	-1.023411754	0.510813455	-2.00349	0.045124278	0.061306292	brown	-0.271689839	0.000577349					NA
Sapur.007G101200.1	1.157997572	-0.583016902	0.293952682	-1.98337	0.047326127	0.064144919	brown	-0.115127642	0.151060287	GO:0006457	AT5G64350.1	ATFKBP12,FKBP12	FK506-binding protein 12	peptidyl-prolyl cis-trans isomerase FKBP12
Sapur.009G033500.1	6.645016052	0.25039016	0.126690723	1.976389	0.048110728	0.065160288	brown	0.128263268	0.109396614	GO:0016758,GO:0008152	AT2G29730.1	UGT71D1	UDP-glucosyl transferase 71D1	UDP-glucosyltransferase, putative
Sapur.002G108700.2	1.081160294	-0.544929068	0.276159002	-1.97324	0.048467781	0.065614317	brown	-0.217034898	0.00632707	GO:0008725,GO:0006284	AT1G75090.1		DNA glycosylase superfamily protein	DNA-3-methyladenine glycosylase I
Sapur.019G044300.1	1.463686758	-0.51942557	0.263572263	-1.97071	0.048756589	0.065983691	brown	-0.125756216	0.116562675		AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.012G033600.1	0.300764217	-1.682722696	0.854391709	-1.9695	0.048895941	0.066153332	brown	-0.276287641	0.000460667		AT3G25170.1	RALFL26	ralf-like 26	rapid aLkalinization factor
Sapur.018G100800.1	0.45117121	0.8198242	0.420016447	1.951886	0.050951747	0.068844598	brown	0.154692245	0.053056595	GO:0009055	AT5G20230.1	ATBCB,BCB,SAG14	blue-copper-binding protein	NA
Sapur.010G126600.2	0.430453979	0.675251579	0.345993597	1.95163	0.050982116	0.068882818	brown	-0.085210144	0.288653877	GO:0005515,GO:0003676	AT1G69440.1	AGO7,ZIP	Argonaute family protein	argonaute protein
Sapur.013G142700.1	0.484528149	-0.897717793	0.461067777	-1.94704	0.051529838	0.069574538	brown	-0.128455674	0.108861226		AT2G30530.1			hypothetical protein
Sapur.T166800.7	0.322511505	0.858408743	0.441163751	1.945783	0.051680862	0.069764206	brown	-0.119859799	0.134853532		AT1G21080.3		DNAJ heat shock N-terminal domain-containing protein	DnaJ heat shock amino-terminal domain protein
Sapur.016G272600.1	1.249155738	-0.728999297	0.374762508	-1.94523	0.051747295	0.069851034	brown	-0.172742709	0.03050625		AT5G53742.1		Protein of unknown function (DUF1278)	prolamin-like protein
Sapur.008G085300.1	0.347953191	-0.833639498	0.429505977	-1.94093	0.052267203	0.070515418	brown	-0.114924621	0.151787115	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G06680.3		Ribosomal L29e protein family	60S ribosomal protein L29
Sapur.003G052500.3	0.873877791	-0.579565907	0.302879918	-1.91352	0.055681885	0.074902292	brown	-0.161898331	0.042789996	GO:0006468,GO:0005524,GO:0004672	AT4G33950.1	ATOST1.OST1.P44.SNRK2-6.	Protein kinase superfamily protein	Serine/Threonine-kinase SAPK3, putative
Sapur.010G161200.1	4.432062451	0.407475834	0.213303216	1.910313	0.056092968	0.075418465	brown	-0.062901819	0.433841643		AT5G02500.1	AT-HSC70-1.HSC70.HSC70-:	heat shock cognate protein 70-1	heat shock cognate 70 kDa protein
Sapur.016G270500.4	1.877304925	-0.358678029	0.189024875	-1.89752	0.057759657	0.077536443	brown	-0.081608864	0.309590942	GO:0043486,GO:0006355,GO:0006338,GO:0005634	AT2G36740.1	ATSWC2,SWC2	sequence-specific DNA binding transcription factors;DNA binding;DNA binding	YL1 nuclear protein
Sapur.002G005800.3	10.46986492	0.203098418	0.107307512	1.892677	0.05840089	0.078352711	brown	-0.130322444	0.103772716		AT1G20670.1		DNA-binding bromodomain-containing protein	bromodomain domain protein
Sapur.014G075900.6	1.192693095	-0.420011896	0.222236212	-1.88993	0.058766713	0.078817935	brown	0.032310139	0.687894046	GO:0046872	AT1G01350.1		Zinc finger (CCCH-type/C3HC4-type RING finger) family protein	RING zinc finger protein, putative
Sapur.T017000.1	7.816712025	-0.258027654	0.13666865	-1.88798	0.059028659	0.079149999	brown	-0.128494586	0.108753197	GO:0005524,GO:0051082,GO:0006457	AT3G02530.1		TCP-1/cpn60 chaperonin family protein	NA
Sapur.016G196900.1	33.35724839	-0.14327185	0.076174387	-1.88084	0.05999366	0.080375514	brown	-0.145030598	0.069939747		AT3G18790.1			NA
Sapur.010G040500.1	0.792019924	0.70151324	0.373231066	1.879568	0.060166952	0.080604414	brown	0.130942746	0.102123941					transmembrane protein, putative
Sapur.002G130600.3	8.469251442	-0.182072198	0.09697944	-1.87743	0.06045906	0.080972786	brown	-0.105799849	0.187242906	GO:0016021,GO:0004190	AT1G01650.1	ATSPPL4,SPPL4	SIGNAL PEPTIDE PEPTIDASE-LIKE 4	signal peptide peptidase-like protein
Sapur.018G115300.1	0.468014397	0.770426553	0.411961403	1.870143	0.061464023	0.082242136	brown	0.124013572	0.121755226	GO:0005515	AT1G58190.2	AtRLP9,RLP9	receptor like protein 9	NA
Sapur.003G039800.1	3.96728388	0.306194194	0.164378052	1.862744	0.062498324	0.083561853	brown	0.142165838	0.075711373	GO:0016192,GO:0016021	AT1G11890.1	ATSEC22,SEC22	Synaptobrevin family protein	25.3 kDa vesicle transporter
Sapur.003G062000.3	12.91968336	0.154168659	0.082946474	1.858652	0.063076431	0.084300719	brown	-0.001137159	0.988722516	GO:0043565,GO:0006355,GO:0005634,GO:0003700	AT1G32330.1	ATHSFA1D,HSFA1D	heat shock transcription factor A1D	heat shock transcription factor 1
Sapur.001G090800.4	3.540755631	-0.289454473	0.156092377	-1.85438	0.063684913	0.085038347	brown	-0.035805759	0.656173406		AT4G11790.1		Pleckstrin homology (PH) domain superfamily protein	RanBP1 domain protein
Sapur.004G112400.1	1.934120709	-0.451272242	0.243942143	-1.84992	0.064325794	0.085869846	brown	-0.173459824	0.029812395	GO:0055114,GO:0047134	AT2G16050.1		Cysteine/Histidine-rich C1 domain family protein	cysteine/histidine-rich C1 domain protein
Sapur.017G123700.1	0.687902975	-0.645541852	0.349224888	-1.8485	0.06453019	0.086121843	brown	-0.156245345	0.050686702		AT4G31980.1			DUF247 domain protein
Sapur.013G038500.3	1.151749141	-0.456098706	0.247304336	-1.84428	0.065142188	0.086903547	brown	-0.157492713	0.048847523	GO:0046983	AT4G02590.1	UNE12	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	helix loop helix protein
Sapur.001G160600.1	0.90224634	-0.602809131	0.326944471	-1.84377	0.065217235	0.086996646	brown	-0.176281139	0.02721152		AT1G52080.1	AR791	actin binding protein family	CHUP1, putative
Sapur.016G134500.3	1.317931557	0.427392802	0.234738202	1.820721	0.068649259	0.091316989	brown	0.008657893	0.914298553	GO:0006511	AT2G29070.1		Ubiquitin fusion degradation UFD1 family protein	ubiquitin fusion degradation 1 protein
Sapur.006G156300.4	0.604210867	0.561177703	0.309578296	1.812717	0.069875549	0.092877222	brown	-0.081608864	0.309590942	GO:0055114,GO:0016717,GO:0006629	AT3G12120.2	FAD2	fatty acid desaturase 2	delta-12 fatty acid desaturase
Sapur.010G194000.1	0.280478016	-1.02859557	0.571176897	-1.80084	0.071728829	0.095180819	brown	-0.218709669	0.00592464					NA
Sapur.008G022000.1	0.339991227	-0.936415136	0.521077062	-1.79708	0.072323539	0.095922875	brown	-0.195373361	0.014201041					NA
Sapur.007G104800.1	0.32761551	-0.744180519	0.416095251	-1.78849	0.073697637	0.09764745	brown	-0.110236604	0.169312723	GO:0005525,GO:0003924	AT4G33650.1	ADL2,DRP3A	dynamin-related protein 3A	dynamin-related protein 3A
Sapur.004G148600.3	1.333281247	-0.427607793	0.240017984	-1.78157	0.074820092	0.099035487	brown	-0.094511092	0.239037946	GO:0016579,GO:0004843	AT2G27350.6		OTU-like cysteine protease family protein	rice genome annotation project, cysteine-type peptidase%2C putative
Sapur.018G079400.2	0.369974142	-0.794555987	0.446604666	-1.7791	0.075222772	0.099550083	brown	-0.195500416	0.014136989	GO:0055114,GO:0016491	AT4G30720.1		FAD/NAD(P)-binding oxidoreductase family protein	FAD/NAD(P)-binding oxidoreductase-like protein
Sapur.002G148200.6	0.382412429	0.699327324	0.393260716	1.778279	0.075358022	0.099723571	brown	-0.023056553	0.774397724	GO:0005515	AT3G61590.2	HS,HWS	Galactose oxidase/kelch repeat superfamily protein	F-box/kelch-repeat plant protein
Sapur.004G057400.3	0.712431581	0.515382022	0.290245765	1.775675	0.075786572	0.100242555	brown	0.078548531	0.32814497	GO:0003676	AT3G54230.1	SUA	suppressor of abi3-5	suppressor of abi3-5 protein
Sapur.012G081100.2	0.217987346	0.929685106	0.524549243	1.77235	0.076336396	0.100925406	brown	-0.116080592	0.147683723		AT5G61970.1		signal recognition particle-related / SRP-related	signal recognition particle subunit SRP68
Sapur.003G052800.4	1.109317195	0.428214301	0.243275056	1.760206	0.078372824	0.103477157	brown	0.149706073	0.061292121	GO:0019887,GO:0005956	AT5G47080.1	CKB1	casein kinase II beta chain 1	casein kinase II beta chain, putative
Sapur.014G121200.3	1.41563787	-0.49452521	0.281421847	-1.75724	0.078877223	0.104076649	brown	-0.099935773	0.21301956		AT5G42390.1		Insulinase (Peptidase family M16) family protein	metalloendopeptidase
Sapur.014G007300.2	1.70466116	0.376185502	0.215247905	1.747685	0.080518614	0.106106966	brown	-0.168138069	0.035296703	GO:0005515	AT1G27840.1	ATCSA-1	Transducin/WD40 repeat-like superfamily protein	ATCSA-1
Sapur.005G014600.9	2.336134341	0.300906579	0.172598849	1.743387	0.081266047	0.107062069	brown	-0.081608864	0.309590942	GO:0005515	AT3G06720.2	AIMP ALPHA.AT-IMP.ATKAP	importin alpha isoform 1	importin subunit alpha
Sapur.005G151300.1	1.282985314	-0.400132081	0.22957394	-1.74293	0.081345254	0.107145079	brown	-0.13560721	0.090378053		AT4G24370.1			NA
Sapur.004G117600.1	0.352951017	-0.787550277	0.453808289	-1.73543	0.082665544	0.108788804	brown	-0.230640657	0.003659509	GO:0042545,GO:0030599,GO:0005618	AT2G21610.1	ATPE11,PE11	pectinesterase 11	pectinesterase
Sapur.019G003600.1	1.956320611	-0.371508727	0.214535698	-1.73169	0.083329267	0.109605575	brown	-0.135037849	0.091751335	GO:0005515,GO:0043531	AT1G12220.1	RPS5	Disease resistance protein (CC-NBS-LRR class) family	NA
Sapur.008G154300.1	0.275278313	-1.204462457	0.695566024	-1.73163	0.083339599	0.109614805	brown	-0.263328902	0.000861794		AT1G70000.2		myb-like transcription factor family protein	MYB transcription factor, putative
Sapur.010G003600.2	4.735255928	0.23760565	0.137731822	1.725133	0.084503586	0.111066269	brown	-0.367746997	2.16E-06	GO:0005524,GO:0003676	AT3G06980.1		DEA(D/H)-box RNA helicase family protein	DEAD-box ATP-dependent RNA helicase, putative
Sapur.016G081200.2	0.288950115	-0.950371516	0.555226183	-1.71168	0.086955005	0.1140933	brown	-0.166474937	0.037176536	GO:0005515,GO:0006468,GO:0004672	AT2G37050.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.002G063900.1	0.218178284	-1.066680861	0.623833568	-1.70988	0.087287971	0.114512013	brown	-0.317102646	5.20E-05	GO:0016020,GO:0006810,GO:0005215	AT1G15960.1	ATNRAMP6,NRAMP6	NRAMP metal ion transporter 6	nramp metal transporter
Sapur.016G246800.1	1.27853668	0.471531865	0.28100902	1.677995	0.093347981	0.121978236	brown	0.135805705	0.089903158	GO:0005515	AT3G49180.1	RID3	Transducin/WD40 repeat-like superfamily protein	NA
Sapur.008G164600.4	9.878407885	0.165109021	0.098823535	1.670746	0.094771868	0.123736174	brown	0.078548531	0.32814497	GO:0017053,GO:0007049,GO:0006351	AT3G21430.2	ALY3,ATALY3	DNA binding	always early protein
Sapur.012G095600.2	0.3876967	0.620588481	0.373433631	1.661844	0.096544035	0.125895888	brown	0.013137477	0.870279301		AT2G35110.1	GRL,NAP1,NAPP	transcription activators	NA
Sapur.005G138900.1	0.640788025	-0.66032771	0.40202537	-1.6425	0.100485891	0.130778355	brown	-0.069331179	0.388239737	GO:0008152,GO:0003824	AT1G77590.1	LACS9	long chain acyl-CoA synthetase 9	long-chain-fatty-acid-CoA ligase
Sapur.001G000400.3	0.223941315	-1.067787423	0.656193777	-1.62724	0.103685274	0.134698408	brown	-0.293746602	0.000188507		AT2G32080.1	PUR ALPHA-1	purin-rich alpha 1	transcription factor Pur-alpha 1
Sapur.002G156100.2	1.193104299	-0.45998882	0.282709856	-1.62707	0.10372216	0.134735742	brown	-0.104064136	0.194622713	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT2G47800.1	ATMRP4,EST3,MRP4	multidrug resistance-associated protein 4	multidrug resistance protein ABC transporter family protein
Sapur.002G014500.1	22.09228015	-0.171677335	0.105563788	-1.62629	0.103887975	0.134935237	brown	-0.139593582	0.081216108		AT1G75810.1			transmembrane protein, putative
Sapur.018G078800.1	0.695478202	0.530513275	0.327950471	1.617663	0.105735288	0.137147164	brown	-0.024187789	0.763647655	GO:0006508,GO:0004185	AT4G30810.1	scpl29	serine carboxypeptidase-like 29	serine carboxypeptidase II-2
Sapur.010G030200.1	0.396100375	0.694269988	0.431179844	1.610163	0.107362197	0.139141744	brown	0.117861827	0.141525935	GO:0016787	AT1G10430.1	PP2A-2	protein phosphatase 2A-2	serine/threonine-protein phosphatase PP2A catalytic subunit
Sapur.014G099900.1	1.28341606	-0.446846416	0.278555184	-1.60416	0.108679317	0.140793566	brown	-0.097966592	0.222219623		AT3G62650.2			hypothetical protein
Sapur.016G184900.1	1.372130232	0.427479533	0.267368413	1.598841	0.109855976	0.142234353	brown	0.123843734	0.122270722	GO:0006351,GO:0005634,GO:0003677	AT5G09850.1		Transcription elongation factor (TFIIS) family protein	transcription elongation factor, putative
Sapur.004G139200.1	65.72254476	0.115229646	0.072464825	1.590146	0.111801916	0.144612302	brown	0.128654732	0.108309489		AT3G07350.1		Protein of unknown function (DUF506)	NA
Sapur.012G053600.2	1.861855376	-0.339811172	0.214240319	-1.58612	0.112711755	0.145743553	brown	-0.126761453	0.113646691		AT5G47390.1		myb-like transcription factor family protein	MYB transcription factor, putative
Sapur.008G013200.1	26.16034369	0.156373618	0.09868626	1.584553	0.113067912	0.146169799	brown	0.130433065	0.103477159					transmembrane protein, putative
Sapur.003G032700.1	9.764282039	0.387416187	0.244797038	1.582602	0.113512296	0.146686534	brown	-0.0385402	0.63177752		AT1G71950.1		Proteinase inhibitor, propeptide	NA
Sapur.002G094900.2	0.690151694	0.492728319	0.313277738	1.572816	0.11576137	0.149488191	brown	0.095732284	0.232995514	GO:0005515	AT3G12350.2		F-box family protein	F-box plant protein
Sapur.004G086700.1	5.199848502	0.168848623	0.107414676	1.571933	0.115966203	0.149711784	brown	0.164275151	0.039791991		AT1G67140.3	SWEETIE	HEAT repeat-containing protein	NA
Sapur.15WG008800.1	3.66453881	0.256118836	0.16391988	1.562464	0.118178828	0.152395765	brown	0.121708338	0.128897122		AT5G26760.2			RNA polymerase II subunit B1 CTD phosphatase RPAP2-like protein, putative
Sapur.017G028900.3	9.183121095	0.154366796	0.098981325	1.559555	0.118865134	0.15324493	brown	-0.173066752	0.030191035		AT3G21865.1	PEX22	peroxin 22	peroxin, putative
Sapur.018G118500.2	0.403071729	-0.683127413	0.438082719	-1.55936	0.118911876	0.153293241	brown	-0.081608864	0.309590942	GO:0046872,GO:0030001	AT1G06330.1		Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.002G084300.1	338.7196423	-0.097346089	0.063042142	-1.54414	0.12255367	0.157754342	brown	-0.147069904	0.066053174		AT5G49700.1		Predicted AT-hook DNA-binding family protein	AT-hook DNA-binding protein, putative
Sapur.001G023500.1	178.7679305	0.103438091	0.067117338	1.541153	0.123279538	0.158626962	brown	0.09964856	0.214344192		AT1G08315.1		ARM repeat superfamily protein	ubiquitin-protein ligase, putative
Sapur.010G137100.1	0.85562482	-0.48474553	0.316221989	-1.53293	0.125293605	0.161080645	brown	-0.082087533	0.306752215	GO:0046872	AT3G12680.1	HUA1	floral homeotic protein (HUA1)	zinc finger CCCH domain protein
Sapur.008G100200.3	2.260050076	0.29325325	0.192010988	1.527273	0.126693074	0.162791248	brown	0.011429236	0.887026164		AT3G02600.2	ATLPP3,LPP3	lipid phosphate phosphatase 3	lipid phosphate phosphatase
Sapur.017G067000.1	1.431019212	0.404235079	0.265833666	1.520632	0.128352306	0.164820786	brown	0.123853877	0.122239889	GO:0055114,GO:0016491,GO:0009073,GO:0003856	AT3G28760.2			3-dehydroquinate synthase
Sapur.004G074000.2	0.407650785	0.6256697	0.411702663	1.519713	0.128583238	0.165078877	brown	-0.121588358	0.129277477	GO:0046983,GO:0003677,GO:0006355,GO:0005634,GO:0003700	AT3G02310.1	AGL4,SEP2	K-box region and MADS-box transcription factor family protein	MADS-box transcription factor
Sapur.010G022700.2	1.587879794	0.361983579	0.239592821	1.510828	0.13083224	0.167835913	brown	0.11047566	0.168384162		AT3G26400.1	EIF4B1	eukaryotic translation initiation factor 4B1	eukaryotic translation initiation factor 4B
Sapur.006G062300.1	1.335756048	0.343154214	0.227436964	1.508788	0.13135291	0.168445045	brown	-0.037653892	0.639643153	GO:0046872,GO:0000166	AT4G30110.1	ATHMA2,HMA2	heavy metal atpase 2	heavy metal transporting P-type ATPase, putative
Sapur.15WG100600.3	1.326239815	-0.319485291	0.2118878	-1.5078	0.131604675	0.167861361	brown	-0.053704722	0.504118781		AT5G63110.1	ATHDA6.AXE1.HDA6.RPD3B	histone deacetylase 6	histone deacetylase family protein
Sapur.005G128400.1	0.518958113	-0.617911508	0.414066492	-1.4923	0.135620465	0.173614772	brown	-0.123544573	0.123182845	GO:0003824,GO:0006470,GO:0004722	AT1G34750.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.016G139600.1	176.1207682	-0.085341765	0.057198847	-1.49202	0.135694171	0.173702404	brown	-0.128009143	0.110106896	GO:0005515	AT1G07310.1		Calcium-dependent lipid-binding (CaLB domain) family protein	C2 domain protein
Sapur.001G107900.5	8.623180915	0.171890917	0.115301269	1.490798	0.136014503	0.174078773	brown	0.20665864	0.009408911	GO:0008168	AT4G19120.1	ERD3	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.15WG123800.1	1.874302632	-0.312787806	0.210981592	-1.48254	0.138197732	0.176712323	brown	-0.137425271	0.086102302		AT5G45470.1		Protein of unknown function (DUF594)	NA
Sapur.014G059400.1	0.294454538	-0.791083265	0.534337885	-1.48049	0.138741844	0.177377185	brown	-0.194592682	0.014600199		AT3G61060.1	AtPP2-A13,PP2-A13	phloem protein 2-A13	F-box protein PP2-A13
Sapur.004G069400.1	0.251707353	-0.814254517	0.551886012	-1.4754	0.140104113	0.179046887	brown	-0.189654674	0.01735923	GO:0016758,GO:0008152	AT3G16520.3	UGT88A1	UDP-glucosyl transferase 88A1	UDP-glucosyltransferase, putative
Sapur.012G030200.1	8.623923287	-0.173596178	0.11823598	-1.46822	0.142045055	0.181284899	brown	-0.12765487	0.11110311	GO:0016020	AT3G17910.1	SURF1	Surfeit locus 1 cytochrome c oxidase biogenesis protein	surfeit locus protein
Sapur.009G105500.1	8.385429637	-0.187408099	0.128501744	-1.45841	0.144727846	0.184502342	brown	-0.116923769	0.144744023	GO:0006950	AT2G21620.1	RD2	Adenine nucleotide alpha hydrolases-like superfamily protein	NA
Sapur.004G084200.1	8.786933999	-0.173093643	0.119123209	-1.45306	0.146205993	0.18629337	brown	-0.091146039	0.256251665	GO:0005524,GO:0051082,GO:0006457	AT3G02530.1		TCP-1/cpn60 chaperonin family protein	NA
Sapur.006G021500.3	0.906410394	-0.389264034	0.269743242	-1.44309	0.148994849	0.189563623	brown	-0.110730555	0.167398257	GO:0046556,GO:0046373	AT3G10740.1	ARAF,ARAF1,ASD1,ATASD1	alpha-L-arabinofuranosidase 1	alpha-L-arabinofuranosidase
Sapur.003G055400.1	8.733305103	0.289466446	0.200779184	1.441715	0.149382672	0.190018941	brown	0.102641475	0.200827322		AT4G21700.1		Protein of unknown function (DUF2921)	transmembrane protein, putative
Sapur.019G005300.1	0.297357735	0.725042615	0.503284804	1.440621	0.149691808	0.190375562	brown	0.147843465	0.064625793		AT4G34990.1	AtMYB32,MYB32	myb domain protein 32	NA
Sapur.011G115600.1	2.289327321	-0.391154744	0.271848417	-1.43887	0.150187137	0.190946774	brown	-0.087864767	0.273839866	GO:0055114,GO:0050660,GO:0016491	AT4G20800.1		FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.010G201300.2	1.120012865	-0.381616635	0.269362567	-1.41674	0.156559053	0.198589941	brown	-0.059888566	0.456226893	GO:0055085,GO:0016021	AT1G55730.2	ATCAX5,CAX5	cation exchanger 5	vacuolar cation/proton exchanger 2
Sapur.005G129300.1	0.349630415	-0.607154074	0.429115148	-1.4149	0.157098467	0.199228324	brown	-0.187292145	0.018832257	GO:0003676	AT5G64200.1	ATSC35,SC35	ortholog of human splicing factor SC35	arginine/serine-rich splicing factor SC30 transcript protein
Sapur.007G070400.1	0.814133754	-0.483227818	0.341675068	-1.41429	0.157276612	0.199408367	brown	-0.128225813	0.109501074		AT5G23340.1		RNI-like superfamily protein	glucose regulated repressor protein, putative
Sapur.002G196600.2	0.495791493	-0.586036441	0.416342501	-1.40758	0.159254716	0.201707597	brown	-0.12775521	0.110820243		AT4G28820.1		HIT-type Zinc finger family protein	HIT zinc finger protein, putative
Sapur.009G043300.1	0.860490571	-0.411668462	0.293385064	-1.40317	0.16056682	0.203229383	brown	-0.145940234	0.068183764		AT5G13760.1		Plasma-membrane choline transporter family protein	NA
Sapur.15WG007000.3	3.564812408	0.186568767	0.133474385	1.397787	0.162177023	0.205102587	brown	0.069770074	0.385235986	GO:0006890	AT5G24350.1			neuroblastoma-amplified sequence protein
Sapur.003G123200.1	7.135159977	-0.223736765	0.160150931	-1.39704	0.162402428	0.205364095	brown	-0.10156036	0.205637037	GO:0005515	AT1G28050.1		B-box type zinc finger protein with CCT domain	B-box type zinc finger protein, putative
Sapur.017G052500.3	13.99295979	0.129668384	0.093053133	1.393488	0.163472401	0.206582844	brown	-0.008024016	0.920551695	GO:0016021,GO:0005783	AT5G14030.3		translocon-associated protein beta (TRAPB) family protein	translocon-associated protein subunit beta
Sapur.014G028600.6	2.826844577	-0.226848114	0.163559392	-1.38695	0.1654581	0.208972437	brown	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004672	AT3G13690.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	receptor tyrosine kinase
Sapur.001G038000.1	0.343391111	-0.558555517	0.403373486	-1.38471	0.166140995	0.209762837	brown	-0.101215484	0.207188635		AT1G80750.1		Ribosomal protein L30/L7 family protein	60S ribosomal protein L7
Sapur.016G244500.3	0.765468716	0.415467954	0.300894316	1.380777	0.167347535	0.211221659	brown	0.100313704	0.211285464	GO:0007165,GO:0006355,GO:0005634,GO:0004871,GO:0003700	AT1G78540.2	ATSHB,SHB,STATLB	SH2 domain protein B	SH2 domain protein A
Sapur.014G111200.1	6.278957663	0.182281872	0.132282231	1.377977	0.16821039	0.212245934	brown	0.116805103	0.145155042	GO:0016021,GO:0008381	AT2G48060.1			FAM38B protein
Sapur.002G173900.1	184.6590735	-0.10602289	0.076991539	-1.37707	0.168489998	0.212574412	brown	-0.103261556	0.198105635		AT5G55160.1	ATSUMO2.SUM2.SUMO 2.S	small ubiquitin-like modifier 2	small ubiquitin-related modifier
Sapur.016G184200.1	0.287404921	-1.022190499	0.749805051	-1.36328	0.17279585	0.217550436	brown	-0.177592999	0.026069792		AT4G39340.1		Protein of unknown function (DUF1278)	prolamin-like protein
Sapur.019G054300.1	0.475273827	-0.696236175	0.511589679	-1.36093	0.173536779	0.218450005	brown	-0.113016928	0.158746087	GO:0016020,GO:0006810,GO:0005215	AT2G40460.1		Major facilitator superfamily protein	peptide transporter
Sapur.016G003900.1	1.84721356	-0.473307126	0.348465142	-1.35826	0.174380413	0.219436814	brown	-0.095877645	0.232283481					NA
Sapur.001G024500.6	0.350244707	0.530741282	0.391484922	1.355713	0.175190433	0.220389045	brown	-0.081608864	0.309590942	GO:0043565,GO:0006355,GO:0003700,GO:0006351	AT3G12250.2	BZIP45,TGA6	TGACG motif-binding factor 6	transcription factor TGA2
Sapur.005G079600.1	5.016989165	0.189276731	0.140034159	1.351647	0.176488313	0.221903611	brown	0.119706836	0.135355697	GO:0016779,GO:0006396,GO:0003723	AT2G17580.1		Polynucleotide adenylyltransferase family protein	poly(A) polymerase, putative
Sapur.011G031400.2	0.339440717	0.56193196	0.416269964	1.349922	0.177041021	0.222539325	brown	0.179485951	0.024494742	GO:0006508,GO:0004185	AT1G11080.2	scpl31	serine carboxypeptidase-like 31	serine carboxypeptidase-like protein
Sapur.012G042300.1	0.400360423	-0.596043309	0.442748842	-1.34623	0.178227234	0.223936768	brown	-0.144804747	0.070381385	GO:0030983,GO:0006298,GO:0005524	AT3G18524.1	ATMSH2,MSH2	MUTS homolog 2	DNA mismatch repair protein Msh2
Sapur.010G101200.2	7.806234422	0.167334993	0.124822372	1.340585	0.180055248	0.226096179	brown	-0.113291485	0.157730071		AT3G25690.1	CHUP1	Hydroxyproline-rich glycoprotein family protein	CHUP1
Sapur.019G009100.1	1.466850929	-0.344998664	0.258681272	-1.33368	0.18230796	0.228751222	brown	-0.083907594	0.296114795	GO:0006886,GO:0005622	AT5G63640.1		ENTH/VHS/GAT family protein	hepatocyte growth factor-regulated tyrosine kinase substrate protein, putative
Sapur.008G048900.4	0.577001655	-0.488580306	0.366553507	-1.3329	0.182563605	0.22904443	brown	-0.094351629	0.239834971		AT2G39855.2			hypothetical protein
Sapur.005G208700.1	0.621960462	-0.524612702	0.393591685	-1.33289	0.182569338	0.22904443	brown	-0.068501075	0.393959372		AT1G21080.1		DNAJ heat shock N-terminal domain-containing protein	DnaJ heat shock amino-terminal domain protein
Sapur.017G045300.1	0.252980684	-0.881408548	0.661694068	-1.33205	0.182844273	0.22932846	brown	-0.167941367	0.035514759		AT3G07550.1		RNI-like superfamily protein	F-box/LRR protein
Sapur.017G003700.2	9.020159575	-0.20466533	0.153666653	-1.33188	0.182900079	0.229389755	brown	-0.098173143	0.221241589	GO:0006412,GO:0005840,GO:0003735,GO:0005622	AT2G44065.1		Ribosomal protein L2 family	ribosomal protein L2
Sapur.002G051300.2	0.5558128	0.493198938	0.371103648	1.329006	0.183846022	0.230462528	brown	0.112402395	0.161037979		AT1G34000.1	OHP2	one-helix protein 2	one helix protein
Sapur.002G154900.2	4.328141328	-0.198831515	0.15026598	-1.3232	0.185769826	0.232724186	brown	-0.366590921	2.33E-06	GO:0005515	AT2G47730.1	ATGSTF5.ATGSTF8.GST6.GST	glutathione S-transferase phi 8	Phi class glutathione S-transferase
Sapur.014G117100.4	94.51974255	0.062960137	0.047772573	1.317914	0.187532481	0.234798958	brown	0.265193821	0.000789008		AT3G19340.1		Protein of unknown function (DUF3754)	transmembrane protein, putative
Sapur.004G114100.2	0.680602179	-0.418745854	0.318699394	-1.31392	0.188872761	0.236351786	brown	-0.024091298	0.764562879	GO:0016773,GO:0048015,GO:0046854	AT1G49340.1	ATPI4K ALPHA	Phosphatidylinositol 3- and 4-kinase family protein	NA
Sapur.016G170800.1	368.0795434	0.530733864	0.405936649	1.30743	0.191066621	0.238898285	brown	0.212652261	0.007497777	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G31500.1	ATR4.CYP83B1.RED1.RNT1.	cytochrome P450, family 83, subfamily B, polypeptide 1	NA
Sapur.008G011300.2	0.530414985	-0.50166719	0.384916406	-1.30332	0.192465282	0.240501615	brown	-0.123297067	0.123941447	GO:0006887,GO:0000145	AT5G03540.1	ATEXO70A1,EXO70A1	exocyst subunit exo70 family protein A1	exocyst subunit EXO70
Sapur.005G148500.1	0.223750296	-0.747690476	0.575131437	-1.30003	0.193589284	0.241833056	brown	-0.254565745	0.001293651		AT5G41470.1		Nuclear transport factor 2 (NTF2) family protein	NA
Sapur.003G131200.3	0.377107419	-0.573707678	0.442524203	-1.29644	0.194822693	0.24330951	brown	-0.067295305	0.402356848	GO:0016020	AT2G33205.1		Serinc-domain containing serine and sphingolipid biosynthesis protein	TMS membrane protein/tumor differentially protein
Sapur.002G192800.1	0.90601434	-0.34076267	0.263732761	-1.29208	0.196330959	0.245045101	brown	-0.093725699	0.242981416	GO:0006457	AT3G25230.1	ATFKBP62,FKBP62,ROF1	rotamase FKBP 1	peptidyl-prolyl cis-trans isomerase FKBP65
Sapur.008G022300.1	0.285601405	-0.786078903	0.615400353	-1.27735	0.201480279	0.25107414	brown	-0.159902164	0.045451862					transmembrane protein, putative
Sapur.017G127700.1	0.313323495	0.618820701	0.484611219	1.276943	0.20162252	0.251232461	brown	0.071053047	0.376536432	GO:0004866	AT1G17860.1		Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor
Sapur.005G111500.4	14.0185314	-0.097272993	0.076268137	-1.27541	0.202164863	0.25181338	brown	-0.08231554	0.305406053		AT2G01710.1		Chaperone DnaJ-domain superfamily protein	AT hook motif protein
Sapur.016G041500.1	1.7938974	0.270758573	0.213640242	1.267358	0.205027472	0.255186792	brown	0.092918084	0.247083461		AT2G42130.4		Plastid-lipid associated protein PAP / fibrillin family protein	plastid-lipid-associated protein, putative
Sapur.008G150900.1	1.64392263	-0.551987031	0.44453347	-1.24172	0.214339115	0.265995719	brown	-0.08646527	0.28158432		AT3G07040.1	RPM1,RPS3	NB-ARC domain-containing disease resistance protein	disease resistance protein RPM1, putative
Sapur.003G112700.2	1.748531903	-0.298114509	0.243242683	-1.22558	0.220355001	0.272890616	brown	-0.099424178	0.215383134					hypothetical protein
Sapur.017G056300.8	7.925446699	0.117166842	0.095667531	1.224729	0.220677176	0.273266573	brown	-0.113172583	0.158169473	GO:0006355,GO:0005634	AT1G07705.2		NOT2 / NOT3 / NOT5 family	CCR4-NOT transcription complex subunit, putative
Sapur.012G088100.1	8.723548843	-0.56073901	0.465269821	-1.20519	0.228129568	0.281851226	brown	-0.154775186	0.052927757					NA
Sapur.019G015800.3	0.182695959	-0.861305524	0.716530071	-1.20205	0.229343858	0.283213933	brown	-0.262689281	0.000888144	GO:0016021,GO:0015693,GO:0015095	AT2G21120.1		Protein of unknown function (DUF803)	Non-imprinted in prader-willi/angelman syndrome region protein
Sapur.008G077400.4	1.007529146	-0.36323189	0.302339033	-1.20141	0.229593798	0.283501411	brown	-0.072789752	0.364953224	GO:0005634,GO:0003677	AT1G69170.1		Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein	LIGULELESS 1 protein, putative
Sapur.005G109900.1	0.169735872	-0.842100856	0.703939034	-1.19627	0.231591374	0.285786624	brown	-0.316529842	5.37E-05	GO:0003676	AT4G36960.1		RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein G RNA recognition motif protein
Sapur.004G113700.1	0.229428246	0.64144028	0.537179625	1.194089	0.232443156	0.286752143	brown	0.143044769	0.073901044					hypothetical protein
Sapur.006G216500.2	5.662442182	-0.175754613	0.14749682	-1.19158	0.233425037	0.287877532	brown	-0.08554933	0.286731822	GO:0005634	AT2G32070.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	CCR4-associated factor-like protein, putative
Sapur.019G073800.3	0.34434482	-0.510254751	0.432929646	-1.17861	0.238553931	0.29372097	brown	-0.137846113	0.085135994		AT1G33810.1			hypothetical protein
Sapur.003G108400.4	0.297368871	-0.58504501	0.496397309	-1.17858	0.238564601	0.293723174	brown	-0.12476833	0.119484706	GO:0006468,GO:0005524,GO:0004672	AT4G10730.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.001G022800.1	1.115685801	0.329555983	0.280271003	1.175848	0.239655786	0.294956851	brown	0.100991022	0.208203003	GO:0005975,GO:0004553,GO:0009341,GO:0004565	AT3G54440.1		glycoside hydrolase family 2 protein	beta-galactosidase
Sapur.001G149600.2	8.911847369	-0.144245643	0.123125261	-1.17154	0.241383504	0.29691751	brown	0.14139455	0.07732936		AT3G13845.1			transmembrane protein, putative
Sapur.15WG025600.2	1.422624296	0.26580797	0.232809157	1.141742	0.253561317	0.310775876	brown	-0.268710344	0.000666916		AT1G66410.2	ACAM-4,CAM4	calmodulin 4	calmodulin
Sapur.013G132400.1	87.82900231	-0.082067572	0.071970704	-1.14029	0.254164937	0.311469529	brown	-0.081761993	0.308680954	GO:0015979,GO:0010207	AT2G20890.1	PSB29,THF1	photosystem II reaction center PSB29 protein	thylakoid FORMATION protein
Sapur.002G011000.2	0.376881886	0.464936145	0.410057656	1.133831	0.25686538	0.314522438	brown	0.096860786	0.227507823	GO:0003824,GO:0005515	AT4G35790.2	ATPLDDELTA,PLDDELTA	phospholipase D delta	phospholipase D
Sapur.005G001200.1	0.330688332	-0.484338411	0.427508047	-1.13293	0.257241961	0.31493691	brown	-0.170558587	0.032704738	GO:0016021	AT3G05880.1	RCI2A	Low temperature and salt responsive protein family	stress-induced hydrophobic peptide protein
Sapur.013G055400.6	0.347655779	-0.482644852	0.426545984	-1.13152	0.257836743	0.315606678	brown	-0.16221659	0.04237791		AT2G23840.1		HNH endonuclease	HNH nuclease, putative
Sapur.006G143000.3	4.979157729	-0.143930911	0.12740951	-1.12967	0.258614612	0.316418307	brown	-0.081608864	0.309590942		AT2G23820.2		Metal-dependent phosphohydrolase	metal-dependent phosphohydrolase HD domain protein
Sapur.006G029200.3	0.292518131	-0.569785393	0.506179073	-1.12566	0.26030958	0.318362572	brown	-0.126095853	0.115571017		AT3G56720.3			hypothetical protein
Sapur.013G001300.1	0.15819311	-0.776240851	0.691003653	-1.12335	0.261287711	0.319464335	brown	-0.093638079	0.243424149	GO:0016021	AT3G05880.1	RCI2A	Low temperature and salt responsive protein family	stress-induced hydrophobic peptide protein
Sapur.018G092100.1	0.289530905	-0.547783805	0.489448366	-1.11919	0.263060757	0.321453908	brown	-0.160204806	0.04503962	GO:0031515,GO:0030488,GO:0016429	AT5G14600.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NA
Sapur.005G201700.1	0.934957655	0.308856222	0.276601959	1.116609	0.264161564	0.322739447	brown	0.081144068	0.312363786		AT1G20640.2		Plant regulator RWP-RK family protein	NA
Sapur.017G076300.1	4.383606509	0.136391055	0.122277351	1.115424	0.264668897	0.323335393	brown	-0.023622843	0.76901081		AT3G02090.1	MPPBETA	Insulinase (Peptidase family M16) protein	processing peptidase beta subunit
Sapur.004G009900.1	1.022520327	-0.347168024	0.314124954	-1.10519	0.269076901	0.328320277	brown	-0.025331267	0.752826926		AT1G11660.1		heat shock protein 70 (Hsp 70) family protein	heat shock 70 kDa protein
Sapur.005G141100.8	1.083525782	0.317270376	0.287309258	1.104282	0.269470929	0.328728294	brown	-0.081608864	0.309590942		AT4G31115.1		Protein of unknown function (DUF1997)	plant/F6E21-30 protein, putative
Sapur.016G288000.1	1.349871637	-0.309983811	0.281302627	-1.10196	0.270479728	0.329885925	brown	-0.054810476	0.4953667		AT1G79160.1			hypothetical protein
Sapur.016G040100.1	0.264261279	-0.729469756	0.663918984	-1.09873	0.271884505	0.331428134	brown	-0.097961372	0.222244379	GO:0016787,GO:0005524,GO:0003677,GO:0016817	AT3G57300.1	ATINO80,INO80	INO80 ortholog	DNA helicase INO80 complex-like protein
Sapur.010G061900.6	0.660442143	-0.341952832	0.311540196	-1.09762	0.272370341	0.331995896	brown	-0.103491805	0.197101845		AT1G05410.1		Protein of unknown function (DUF1423)	CDPK adapter protein, putative
Sapur.009G106900.1	11.21703454	-0.125419117	0.114656369	-1.09387	0.27401217	0.333861798	brown	-0.093303967	0.245117526	GO:0004842	AT4G38600.1	KAK,UPL3	HEAT repeat ;HECT-domain (ubiquitin-transferase)	E3 ubiquitin-protein ligase UPL3
Sapur.15WG062000.1	3.397966903	-0.27035023	0.247833644	-1.09085	0.275337295	0.335303424	brown	-0.078573882	0.327988398		AT4G08910.1			NA
Sapur.008G048900.2	0.236091586	-0.761100421	0.69787244	-1.0906	0.275448464	0.335426455	brown	-0.143868802	0.072235772		AT2G39855.2			hypothetical protein
Sapur.010G205700.2	0.3224983	0.451505151	0.415058349	1.087811	0.276678431	0.336849828	brown	-0.113047939	0.158631083	GO:0016887,GO:0005524	AT3G54540.1	ATGCN4,GCN4	general control non-repressible 4	ABC transporter F family protein
Sapur.007G124700.1	0.212536676	0.605294731	0.557534739	1.085663	0.277628201	0.337906643	brown	0.138820494	0.082932007	GO:0006468,GO:0005524,GO:0004672	AT2G43790.1	ATMAPK6.ATMPK6.MAPK6.I	MAP kinase 6	MAP kinase
Sapur.T062600.1	0.259902264	1.000110708	0.926282829	1.079703	0.280274285	0.340826226	brown	0.177251804	0.02636272		AT1G67020.1			NA
Sapur.009G103200.1	1.926413974	-0.200096888	0.186011205	-1.07572	0.282050299	0.342834678	brown	-0.105254788	0.189537987	GO:0005634	AT2G21150.1	XCT	XAP5 family protein	XAP5 circadian timekeeper
Sapur.018G096100.1	2.813261282	-0.231201647	0.215583546	-1.07245	0.283519889	0.344481717	brown	-0.053584248	0.505077197	GO:0007165	AT1G30270.1	ATCIPK23.CIPK23.LKS1.SnRI	CBL-interacting protein kinase 23	CBL-interacting Serine/Threonine-kinase
Sapur.004G142400.1	0.234588657	-0.711894348	0.664228196	-1.07176	0.283827074	0.344816951	brown	-0.147340028	0.065551843	GO:0003676,GO:0046872,GO:0005634,GO:0003723	AT5G42820.1	ATU2AF35B,U2AF35B	Zinc finger C-x8-C-x5-C-x3-H type family protein	splicing factor U2af small protein, putative
Sapur.018G100900.1	0.306452693	-0.631425902	0.595480332	-1.06036	0.288979037	0.350599489	brown	-0.150527119	0.059868084	GO:0009055	AT2G25060.1	AtENODL14,ENODL14	early nodulin-like protein 14	NA
Sapur.003G053900.3	3.88954279	-0.137466192	0.130820229	-1.0508	0.293349419	0.355406377	brown	-0.081234473	0.31182319	GO:0005524,GO:0030163,GO:0004252,GO:0004176	AT5G47040.1	LON2	lon protease 2	Lon protease-like, peroxisomal protein
Sapur.017G018400.1	2.364028811	-0.234144536	0.224542679	-1.04276	0.297058611	0.359663085	brown	-0.067985047	0.397540269	GO:0016747	AT3G26040.1		HXXXD-type acyl-transferase family protein	benzylalcohol acetyltransferase
Sapur.008G130700.3	1.15247323	-0.244737296	0.23640915	-1.03523	0.300562594	0.363477189	brown	-0.089823893	0.263242802	GO:0016020,GO:0005509,GO:0004571	AT5G43710.1		Glycosyl hydrolase family 47 protein	alpha-mannosidase, putative
Sapur.018G030400.1	0.229230268	-0.877655708	0.848598875	-1.03424	0.301023534	0.363957316	brown	-0.132510764	0.098048119	GO:0005525	AT5G11480.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	ribosome biogenesis GTP-binding protein YsxC
Sapur.15WG092200.3	2.05102884	0.214466928	0.207428988	1.033929	0.30116917	0.36409347	brown	-0.141768803	0.076540812	GO:0005992,GO:0003824	AT1G23870.1	ATTPS9,TPS9	trehalose-phosphatase/synthase 9	trehalose-6-phosphate synthase
Sapur.005G149900.3	1.013305958	0.35010351	0.33957728	1.030998	0.302541739	0.365605812	brown	0.058337835	0.467993199	GO:0030170,GO:0019752,GO:0016831	AT1G43710.1	emb1075	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	serine decarboxylase
Sapur.010G037100.1	0.39182878	-0.402280227	0.391855729	-1.0266	0.304607489	0.367860229	brown	-0.127166485	0.112487983	GO:0016021	AT1G09330.1			NA
Sapur.008G032700.2	0.226776082	-0.643301521	0.630040934	-1.02105	0.307232085	0.370840261	brown	-0.158033676	0.048067327		AT2G35795.1		Chaperone DnaJ-domain superfamily protein	import inner membrane translocase subunit TIM14
Sapur.013G086000.1	1.059445321	0.237335018	0.234369628	1.012653	0.311226117	0.375305086	brown	0.15309793	0.055584001		AT3G03140.1		Tudor/PWWP/MBT superfamily protein	PWWP domain protein
Sapur.016G223200.1	0.385307925	0.382618705	0.378836966	1.009982	0.312503676	0.376708335	brown	-0.060401171	0.452373997	GO:0008484,GO:0008152,GO:0016740,GO:0006506,GO:0005789	AT3G01380.1		transferases;sulfuric ester hydrolases;catalytics;transferases	phosphatidylinositolglycan class N protein
Sapur.005G003800.1	0.219030012	-0.599074727	0.594928768	-1.00697	0.313949752	0.378341195	brown	-0.225183661	0.004575293		AT1G56700.2		Peptidase C15, pyroglutamyl peptidase I-like	pyrrolidone-carboxylate peptidase
Sapur.009G005400.2	1.673127292	-0.252030157	0.250380682	-1.00659	0.314132868	0.378534284	brown	-0.050013134	0.533912604	GO:0006355,GO:0003677	AT2G27990.1	BLH8,PNF	BEL1-like homeodomain 8	BEL1 homeotic protein, putative
Sapur.004G089300.1	0.593307065	-0.405247672	0.40283842	-1.00598	0.314424859	0.378872333	brown	-0.095732944	0.232992274		AT4G34419.1			hypothetical protein
Sapur.005G080400.3	29.34749844	-0.070371929	0.071030148	-0.99073	0.321815852	0.386946504	brown	-0.081608864	0.309590942	GO:0006468,GO:0004672	AT4G35600.2	CONNEXIN 32	Protein kinase superfamily protein	Serine/Threonine-kinase Cx32, putative
Sapur.014G058300.1	0.208203718	-0.59341457	0.601426717	-0.98668	0.32380047	0.389205435	brown	-0.203834072	0.010450213	GO:0003677	AT5G42700.1		AP2/B3-like transcriptional factor family protein	B3 DNA-binding domain protein
Sapur.016G132000.3	0.168059527	-0.656774025	0.666997969	-0.98467	0.324785357	0.390289972	brown	-0.098435559	0.220003449		AT3G46540.1		ENTH/VHS family protein	hypothetical protein
Sapur.013G000800.4	0.233347252	-0.641437329	0.651742661	-0.98419	0.325023067	0.390533057	brown	-0.20764759	0.009066616	GO:0016787	AT3G05910.2		Pectinacetylesterase family protein	pectin acetylesterase, putative
Sapur.010G155200.6	2.219578535	-0.186305869	0.190225041	-0.9794	0.327383769	0.393041155	brown	-0.08863982	0.269613532		AT2G39805.2		Integral membrane Yip1 family protein	integral membrane Yip1 family protein
Sapur.005G184200.10	13.33390504	-0.087997908	0.089884121	-0.97902	0.327572537	0.393253506	brown	-0.081608864	0.309590942	GO:0004518	AT1G75380.1	ATBBD1,BBD1	bifunctional nuclease in basal defense response 1	wound responsive protein, putative
Sapur.011G036900.1	1.655037114	-0.225188198	0.230433843	-0.97724	0.328452435	0.394252589	brown	-0.09385095	0.242349511	GO:0006468,GO:0005524,GO:0004672,GO:0030246	AT4G04960.1		Concanavalin A-like lectin protein kinase family protein	lectin-receptor-like kinase
Sapur.007G102600.1	63.81928498	0.054360191	0.055692562	0.976076	0.329026642	0.394913164	brown	0.060685555	0.450244359		AT5G64360.3		Chaperone DnaJ-domain superfamily protein	DnaJ heat shock amino-terminal domain protein, putative
Sapur.004G013900.1	0.530136091	0.325716358	0.336530741	0.967865	0.333111747	0.399526325	brown	-0.053682595	0.504294737	GO:0005515,GO:0008081,GO:0006281,GO:0005634	AT5G15170.1	TDP1	tyrosyl-DNA phosphodiesterase-related	tyrosyl-DNA phosphodiesterase
Sapur.15WG091000.2	0.168219581	-0.850835928	0.886536626	-0.95973	0.337191046	0.403935552	brown	-0.249471072	0.001627927		AT5G50090.1			DUF4228 domain protein
Sapur.004G031200.4	58.33509292	-0.074204932	0.077454983	-0.95804	0.338042848	0.404895741	brown	-0.105591742	0.188116767		AT1G28330.4	DRM1,DYL1	dormancy-associated protein-like 1	auxin-repressed/dormancy-associated protein, putative
Sapur.009G061700.1	0.195424858	-0.548947231	0.573527037	-0.95714	0.338495221	0.405351061	brown	-0.208791548	0.008684443	GO:0055114,GO:0016491,GO:0008152	AT2G14170.1	ALDH6B2	aldehyde dehydrogenase 6B2	methylmalonate-semialdehyde dehydrogenase (acylating)
Sapur.008G151700.2	0.206733461	-0.564126806	0.589729292	-0.95659	0.33877624	0.405638071	brown	-0.202584248	0.010942498	GO:0008168,GO:0008152	AT1G23360.2	MENG	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ubiquinone/menaquinone biosynthesis methyltransferase
Sapur.004G047700.1	0.208953219	-0.579954642	0.606946294	-0.95553	0.339310366	0.406194841	brown	-0.243515811	0.002117328		AT3G54710.1	ATCDT1B,CDT1,CDT1B	homolog of yeast CDT1 B homolog of yeast CDT1 B	DNA replication factor CDT1-like protein
Sapur.018G083200.1	2.598040252	-0.157904319	0.165513904	-0.95402	0.340071242	0.406943676	brown	-0.049293967	0.539817625		AT5G58003.1	CPL4	C-terminal domain phosphatase-like 4	RNA polymerase II carboxy-terminal domain phosphatase-like protein
Sapur.010G169900.1	0.195073933	-0.906933392	0.958703977	-0.946	0.34414889	0.411272596	brown	-0.12322531	0.124162053		AT2G39340.1		SAC3/GANP/Nin1/mts3/eIF-3 p25 family	leukocyte receptor cluster (Lrc) protein, putative
Sapur.009G013800.1	2.777277984	0.149088934	0.160529405	0.928733	0.353027544	0.420985506	brown	0.067731706	0.399305373	GO:0016853,GO:0005975	AT5G57330.1		Galactose mutarotase-like superfamily protein	NA
Sapur.15WG045200.1	0.143826444	-0.808918596	0.872960957	-0.92664	0.354114637	0.422084024	brown	-0.295008998	0.000176314		AT1G67060.1			peptidase M50B-like protein
Sapur.001G160200.1	0.225634162	-1.29078371	1.394004931	-0.92595	0.354470159	0.422477335	brown	-0.200123599	0.011971668		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.010G206500.1	0.415306203	-0.388575994	0.419711595	-0.92582	0.354541259	0.422533163	brown	-0.03951502	0.623173838		AT5G08400.2		Protein of unknown function (DUF3531)	plant/F8L15-130 protein, putative
Sapur.016G224600.1	1.085248364	-0.278403878	0.300894529	-0.92525	0.35483378	0.422834532	brown	-0.057756014	0.472450375		AT2G34410.2		O-acetyltransferase family protein	O-acetyltransferase-like protein
Sapur.013G001100.4	0.305573863	-0.406253256	0.439257985	-0.92486	0.355037414	0.423016226	brown	-0.121212945	0.130473167	GO:0046983	AT1G09530.2	PAP3,PIF3,POC1	phytochrome interacting factor 3	phytochrome-interacting factor 3.1, putative
Sapur.007G024800.1	0.207644101	-0.704761736	0.763126425	-0.92352	0.355736815	0.42380374	brown	-0.110546665	0.168109092	GO:0017025,GO:0008270,GO:0006355,GO:0006352	AT4G36650.1	ATPBRP,PBRP	plant-specific TFIIB-related protein	transcription factor IIB
Sapur.009G068500.3	7.149042267	0.095721157	0.105440386	0.907823	0.363971999	0.432710636	brown	-0.049291835	0.539835179	GO:0005525	AT3G49870.1	ARLA1C,ATARLA1C	ADP-ribosylation factor-like A1C	ADP-ribosylation factor-like protein 8a
Sapur.003G166200.1	0.29095326	-0.418371125	0.461325928	-0.90689	0.364465825	0.43314203	brown	-0.145614118	0.068809133	GO:0055114,GO:0051537,GO:0016491,GO:0010277	AT4G25650.1	ACD1-LIKE,PTC52,TIC55-IV	ACD1-like	pheophorbide A oxygenase
Sapur.003G116200.2	0.233398014	-0.440535072	0.488613551	-0.9016	0.367268201	0.436143351	brown	0.017387466	0.828878863	GO:0006367,GO:0005634	AT4G20280.1	TAF11	TBP-associated factor 11	transcription initiation factor TFIID subunit 11
Sapur.017G101600.1	0.810350129	0.254860431	0.282910414	0.900852	0.367666981	0.436585564	brown	0.054664067	0.496520899		AT5G38060.1			hypothetical protein
Sapur.006G082600.1	0.685816457	-0.278120728	0.310074584	-0.89695	0.369746751	0.438818862	brown	-0.090085655	0.261848428	GO:0005515,GO:0042393,GO:0006355	AT5G05610.1	AL1	alfin-like 1	PHD finger protein

Sapur.001G189900.1	0.175899529	0.781291884	0.87450539	0.89341	0.371637635	0.440809896	brown	0.132408515	0.098309917		AT1G67020.1			NA
Sapur.012G073500.3	0.949363883	0.258082804	0.289076873	0.892783	0.371973604	0.441176755	brown	-0.073974136	0.357181665		AT3G48550.1			nucleic acid-binding protein, putative
Sapur.001G101800.2	0.274610212	-0.490982778	0.550611701	-0.8917	0.37255149	0.441735427	brown	-0.133343828	0.095935651	GO:0005515,GO:0006468,GO:0004672	AT1G16270.2		Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain	Serine/Threonine kinase, putative
Sapur.005G105600.1	0.322496343	0.385510106	0.434465095	0.887321	0.374905973	0.444320069	brown	-0.046391479	0.56397375	GO:0006468,GO:0005524,GO:0004672	AT5G66880.1	SNRK2-3,SNRK2.3,SRK2I	sucrose nonfermenting 1(SNF1)-related protein kinase 2.3	Serine/Threonine kinase, putative
Sapur.010G116900.1	0.423957142	-0.372207166	0.421382083	-0.8833	0.377073727	0.446681104	brown	-0.047441459	0.555175955		AT3G17210.1	ATHS1,HS1	heat stable protein 1	stress responsive A/B barrel domain protein
Sapur.017G031300.1	0.198398369	-0.522831906	0.592731494	-0.88207	0.377737826	0.447406937	brown	-0.118402297	0.139696687	GO:0005525,GO:0003924	AT4G33650.1	ADL2,DRP3A	dynamin-related protein 3A	dynamin-related protein 3A
Sapur.010G060700.4	0.35971506	0.408309579	0.462900852	0.882067	0.377740561	0.447406937	brown	0.061471694	0.444386634	GO:0006468,GO:0005524,GO:0004672	AT3G04910.1	ATWNK1,WNK1,ZIK4	with no lysine (K) kinase 1	Serine/Threonine-kinase WNK1, putative
Sapur.T169700.1	0.149829408	-0.696084227	0.79088409	-0.88013	0.378786551	0.448485229	brown	-0.286873808	0.000269832		AT4G00850.1	GIF3	GRF1-interacting factor 3	SSXT protein (amino-terminal region) protein
Sapur.007G034200.1	10.30227827	-0.11227244	0.127707632	-0.87914	0.379327273	0.449061143	brown	-0.051713457	0.520081118		AT2G23610.1	ATMES3,MES3	methyl esterase 3	polyneuridine-aldehyde esterase, putative
Sapur.008G085200.3	35.95038507	0.085620223	0.097724212	0.876141	0.380953197	0.450873002	brown	-0.079467263	0.322501394		AT3G06670.1		binding	serine/threonine protein phosphatase 4 regulatory subunit
Sapur.009G063000.2	0.999082706	0.234686747	0.269509769	0.870791	0.383868147	0.453981803	brown	-0.081608864	0.309590942		AT5G64460.3		Phosphoglycerate mutase family protein	phosphoglycerate mutase-like protein
Sapur.016G140400.4	0.978715134	0.248642335	0.286122993	0.869005	0.384844352	0.454973624	brown	-0.004345567	0.956923261		AT2G29670.1		Tetratricopeptide repeat (TPR)-like superfamily protein	plant/F22G5-32 protein, putative
Sapur.003G133200.1	1.317792271	0.212970491	0.245707116	0.866766	0.38607042	0.456129637	brown	0.082618665	0.30362241	GO:0016747,GO:0008152	AT2G33150.1	KAT2,PED1,PKT3	peroxisomal 3-ketoacyl-CoA thiolase 3	3-ketoacyl-CoA thiolase
Sapur.002G063200.1	1035.743336	0.070782245	0.082155894	0.86156	0.388929604	0.459097674	brown	0.068731239	0.392368444		AT1G77380.1	AAP3,ATAAP3	amino acid permease 3	amino acid permease
Sapur.T115500.1	0.760363517	-0.228063374	0.264762029	-0.86139	0.38902326	0.459191838	brown	-0.107630649	0.179682797	GO:0005515,GO:0043531	AT4G27220.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.002G184300.1	0.61639871	-0.283399685	0.329362721	-0.86045	0.389541817	0.459721893	brown	-0.081608864	0.309590942	GO:0016758,GO:0008152,GO:0030259,GO:0005975	AT3G07020.2		UDP-Glycosyltransferase superfamily protein	sterol 3-beta-glucosyltransferase
Sapur.003G019600.1	0.182580381	-0.631124645	0.737542523	-0.85571	0.392156607	0.46249421	brown	-0.219053118	0.005844993		AT1G76750.1		Protein of unknown function (DUF1278)	NA
Sapur.010G072400.3	0.293792859	0.388467545	0.471499064	0.823899	0.409997024	0.48152557	brown	0.099346888	0.215741836		AT1G68130.1	AtIDD14,IDD14	indeterminate(ID)-domain 14	NA
Sapur.007G016100.1	0.736551434	0.278244106	0.338653273	0.821619	0.411293533	0.482859659	brown	0.040088681	0.618134353		AT3G51000.1		alpha/beta-Hydrolases superfamily protein	NA
Sapur.T115300.1	0.366222202	0.391957995	0.479917871	0.816719	0.414089088	0.485658954	brown	0.07446322	0.354002788					NA
Sapur.011G114500.4	1.890441061	0.154855932	0.189886555	0.815518	0.414775781	0.486343609	brown	-0.060859963	0.448941071		AT1G32540.1	LOL1	lsd one like 1	LSD1 zinc finger protein
Sapur.004G155000.1	0.173019589	0.509823534	0.627149544	0.812922	0.416262897	0.487862476	brown	0.106527081	0.184212494		AT4G38260.1		Protein of unknown function (DUF833)	ser/thr-rich protein T10 in DGCR region protein
Sapur.006G140100.2	0.278110046	-0.522150722	0.647240756	-0.80673	0.419820108	0.491717907	brown	-0.059193263	0.461482081	GO:0008152,GO:0003824,GO:0016114,GO:0008661	AT4G15560.1	CLA,CLA1,DEF,DXPS2,DXS	Deoxyxylulose-5-phosphate synthase	1-deoxy-D-xylulose-5-phosphate synthase
Sapur.004G089400.1	1.569902292	-0.192586422	0.241457152	-0.7976	0.425102176	0.497376162	brown	-0.053969909	0.502012482	GO:0006914	AT3G19190.1	ATATG2,ATG2	autophagy 2	autophagy-related protein
Sapur.T047500.4	0.184397397	-0.565333114	0.710111113	-0.79612	0.425962737	0.498277271	brown	-0.150894078	0.05924047		AT3G17668.1	ENA	DnaJ/Hsp40 cysteine-rich domain superfamily protein	hypothetical protein
Sapur.011G070800.5	8.307513296	0.079739501	0.100531429	0.79318	0.427673062	0.500101077	brown	-0.081608864	0.309590942		AT1G78420.2		RING/U-box superfamily protein	RING E3 ubiquitin ligase
Sapur.001G096700.1	0.181063631	0.463882414	0.585085481	0.792846	0.42786782	0.500222704	brown	0.107163393	0.181590581	GO:0055114,GO:0048038,GO:0009308,GO:0008131,GO:0005507	AT1G62810.1		Copper amine oxidase family protein	amine oxidase [copper containing] protein, putative
Sapur.005G027800.2	1.172134647	-0.211353901	0.266966186	-0.79169	0.428542675	0.500923147	brown	-0.068758266	0.392181882	GO:0016020	AT5G27490.1		Integral membrane Yip1 family protein	integral membrane Yip1 family protein
Sapur.019G006300.1	4.247952403	0.138069354	0.175211256	0.788016	0.430687078	0.503091913	brown	0.053631034	0.504704881		AT5G23630.1	MIA,PDR2	phosphate deficiency response 2	NA
Sapur.006G158300.1	0.523834757	-0.376289439	0.480193198	-0.78362	0.433262573	0.50583241	brown	-0.036646555	0.648631772	GO:0007275,GO:0006511,GO:0005634	AT3G58040.1	SINAT2	seven in absentia of Arabidopsis 2	E3 ubiquitin-protein ligase SINAT2
Sapur.012G056800.3	0.467990797	-0.303943883	0.392189138	-0.77499	0.438343725	0.511259314	brown	-0.078563653	0.32805157	GO:0055085,GO:0016020,GO:0006810,GO:0005215	AT5G62890.1		Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.013G127300.1	1.052566754	0.215545447	0.278580878	0.773727	0.439092462	0.512078423	brown	0.058600689	0.465987129	GO:0051536,GO:0003824,GO:0051539,GO:0016992,GO:0009107	AT5G08415.1		Radical SAM superfamily protein	lipoyl synthase
Sapur.017G122100.2	0.178160348	-0.493270063	0.65343034	-0.75489	0.450313119	0.523852699	brown	-0.167120941	0.036436568	GO:0046872,GO:0030001	AT1G01490.2		Heavy metal transport/detoxification superfamily protein	metal ion-binding protein, putative
Sapur.004G040900.1	0.775593665	-0.234456193	0.310964818	-0.75396	0.450871003	0.524464796	brown	-0.085754198	0.285575053	GO:0006468,GO:0004672	AT4G18710.1	ATSK21.BIN2.DWF12.SK21.U	Protein kinase superfamily protein	shaggy-related kinase
Sapur.013G060900.2	0.214786537	-0.409522523	0.54326534	-0.75382	0.450959254	0.524549003	brown	-0.16579442	0.037969699		AT5G16450.2		Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase	NA
Sapur.019G112900.1	0.193288633	-0.611673506	0.813446828	-0.75195	0.452079528	0.525778124	brown	-0.105684778	0.187725733		AT5G41700.2	ATUBC8,UBC8	ubiquitin conjugating enzyme 8	ubiquitin-conjugating enzyme E2
Sapur.006G106500.1	0.187866326	-0.600928171	0.809316729	-0.74251	0.457776595	0.531600122	brown	-0.122557863	0.12622859	GO:0005515	AT3G09740.1	ATSYP71,SYP71	syntaxin of plants 71	syntaxin-71 protein
Sapur.001G158900.1	0.195661164	-1.100276559	1.482325065	-0.74226	0.457927388	0.531737894	brown	-0.186029152	0.019663253		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.016G272700.2	0.208608118	-0.682698328	0.922300552	-0.74021	0.459171109	0.533069791	brown	-0.078512236	0.328369222	GO:0005515	AT5G54520.1		Transducin/WD40 repeat-like superfamily protein	WD domain, G-beta repeat protein
Sapur.005G000700.3	0.174257124	-0.487996537	0.660793778	-0.7385	0.460210362	0.534088829	brown	-0.055884773	0.486941189	GO:0016787	AT3G05910.2		Pectinacetylesterase family protein	pectin acetylesterase, putative
Sapur.016G110100.1	0.477574412	-0.330839525	0.450556108	-0.73429	0.462771091	0.536740464	brown	-0.072902936	0.364206056					NA
Sapur.014G117900.2	0.989747954	-0.199607468	0.271999388	-0.73385	0.463038558	0.536983785	brown	-0.252764109	0.001403928	GO:0005515	AT5G46860.1	ATSYP22.ATVAM3.SGR3.SYF	Syntaxin/t-SNARE family protein	syntaxin
Sapur.016G061700.3	0.778373234	-0.212060951	0.289656236	-0.73211	0.464099907	0.538130708	brown	-0.081608864	0.309590942	GO:0008270,GO:0005515	AT5G22000.1	RHF2A	RING-H2 group F2A	RING-H2 zinc finger protein
Sapur.002G063000.1	0.258641134	0.385015255	0.526824879	0.730822	0.464887833	0.538893179	brown	0.073517924	0.360162884		AT1G21660.1		Chaperone DnaJ-domain superfamily protein	heat shock protein-binding protein
Sapur.004G110600.1	0.175117973	-0.814318247	1.119340007	-0.7275	0.466920595	0.540965137	brown	-0.10787221	0.178702317	GO:0009512	AT2G26500.1		cytochrome b6f complex subunit (petM), putative	plastoquinol-plastocyanin reductase, putative
Sapur.012G059500.2	0.438266452	0.294084958	0.410423255	0.716541	0.473657557	0.54797512	brown	-0.123960599	0.12191583	GO:0003723,GO:0000178	AT4G32175.1		PNAS-3 related	exosome complex exonuclease RRP40
Sapur.016G031200.1	0.116668519	-0.617959961	0.864751899	-0.71461	0.474850345	0.54909448	brown	-0.325309646	3.22E-05	GO:0055085,GO:0016021	AT1G73590.1	ATPIN1,PIN1	Auxin efflux carrier family protein	auxin efflux facilitator PIN1
Sapur.005G094900.2	0.183745247	-0.388602631	0.552942121	-0.70279	0.482186136	0.556740244	brown	-0.188086679	0.018325221		AT4G36280.1		Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	zinc finger protein, putative
Sapur.016G160900.1	0.143523071	-0.615760138	0.887972204	-0.69345	0.488030151	0.562584407	brown	-0.169310772	0.034020034		AT5G12330.4	LRP1	Lateral root primordium (LRP) protein-related	transcription factor, putative
Sapur.001G045500.2	0.240759262	-0.407837688	0.591199687	-0.68985	0.490290029	0.564857446	brown	-0.092826113	0.247553627	GO:0005634,GO:0003677	AT5G43270.3	SPL2	squamosa promoter binding protein-like 2	squamosa promoter-binding-like protein
Sapur.003G055700.2	1.522696518	-0.18216766	0.265140079	-0.68706	0.49204369	0.566638336	brown	-0.039815513	0.620531869		AT1G32410.2		Vacuolar protein sorting 55 (VPS55) family protein	vacuolar protein sorting-associated-like protein
Sapur.018G006400.1	1.650871152	0.154445096	0.226103817	0.683072	0.4945616	0.569220851	brown	-0.040997504	0.610186911	GO:0030126,GO:0016192,GO:0006886,GO:0005198,GO:0030117,GO:0005737	AT4G31480.1		Coatomer, beta subunit	coatomer subunit beta
Sapur.005G117800.4	6.277810762	-0.076036718	0.11247686	-0.67602	0.499027324	0.573781669	brown	0.008255794	0.918264641		AT2G34320.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	ribonuclease HI
Sapur.019G017700.1	0.112163566	0.556654822	0.826686576	0.673357	0.500720483	0.575548386	brown	0.210020834	0.00828972					NA
Sapur.003G014500.1	2.804433728	-0.13274874	0.197537993	-0.67202	0.501573355	0.576408518	brown	-0.021954114	0.784915531		AT1G15780.1			transcription cofactor, putative
Sapur.010G154500.4	1.762640713	0.141015209	0.212652239	0.663126	0.50724992	0.582223976	brown	0.078548531	0.32814497	GO:0008270	AT2G39830.1	DAR2	DA1-related protein 2	zinc ion-binding protein, putative
Sapur.006G095900.1	0.181568791	0.547810968	0.830451434	0.659654	0.509475616	0.584575768	brown	0.074303129	0.355041366	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT3G52970.1	CYP76G1	cytochrome P450, family 76, subfamily G, polypeptide 1	cytochrome P450 family protein
Sapur.002G103800.1	0.135449911	-0.683127926	1.03586928	-0.65947	0.509592014	0.58468904	brown	-0.184075508	0.021011108		AT4G33380.1			plant/F17M5-140 protein, putative
Sapur.006G046300.1	0.324520234	-0.270548592	0.410345585	-0.65932	0.509691021	0.584762066	brown	-0.103225995	0.198260993	GO:0005515	AT3G57880.1		Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein	anthranilate phosphoribosyltransferase-like protein
Sapur.018G036300.4	4.125820892	0.089910644	0.13682691	0.657112	0.511108718	0.586080678	brown	-0.08727045	0.277110875	GO:0006508,GO:0004176	AT2G25740.1		ATP-dependent protease La (LON) domain protein	ATP-dependent protease LA (LON) domain protein
Sapur.017G123700.2	0.177164426	-0.451425673	0.688459024	-0.6557	0.51201428	0.58693887	brown	-0.08690621	0.279128556		AT4G31980.1			DUF247 domain protein
Sapur.005G075800.1	0.195516379	-0.49775193	0.762139469	-0.6531	0.513692961	0.588699965	brown	-0.123573093	0.123095662	GO:0030170,GO:0008483	AT1G80600.1	WIN1	HOPW1-1-interacting 1	acetylornithine aminotransferase
Sapur.018G012000.2	6.028017996	-0.235485886	0.361091794	-0.65215	0.514304638	0.589319277	brown	-0.080876687	0.313966224	GO:0005515	AT2G02230.1	AtPP2-B1,PP2-B1	phloem protein 2-B1	NA
Sapur.004G110200.4	0.476413039	-0.254573639	0.390736157	-0.65152	0.51470886	0.589700736	brown	-0.081608864	0.309590942	GO:0003677	AT1G49480.1	RTV1	related to vernalization1 1	B3 domain transcription factor VRN1
Sapur.005G032600.4	1.874356943	0.151118307	0.234463666	0.644528	0.519233358	0.594554912	brown	-0.113520383	0.156886751	GO:0055114,GO:0004764,GO:0003855	AT3G06350.1	EMB3004,MEE32	dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative	dehydroquinate dehydratase/shikimate dehydrogenase
Sapur.15WG007600.3	0.190033901	-0.551824509	0.85707911	-0.64384	0.519677154	0.59498069	brown	-0.081348192	0.311144047		AT3G26100.2		Regulator of chromosome condensation (RCC1) family protein	RCC1 and BTB domain protein, putative
Sapur.016G177400.1	0.228455863	-0.500339899	0.782280928	-0.63959	0.522438487	0.597728329	brown	-0.073703899	0.358945723	GO:0008270,GO:0005515	AT1G49850.1		RING/U-box superfamily protein	RING-H2 finger protein, putative
Sapur.014G120600.1	0.156527714	-0.37447784	0.585890295	-0.63916	0.522718629	0.597966102	brown	-0.132095106	0.09911581		AT4G29400.1		Protein of unknown function (DUF3531)	oxidoreductase/transition metal ion-binding protein, putative
Sapur.019G029200.1	1.203324214	-0.155895126	0.244953451	-0.63643	0.524497787	0.599628061	brown	-0.056338823	0.483403348		AT3G04450.2		Homeodomain-like superfamily protein	transcription factor, putative
Sapur.007G067500.2	0.383075531	-0.246919345	0.389436931	-0.63404	0.526053456	0.601115672	brown	-0.094142785	0.240881618	GO:0005681,GO:0000398	AT5G08290.1	YLS8	mRNA splicing factor, thioredoxin-like U5 snRNP	thioredoxin-like protein 4A
Sapur.014G104800.6	2.247844393	-0.140198058	0.222013105	-0.63149	0.527723124	0.602794495	brown	-0.075807744	0.345355424	GO:0030975,GO:0009229,GO:0005524,GO:0004788	AT1G02880.1	TPK1	thiamin pyrophosphokinase1	thiamine pyrophosphokinase
Sapur.006G026100.1	0.774139851	-0.200552486	0.321340409	-0.62411	0.532553869	0.60770379	brown	-0.115782905	0.148732318	GO:0006508,GO:0004185	AT1G28110.1	SCPL45	serine carboxypeptidase-like 45	serine carboxypeptidase
Sapur.016G144600.1	0.522132777	0.243233688	0.393050814	0.618835	0.536024915	0.611390421	brown	0.011641541	0.884941943	GO:0006468,GO:0004672	AT5G12480.1	CPK7	calmodulin-domain protein kinase 7	calcium-dependent kinase
Sapur.008G143300.2	0.418284691	0.232703258	0.376687624	0.617762	0.536732309	0.612049524	brown	-0.151017222	0.059031071	GO:0051603,GO:0005839,GO:0004298	AT3G26340.1		N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	proteasome subunit beta type-5 protein
Sapur.005G161300.3	0.192909026	0.444327253	0.719977668	0.61714	0.537142171	0.612474667	brown	0.084502307	0.292692607		AT1G53580.1	ETHE1,GLX2-3,GLY3	glyoxalase II 3	hydroxyacylglutathione hydrolase
Sapur.001G166200.2	0.326964009	0.262004943	0.424617041	0.617038	0.537209516	0.612530339	brown	0.000309292	0.996932577	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G79850.1	CS17,PRPS17,RPS17	ribosomal protein S17	30S ribosomal protein S17
Sapur.006G086600.1	0.186554887	-0.589183059	0.95742511	-0.61538	0.538301869	0.613691221	brown	-0.090253814	0.26095534	GO:0030036,GO:0005856	AT5G01730.1	ATSCAR4,SCAR4,WAVE3	SCAR family protein 4	SCAR2
Sapur.010G170400.2	0.222102526	0.341953814	0.556130417	0.614881	0.538633564	0.61402704	brown	-0.132856757	0.097166331					HMG (high mobility group) box protein
Sapur.002G051000.3	1.217624802	0.148843313	0.242267505	0.614376	0.538966969	0.614343587	brown	0.078548531	0.32814497		AT4G09810.1		Nucleotide-sugar transporter family protein	triose-phosphate transporter family protein
Sapur.002G112700.1	1.936511003	-0.126362568	0.207850286	-0.60795	0.543220677	0.618765693	brown	-0.041204179	0.608385875		AT4G17520.1		Hyaluronan / mRNA binding family	nuclear RNA-binding protein
Sapur.009G024400.1	0.105651651	-0.547948614	0.908883289	-0.60288	0.546587748	0.622151054	brown	-0.316115004	5.50E-05		AT1G07530.1	ATGRAS2,GRAS2,SCL14	SCARECROW-like 14	GRAS family transcription factor
Sapur.017G100200.4	0.132016741	-0.411835058	0.686713052	-0.59972	0.548693335	0.624078887	brown	-0.081608864	0.309590942		AT2G24960.1			Myb/SANT-like DNA-binding domain protein
Sapur.002G128800.2	0.116715449	-0.609590182	1.021571641	-0.59672	0.550695676	0.625959602	brown	-0.238598614	0.00261826		AT2G45820.1		Remorin family protein	remorin, amino-terminal region protein
Sapur.013G003900.1	0.713399761	-0.175765175	0.296701792	-0.5924	0.553584948	0.628838734	brown	-0.049676763	0.536670493		AT1G09430.1	ACLA-3	ATP-citrate lyase A-3	ATP-citrate synthase
Sapur.001G173500.1	0.181504567	-0.452435022	0.773052029	-0.58526	0.558374132	0.633865318	brown	-0.133162772	0.096391675		AT3G26070.1		Plastid-lipid associated protein PAP / fibrillin family protein	PAP fibrillin
Sapur.016G062200.7	0.154439781	-0.445781097	0.763569602	-0.58381	0.559346804	0.634773408	brown	-0.181606257	0.022828152		AT5G06440.2			START-2 domain protein, putative
Sapur.011G031100.5	1.02535901	0.144066143	0.249920492	0.576448	0.564312474	0.639706292	brown	-0.063887384	0.426658752	GO:0005515	AT1G61150.1		LisH and RanBPM domains containing protein	Ran-binding protein in the microtubule-organising centre protein
Sapur.010G206600.4	0.174688751	-0.326020511	0.573210345	-0.56876	0.569517372	0.644899259	brown	-0.141143795	0.077861357	GO:0005515,GO:0051013,GO:0008352,GO:0008017	AT5G23430.1		Transducin/WD40 repeat-like superfamily protein	katanin p80 subunit-like protein
Sapur.003G074400.3	11.60037284	-0.055757086	0.098119154	-0.56826	0.569859162	0.645220017	brown	-0.035938308	0.654982164		AT2G45010.1		PLAC8 family protein	cell number regulator 6
Sapur.014G127100.2	0.542519483	0.2217621	0.390348642	0.568113	0.569958308	0.645310183	brown	0.009389431	0.907088552		AT3G21610.1		Acid phosphatase/vanadium-dependent haloperoxidase-related protein	NA
Sapur.014G114800.6	0.177189326	-0.402910484	0.709269626	-0.56806	0.569991566	0.645325747	brown	-0.067118091	0.403599932		AT1G06460.1	ACD31.2,ACD32.1	alpha-crystallin domain 32.1	small heat-shock protein, putative
Sapur.018G001800.1	0.090659331	0.544857175	0.959698423	0.567738	0.570212947	0.64555429	brown	-0.045749625	0.569384396		AT4G15060.1			NA
Sapur.016G119700.3	0.138256655	-0.742866326	1.31858192	-0.56338	0.573174271	0.648596067	brown	-0.121570996	0.129332589	GO:0005975,GO:0004553	AT2G44480.1	BGLU17	beta glucosidase 17	glycoside hydrolase family 1 protein
Sapur.016G119700.4	0.138683339	-0.445038181	0.790715643	-0.56283	0.573550912	0.648933459	brown	-0.010354245	0.89759107	GO:0005975,GO:0004553	AT2G44480.1	BGLU17	beta glucosidase 17	glycoside hydrolase family 1 protein
Sapur.019G078600.1	3.383922989	-0.081714692	0.145707103	-0.56081	0.574923831	0.650153206	brown	-0.063926472	0.426375295		AT1G07400.1		HSP20-like chaperones superfamily protein	17.5 kDa class I heat shock protein
Sapur.001G089100.1	0.134590413	-0.57434836	1.026662877	-0.55943	0.575866733	0.65106366	brown	-0.133926031	0.094480849		AT1G63100.1		GRAS family transcription factor	GRAS family transcription factor
Sapur.003G131900.1	0.728929377	-0.164730276	0.294484627	-0.55938	0.575899013	0.651077899	brown	-0.044861929	0.576907604	GO:0006468,GO:0005524,GO:0004672	AT2G33170.1		Leucine-rich repeat receptor-like protein kinase family protein	LRR receptor-like kinase plant, putative
Sapur.15WG019200.1	0.208336988	-0.309752278	0.561697474	-0.55146	0.581320102	0.656107734	brown	-0.100494757	0.210458313	GO:0005524,GO:0003676,GO:0004386	AT3G26560.1		ATP-dependent RNA helicase, putative	ATP-dependent RNA helicase DHX8
Sapur.004G009100.2	0.105865287	-0.583885357	1.068852222	-0.54627	0.584878134	0.659650789	brown	-0.29819967	0.000148692	GO:0003824	AT1G78960.1	ATLUP2,LUP2	lupeol synthase 2	beta-amyrin synthase
Sapur.006G140200.1	7.516881285	-0.137919221	0.25261608	-0.54596	0.585090858	0.659845707	brown	-0.045866463	0.568397661	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G31500.1	ATR4.CYP83B1.RED1.RNT1.	cytochrome P450, family 83, subfamily B, polypeptide 1	NA
Sapur.008G037100.1	0.261956069	-0.343889836	0.632057116	-0.54408	0.586386205	0.661103672	brown	-0.052073838	0.517173237		AT5G13560.1			hypothetical protein
Sapur.006G126700.4	24.49068785	-0.038317554	0.070813291	-0.54111	0.588433966	0.66307332	brown	-0.087772236	0.274347414		AT4G29330.1	DER1	DERLIN-1	derlin protein
Sapur.001G039600.1	0.108419075	-0.547676064	1.012800247	-0.54075	0.588676963	0.663324539	brown	-0.119706309	0.13535743					transmembrane protein, putative
Sapur.019G044400.1	0.205995893	0.387049832	0.716011621	0.540564	0.5888084	0.663427439	brown	0.103233841	0.198226709		AT5G14930.2	SAG101	senescence-associated gene 101	NA
Sapur.005G145000.1	0.176781333	-0.399965266	0.740353511	-0.54024	0.589034618	0.663591898	brown	-0.114502612	0.153306369	GO:0008168	AT2G34300.2		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase PMT24, putative
Sapur.008G143100.1	6.585255512	0.065572384	0.121768586	0.5385	0.590231902	0.664736947	brown	0.036045058	0.65402341		AT5G20165.1			NA
Sapur.008G148900.1	0.130162847	-0.514104793	0.959889028	-0.53559	0.592243505	0.666820824	brown	-0.205910025	0.009675562		AT1G13030.1		sphere organelles protein-related	hypothetical protein
Sapur.003G113200.1	0.401729981	-0.203514461	0.382251184	-0.53241	0.594441864	0.66906824	brown	-0.062108632	0.439672402	GO:0006281,GO:0003684	AT5G44740.2	POLH	Y-family DNA polymerase H	DNA polymerase eta
Sapur.009G011900.1	0.153157425	-0.74573927	1.401185234	-0.53222	0.594573403	0.669170746	brown	-0.134053703	0.094164176	GO:0019773,GO:0006511,GO:0004175,GO:0051603,GO:0005839,GO:0004298	AT2G27020.1	PAG1	20S proteasome alpha subunit G1	proteasome subunit alpha type-3 protein
Sapur.018G002100.1	0.153423645	-0.447503498	0.841953351	-0.53151	0.595067987	0.669806806	brown	-0.154961016	0.052640035		AT3G14470.1		NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.T032000.1	0.224396774	-0.300154656	0.565807178	-0.53049	0.595772723	0.670292446	brown	-0.102815932	0.200058868	GO:0005509	AT4G13440.1		Calcium-binding EF-hand family protein	calcium ion-binding protein, putative
Sapur.008G051500.1	448.8377285	-0.020106851	0.037992616	-0.52923	0.596645556	0.671114648	brown	-0.079387108	0.322991255	GO:0005515	AT1G07310.1		Calcium-dependent lipid-binding (CaLB domain) family protein	C2 domain protein
Sapur.016G251600.3	0.969866377	0.171662002	0.324562315	0.528903	0.596872698	0.671278823	brown	0.073300178	0.361591226	GO:0004635,GO:0000105	AT1G31860.1	AT-IE,HISN2	histidine biosynthesis bifunctional protein (HISIE)	histidine biosynthesis hisIE protein
Sapur.009G055500.1	0.118266075	-0.609625458	1.155743641	-0.52747	0.597864024	0.672233716	brown	-0.157238243	0.049218152	GO:0006412,GO:0005840,GO:0003735	AT4G29430.1	rps15ae	ribosomal protein S15A E	40S ribosomal protein S15a
Sapur.010G165700.2	0.106316285	-0.603238917	1.14985054	-0.52462	0.599844764	0.674094177	brown	-0.208977757	0.008623602	GO:0019898,GO:0015979,GO:0009654,GO:0009523,GO:0005509	AT2G39470.1	PPL2	PsbP-like protein 2	photosystem II reaction center PsbP family protein
Sapur.016G054200.2	0.139999558	-0.39989589	0.763401314	-0.52383	0.600393706	0.674622799	brown	-0.205396882	0.009862172	GO:0017025,GO:0008270,GO:0006355,GO:0006352	AT3G10330.1		Cyclin-like family protein	transcription initiation factor IIB
Sapur.008G010600.1	12.4892212	-0.066116465	0.127041409	-0.52043	0.602762237	0.676911134	brown	-0.049633334	0.538424059	GO:0048544	AT5G03700.1		D-mannose binding lectin protein with Apple-like carbohydrate-binding domain	D-mannose-binding lectin protein
Sapur.006G194800.1	0.872150004	-0.162509105	0.316805298	-0.51296	0.607977846	0.681867049	brown	-0.089502868	0.264959771		AT2G19770.1	PRF5	profilin 5	profilin
Sapur.001G038600.3	0.20071973	-0.31345612	0.61538142	-0.50937	0.610493713	0.684294204	brown	-0.098197112	0.221128293	GO:0005515	AT1G80670.1		Transducin/WD40 repeat-like superfamily protein	RNA export protein
Sapur.008G071800.7	0.599571201	-0.180931285	0.356533435	-0.50747	0.611822595	0.685667543	brown	-0.04448641	0.580104026	GO:0016020	AT1G69450.1		Early-responsive to dehydration stress protein (ERD4)	early-responsive to dehydration stress protein (ERD4), putative
Sapur.002G186500.1	0.125030094	-0.665842248	1.31656227	-0.50574	0.613037026	0.686820535	brown	-0.133295837	0.096056359	GO:0005525	AT3G07050.1		GTP-binding family protein	GTP-binding protein, putative
Sapur.018G066900.1	0.487324236	0.188928738	0.377482394	0.500497	0.616725295	0.690273178	brown	-0.05574026	0.488070096	GO:0016021,GO:0004659	AT2G18950.1	ATHPT,HPT1,TPT1,VTE2	homogentisate phytyltransferase 1	homogentisate phytyltransferase
Sapur.014G034900.1	0.205819127	-0.28228178	0.564968536	-0.49964	0.617327464	0.690853642	brown	-0.120803464	0.131787034	GO:0006457	AT3G60370.1		FKBP-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase
Sapur.019G006100.1	0.200195403	0.290532715	0.58193766	0.499251	0.617602865	0.691091693	brown	0.056234349	0.484216154					hypothetical protein
Sapur.006G128300.1	4.99922614	-0.127960041	0.25670849	-0.49846	0.618156762	0.691571111	brown	-0.034244468	0.670269588	GO:0005515	AT1G76900.2	AtTLP1,TLP1	tubby like protein 1	tubby-like F-box protein
Sapur.007G013900.2	0.161106606	-0.49910671	1.005442161	-0.49641	0.619608562	0.693007798	brown	-0.090480608	0.259754149	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT5G66320.2	GATA5	GATA transcription factor 5	GATA transcription factor
Sapur.008G039700.1	0.200496776	-0.364111718	0.739137935	-0.49262	0.62228342	0.695458601	brown	-0.058682934	0.465360419	GO:0005525	AT5G59840.1		Ras-related small GTP-binding family protein	Ras small GTPase family Ras protein
Sapur.012G077200.1	3.01501218	-0.087395434	0.177557983	-0.49221	0.622572412	0.695687545	brown	-0.033203956	0.679728541		AT4G24960.1	ATHVA22D,HVA22D	HVA22 homologue D	TB2/DP1, HVA22 family protein
Sapur.006G164800.1	0.2016689	0.276506835	0.56793762	0.486861	0.626356642	0.699296948	brown	0.073139224	0.362649294	GO:0008270,GO:0005515	AT5G06490.1		RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.002G030700.3	0.172111061	-0.325845753	0.670369709	-0.48607	0.626918436	0.699881873	brown	-0.17573575	0.027698605		AT2G31260.1	APG9,ATAPG9	autophagy 9 (APG9)	autophagy protein Apg9 containing protein
Sapur.013G085000.5	4.041396492	0.1014771	0.209184679	0.485108	0.627599945	0.700571757	brown	-0.290142606	0.000227772		AT3G26580.1		Tetratricopeptide repeat (TPR)-like superfamily protein	transmembrane protein, putative
Sapur.006G028500.2	0.12042594	0.419411556	0.865385542	0.484653	0.627922629	0.700884648	brown	-0.081608864	0.309590942		AT5G09225.1			transmembrane protein, putative
Sapur.001G046300.1	5.143850074	-0.084858383	0.178394295	-0.47568	0.63430323	0.707099836	brown	-0.046089649	0.566515038		AT1G67340.1		HCP-like superfamily protein with MYND-type zinc finger	zinc finger protein, putative
Sapur.012G110600.4	0.123465236	-0.515433246	1.083923452	-0.47553	0.634412459	0.707197765	brown	-0.177835004	0.025863715	GO:0055085,GO:0016021	AT1G02260.1		Divalent ion symporter	silicon transporter
Sapur.016G286300.1	0.182965488	0.355888269	0.750710036	0.474069	0.635450787	0.708164274	brown	-0.074944011	0.350895124	GO:0004674,GO:0006468,GO:0004672	AT3G16030.1	CES101	lectin protein kinase family protein	Serine/Threonine-kinase
Sapur.014G037100.1	0.165984781	-0.371985781	0.788508675	-0.47176	0.637099075	0.709690304	brown	-0.105047747	0.190415129		AT4G17520.1		Hyaluronan / mRNA binding family	nuclear RNA-binding protein, putative
Sapur.002G173800.1	0.149995408	-0.391764426	0.833605344	-0.46996	0.638380803	0.711022283	brown	-0.158798103	0.046982547		AT2G31340.1	emb1381	embryo defective 1381	embryo defective 1381 protein
Sapur.017G014700.1	0.503574553	0.145037785	0.313904851	0.462044	0.644049922	0.716491998	brown	0.00296865	0.970564806		AT2G28580.1		Plant protein of unknown function (DUF247)	NA
Sapur.15WG078400.1	1.95353649	0.084569878	0.183137007	0.461785	0.644235684	0.716650444	brown	0.055451343	0.490331243	GO:0031225,GO:0016049,GO:0010215	AT5G60920.1	COB	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family	phytochelatin synthetase-like protein
Sapur.001G016600.5	3.912874615	-0.065006158	0.141599003	-0.45909	0.646172219	0.718562973	brown	0.048620683	0.544878692	GO:0008270,GO:0005515	AT3G63530.1	BB,BB2	RING/U-box superfamily protein	E3 ubiquitin-protein ligase
Sapur.014G081500.5	20.4369506	0.031149356	0.067911833	0.458673	0.646468664	0.71883676	brown	-0.108817865	0.174901877	GO:0016773,GO:0016020,GO:0005524	AT2G46700.1	ATCRK3,CRK3	CDPK-related kinase 3	CDPK-related kinase, putative
Sapur.016G115600.1	0.150954516	-0.299599837	0.660209728	-0.45379	0.649974422	0.721992282	brown	-0.102577387	0.201110152	GO:0006468,GO:0005524,GO:0004672	AT3G23750.1		Leucine-rich repeat protein kinase family protein	receptor-like kinase, putative
Sapur.004G165500.1	0.183793455	-0.453714322	0.999907231	-0.45376	0.650004156	0.72199884	brown	-0.076212776	0.342776806		AT1G08470.1	SSL3	strictosidine synthase-like 3	strictosidine synthase
Sapur.006G043700.7	0.240772708	-0.277873198	0.613928615	-0.45261	0.650826115	0.722741931	brown	-0.092719099	0.248101476	GO:0006468,GO:0005524,GO:0004672	AT3G20860.1	ATNEK5,NEK5	NIMA-related kinase 5	Serine/Threonine kinase domain protein
Sapur.001G117300.2	0.112415893	-0.548082703	1.212622484	-0.45198	0.651282445	0.72317584	brown	-0.188474214	0.018082237					transmembrane protein, putative
Sapur.006G134900.1	184.7587442	-0.022382131	0.04957602	-0.45147	0.651650187	0.723389887	brown	-0.073692335	0.359021337	GO:0015450,GO:0006886,GO:0005744	AT1G20350.1	ATTIM17-1,TIM17-1	translocase inner membrane subunit 17-1	import inner membrane translocase subunit Tim17
Sapur.016G032100.1	0.669392493	0.146689129	0.325213139	0.451055	0.651949651	0.723698028	brown	0.0244157	0.761487208	GO:0008017,GO:0007010	AT1G68060.1	ATMAP70-1,MAP70-1	microtubule-associated proteins 70-1	microtubule associated protein
Sapur.008G051900.2	0.167917322	-0.38169403	0.850672643	-0.4487	0.653650447	0.725391231	brown	-0.100514853	0.21036665	GO:0016020,GO:0006810,GO:0005215	AT2G45960.2	ATHH2.PIP1:2.PIP1B.TMP-A	plasma membrane intrinsic protein 1B	plasma membrane intrinsic protein PIP1-1
Sapur.009G041800.1	0.126418215	-0.352373737	0.786944823	-0.44777	0.654316029	0.726056778	brown	-0.242168091	0.00224516		AT3G51970.1	ASAT1,ATASAT1,ATSAT1	acyl-CoA sterol acyl transferase 1	membrane-bound O-acyltransferase family MBOAT protein
Sapur.T138000.1	1.418809606	-0.116162062	0.259453947	-0.44772	0.65435712	0.726078015	brown	-0.107039892	0.182097306	GO:0005524,GO:0051082,GO:0006457	AT3G02530.1		TCP-1/cpn60 chaperonin family protein	NA
Sapur.013G136600.2	0.14995224	-0.333160657	0.745083487	-0.44715	0.654770077	0.726390016	brown	-0.134560862	0.092914553		AT5G37055.1	ATSWC6,SEF	HIT-type Zinc finger family protein	zinc finger protein
Sapur.007G041600.1	0.149797806	-0.493218034	1.10380877	-0.44683	0.65499574	0.726591619	brown	-0.098128077	0.221454721	GO:0003676	AT4G36960.2		RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein G RNA recognition motif protein
Sapur.006G131200.3	0.106282433	-0.512556901	1.147439809	-0.4467	0.65509449	0.726652418	brown	-0.181153323	0.023175729		AT2G18660.1	PNP-A	plant natriuretic peptide A	rare lipoprotein A-like double-psi beta-barrel protein
Sapur.016G194300.1	0.139152045	-0.77837881	1.750686973	-0.44461	0.656599194	0.728101715	brown	-0.122846506	0.125331668		AT4G30990.1		ARM repeat superfamily protein	small subunit processome component-like protein, putative
Sapur.018G017900.1	0.090918958	-0.476392054	1.079748636	-0.44121	0.65906355	0.730540514	brown	-0.267367835	0.000711312		AT5G10970.1		C2H2 and C2HC zinc fingers superfamily protein	NA
Sapur.007G081900.1	0.100978596	-0.474368175	1.080456189	-0.43904	0.660629408	0.732104441	brown	-0.213563224	0.007239705	GO:0005975,GO:0004553,GO:0051015,GO:0007015				glucan 1%2C3-beta-glucosidase
Sapur.014G009300.3	0.201149782	0.208275111	0.478700348	0.435085	0.66350108	0.735089764	brown	-0.081608864	0.309590942	GO:0006352,GO:0005669	AT5G43130.2	TAF4,TAF4B	TBP-associated factor 4	transcription initiation factor, putative
Sapur.002G087700.1	0.278112248	-0.242773858	0.56000176	-0.43352	0.664634582	0.736222258	brown	-0.053483621	0.505878445		AT2G22660.2		Protein of unknown function (duplicated DUF1399)	NA
Sapur.002G152300.2	0.266535099	-0.182213802	0.420883274	-0.43293	0.665064233	0.736565368	brown	-0.107629849	0.179686048		AT2G47940.1	DEGP2	DEGP protease 2	NA
Sapur.016G016300.2	0.313190928	0.164083877	0.37958134	0.432276	0.665540878	0.737028695	brown	-0.088579536	0.269940664		AT3G48880.2		RNI-like superfamily protein	F-box protein
Sapur.008G125300.1	0.098562001	-0.435994109	1.015168847	-0.42948	0.667574381	0.738735096	brown	-0.239793555	0.002487533		AT3G22550.1		Protein of unknown function (DUF581)	DUF581 family protein
Sapur.002G135600.1	0.17480967	-0.399880032	0.934181152	-0.42805	0.668611765	0.739562741	brown	-0.105260864	0.189512287	GO:0005525	AT1G02280.1	ATTOC33,PPI1,TOC33	translocon at the outer envelope membrane of chloroplasts 33	translocase of protein
Sapur.011G082200.1	0.122261484	-0.550802712	1.291739999	-0.4264	0.669813708	0.740514081	brown	-0.213487011	0.007260989		AT1G53035.1			transmembrane protein, putative
Sapur.007G016700.1	0.120285989	-0.512479952	1.208046702	-0.42422	0.67140394	0.741906849	brown	-0.207122461	0.009246977	GO:0005515	AT4G18905.1		Transducin/WD40 repeat-like superfamily protein	transducin/WD40 domain protein
Sapur.15WG073600.1	0.103142122	-0.459298291	1.086857472	-0.42259	0.672592281	0.743001346	brown	-0.167283264	0.036252601	GO:0016747	AT5G48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	NA
Sapur.006G064500.1	0.157287839	-0.339304656	0.805413408	-0.42128	0.673550546	0.743831539	brown	-0.129095965	0.107094324		AT2G07170.1		ARM repeat superfamily protein	microtubule-associated protein TORTIFOLIA protein
Sapur.T115200.1	0.129050435	-0.318303252	0.757601444	-0.42015	0.674378766	0.744621864	brown	-0.09301752	0.246575828		AT4G38620.1	ATMYB4,MYB4	myb domain protein 4	NA
Sapur.005G101400.1	28.73416483	0.032425255	0.077624937	0.417717	0.676154044	0.746357803	brown	0.02376023	0.767705544		AT1G75080.1	BZR1	Brassinosteroid signalling positive regulator (BZR1) family protein	brassinazole-resistant 1 protein, putative
Sapur.008G027700.1	0.098924294	0.446793432	1.07608194	0.415204	0.677992635	0.748137604	brown	-0.055353251	0.491100204		AT5G03300.1	ADK2	adenosine kinase 2	adenosine kinase
Sapur.004G084500.1	0.099380561	0.420896242	1.021651282	0.411976	0.680356704	0.750395759	brown	0.122341784	0.126903266		AT5G16080.1	AtCXE17,CXE17	carboxyesterase 17	carboxylesterase
Sapur.008G050400.1	0.170114388	-0.350547327	0.85382732	-0.41056	0.681395215	0.751415888	brown	-0.119276144	0.136777309		AT2G39910.1		ARM repeat superfamily protein	DUF2454 family protein
Sapur.005G074800.1	0.109272124	-0.606499874	1.501256854	-0.40399	0.686216586	0.75595135	brown	-0.160817185	0.044215015	GO:0005515,GO:0006396,GO:0003723	AT1G14650.1		SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin family protein	suppressor-of-white-APricot splicing regulator, putative
Sapur.007G090200.2	2.54130316	0.090178003	0.233368833	0.386418	0.699186852	0.768243777	brown	-0.057620803	0.473489504		AT5G09220.1	AAP2	amino acid permease 2	amino acid permease
Sapur.010G023000.1	0.11662888	-0.436356351	1.131186288	-0.38575	0.699681016	0.768684602	brown	-0.184619398	0.020628088	GO:0003824,GO:0006470,GO:0004722	AT1G67820.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.014G136500.1	1.021412775	-0.117571187	0.308633092	-0.38094	0.703246575	0.771858274	brown	-0.029082652	0.717674064	GO:0005515	AT4G16360.3		5\'-AMP-activated protein kinase beta-2 subunit protein	SNF1-related kinase regulatory subunit beta-2
Sapur.007G006400.3	0.317514774	-0.161403365	0.425668923	-0.37918	0.704557303	0.772930918	brown	-0.081608864	0.309590942		AT5G65740.2		zinc ion binding	NA
Sapur.001G042600.1	0.081780337	-0.432300118	1.140492902	-0.37905	0.704653154	0.772969095	brown	-0.29817397	0.000148897					transmembrane protein, putative
Sapur.15WG107300.1	0.107689941	0.360817789	0.962081893	0.375039	0.707631804	0.775641754	brown	0.100891118	0.208655624	GO:0055085,GO:0016020,GO:0006810,GO:0005215,GO:0006863,GO:0005345	AT5G50300.1	ATAZG2,AZG2	Xanthine/uracil permease family protein	adenine/guanine permease
Sapur.010G023300.2	0.159577535	-0.28733407	0.770513943	-0.37291	0.709213772	0.777118218	brown	-0.114646807	0.152785977		AT1G67850.2		Protein of unknown function (DUF707)	lysine ketoglutarate reductase trans-splicing protein
Sapur.009G060800.1	2.936301944	0.062836997	0.168555954	0.372796	0.709300231	0.777187206	brown	0.014587437	0.856109274		AT1G07030.1		Mitochondrial substrate carrier family protein	substrate carrier family protein
Sapur.006G017900.1	0.145364825	-0.284405606	0.764412219	-0.37206	0.709849739	0.777686253	brown	-0.148508728	0.063418498	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G46950.1	CYP709B2	cytochrome P450, family 709, subfamily B, polypeptide 2	cytochrome P450 family protein
Sapur.010G028000.8	0.64326285	-0.116130523	0.315627476	-0.36794	0.712921399	0.78037936	brown	-0.114218666	0.154335013	GO:0005975,GO:0004650	AT1G60590.1		Pectin lyase-like superfamily protein	polygalacturonase
Sapur.006G144100.1	0.713064239	-0.106149414	0.291206087	-0.36452	0.71547238	0.782731328	brown	-0.060619457	0.450738837					NA
Sapur.003G148500.1	0.11246572	-0.438558428	1.212988699	-0.36155	0.717686878	0.784505265	brown	-0.190532819	0.016837795	GO:0008017,GO:0000910,GO:0000226	AT2G38720.1	MAP65-5	microtubule-associated protein 65-5	microtubule-associated protein
Sapur.15WG075100.1	0.139381931	-0.274352401	0.76495917	-0.35865	0.719857138	0.786487678	brown	-0.133810726	0.094767571	GO:0016747	AT5G48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	NA
Sapur.011G100300.1	0.379096508	-0.172343567	0.480601792	-0.3586	0.719894714	0.786502751	brown	-0.01340157	0.867695185	GO:0044599	AT3G15160.1			NA
Sapur.005G162700.1	0.231003892	-0.19379038	0.545346268	-0.35535	0.722325226	0.788897551	brown	-0.060163039	0.454161601	GO:0005524,GO:0003676,GO:0004386	AT2G30800.1	ATVT-1,HVT1	helicase in vascular tissue and tapetum	ATP-dependent RNA helicase, putative
Sapur.011G011300.1	0.096219333	-0.494501861	1.406987176	-0.35146	0.725242131	0.79161276	brown	-0.134494686	0.093076857	GO:0005515	AT1G62390.1		Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protei	heat shock protein 70 (HSP70)-interacting protein, putative
Sapur.15WG004600.1	0.090058996	-0.529742914	1.511307212	-0.35052	0.725948727	0.792227148	brown	-0.16203879	0.042607715	GO:0005515	AT4G00820.1	iqd17	IQ-domain 17	IQ calmodulin-binding motif protein, putative
Sapur.003G079600.3	3.252117272	-0.05615465	0.16046257	-0.34995	0.726372606	0.792663573	brown	-0.02584339	0.747996114		AT4G12230.1		alpha/beta-Hydrolases superfamily protein	esterase/lipase/thioesterase family protein, putative
Sapur.008G055800.1	0.842385599	0.102591159	0.300037562	0.341928	0.732405289	0.797746501	brown	0.019822332	0.805362898	GO:0030132,GO:0030130,GO:0016192,GO:0006886,GO:0005198	AT3G11130.1		Clathrin, heavy chain	clathrin heavy chain
Sapur.010G153800.3	1.312668411	0.101159206	0.296898695	0.34072	0.733314678	0.798579226	brown	0.013203344	0.869634671		AT2G39855.1			hypothetical protein
Sapur.003G002300.3	0.116434185	-0.386101776	1.143855711	-0.33754	0.735706754	0.800630599	brown	-0.109526427	0.172093669	GO:0005515,GO:0006414,GO:0003746	AT1G09640.1		Translation elongation factor EF1B, gamma chain	elongation factor 1-gamma 1
Sapur.011G057800.1	0.107939455	-0.364636834	1.081605857	-0.33713	0.736022352	0.800894992	brown	-0.150988928	0.05907913		AT4G18260.1		Cytochrome b561/ferric reductase transmembrane protein family	cytochrome b561/ferric reductase transmembrane family protein, putative
Sapur.009G033900.1	0.132838254	-0.260019193	0.78998621	-0.33674	0.736313635	0.801132876	brown	-0.1646516	0.039333745	GO:0007010,GO:0003779,GO:0051017	AT2G29890.2	ATVLN1,VLN1	villin-like 1	villin, putative
Sapur.003G127100.1	0.261227788	-0.284178031	0.852113624	-0.3335	0.738758539	0.803359174	brown	-0.067562914	0.400483991					NA
Sapur.014G089100.4	0.106837832	-0.400622932	1.216394689	-0.32935	0.74188908	0.806191333	brown	-0.16701653	0.036555317		AT4G01790.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	ribonuclease P, putative
Sapur.016G101100.1	0.120275293	-0.339672302	1.032917061	-0.32885	0.742270878	0.806526727	brown	-0.13176805	0.099962353		AT5G01450.1		RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.008G033000.1	0.213590591	-0.217110153	0.664360367	-0.3268	0.743822365	0.807947088	brown	-0.065527139	0.414861476	GO:0015986,GO:0015078,GO:0000276	AT3G52300.1	ATPQ	ATP synthase D chain, mitochondrial	ATP synthase subunit D
Sapur.15WG012100.2	0.139175014	-0.248636516	0.763598172	-0.32561	0.744718142	0.808734168	brown	-0.107495371	0.180233604	GO:0005515	AT4G27910.1	ATX4,SDG16	SET domain protein 16	histone-lysine N-methyltransferase ATX5
Sapur.012G102900.3	0.132866686	-0.29630879	0.920765231	-0.32181	0.747598834	0.811249839	brown	-0.210786522	0.008051969		AT5G52030.2		TraB family protein	TraB family protein
Sapur.005G027600.6	0.391078131	-0.111898671	0.350709981	-0.31906	0.749678541	0.813053124	brown	-0.081608864	0.309590942	GO:0007264,GO:0005525	AT5G27540.2	emb2473,MIRO1	MIRO-related GTP-ase 1	Rho GTPase
Sapur.013G135300.2	0.166854222	-0.229933508	0.726325513	-0.31657	0.751569233	0.81464952	brown	-0.131600901	0.100397196	GO:0009378,GO:0006310,GO:0006281	AT3G01610.1	CDC48C,emb1354	cell division cycle 48C	cell division control-like protein
Sapur.006G141500.3	0.541780076	0.13051704	0.413031336	0.315998	0.752004093	0.815067454	brown	0.002905577	0.97118993	GO:0005992,GO:0003824	AT2G18700.1	ATTPS11,ATTPSB,TPS11	trehalose phosphatase/synthase 11	trehalose-6-phosphate synthase
Sapur.001G150100.1	0.295342579	-0.144862635	0.46003576	-0.31489	0.752841916	0.815868591	brown	-0.064337646	0.423400182		AT4G08520.1		SNARE-like superfamily protein	nonclathrin coat protein
Sapur.013G036500.2	3.558586837	0.059677788	0.189604865	0.314748	0.752952854	0.815914912	brown	-0.090440828	0.259964563		AT5G28150.1		Plant protein of unknown function (DUF868)	plant/T9J14-19 protein
Sapur.017G127300.1	0.065714757	0.408737658	1.316553185	0.31046	0.756210852	0.81876838	brown	-0.02991047	0.709993026	GO:0055085,GO:0016021,GO:0016020,GO:0006810,GO:0005215	AT5G14940.1		Major facilitator superfamily protein	peptide transporter
Sapur.018G068500.2	3.540234265	0.058083821	0.189233234	0.306943	0.758886741	0.821047435	brown	-0.081608864	0.309590942	GO:0016020,GO:0009055,GO:0008137	AT4G26965.1		NADH:ubiquinone oxidoreductase, 17.2kDa subunit	NA
Sapur.007G000500.1	0.106312885	-0.350831875	1.157593948	-0.30307	0.761836597	0.823646169	brown	-0.106024547	0.18630271	GO:0005524	AT1G50410.1		SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related	DNA helicase
Sapur.008G003300.3	0.182992179	0.208695001	0.695638512	0.300005	0.764173375	0.825929552	brown	0.0018179	0.981972361		AT1G51560.1		Pyridoxamine 5\'-phosphate oxidase family protein	pyridoxamine 5'-phosphate oxidase family protein
Sapur.002G197800.6	0.231950467	-0.152089009	0.515116576	-0.29525	0.767801663	0.829210735	brown	-0.081608864	0.309590942	GO:0005515,GO:0016459,GO:0005524,GO:0003774	AT1G04160.1	ATXIB,XI-8,XI-B,XIB	myosin XI B	myosin XI, putative
Sapur.003G074600.1	0.126333766	-0.416720366	1.414184931	-0.29467	0.768244636	0.829516604	brown	-0.069469733	0.387289961	GO:0006376,GO:0005685,GO:0003729	AT5G51410.2		LUC7 N_terminus domain-containing protein	LUC7 amino-terminal protein
Sapur.014G061500.1	0.192605742	-0.193411696	0.658577622	-0.29368	0.769001719	0.830252754	brown	-0.047063607	0.558334319		AT4G00585.1			hypothetical protein
Sapur.007G066100.2	0.07336734	0.352673473	1.216984039	0.289793	0.771974592	0.833008751	brown	-0.304028922	0.000108358		AT5G23120.1	HCF136	photosystem II stability/assembly factor, chloroplast (HCF136)	photosystem II stability/assembly factor HCF136
Sapur.019G081900.1	0.108133148	-0.51211446	1.767250705	-0.28978	0.771984311	0.833008751	brown	-0.097016228	0.22675915	GO:0052726,GO:0052725,GO:0047325,GO:0032957,GO:0005622,GO:0005524,GO:000028	AT5G16760.1		Inositol 1,3,4-trisphosphate 5/6-kinase family protein	inositol 1%2C3%2C4-trisphosphate 5/6-kinase
Sapur.008G151700.4	0.154107291	-0.210954971	0.72977787	-0.28907	0.772529821	0.833463312	brown	-0.101098129	0.207718533		AT1G23360.1	MENG	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ubiquinone/menaquinone biosynthesis methyltransferase
Sapur.013G087500.1	0.257422348	0.161013449	0.558272504	0.288414	0.773030067	0.833975811	brown	0.004610556	0.954299248	GO:0006468,GO:0005524,GO:0004672	AT1G17910.1		Wall-associated kinase family protein	NA
Sapur.006G017800.2	0.078417473	0.375374985	1.304334244	0.28779	0.773507121	0.834381274	brown	0.032948889	0.682054971		AT4G16660.1		heat shock protein 70 (Hsp 70) family protein	heat shock 70 kDa protein
Sapur.004G084600.1	0.224625227	-0.129209505	0.450188199	-0.28701	0.77410298	0.834833767	brown	-0.133922082	0.094490656		AT1G67140.3	SWEETIE	HEAT repeat-containing protein	NA
Sapur.003G108900.2	0.283401594	0.168298407	0.593234362	0.283696	0.776643113	0.83691823	brown	-0.14191208	0.076240653		AT3G50790.1		esterase/lipase/thioesterase family protein	alpha/beta hydrolase family protein
Sapur.011G089900.1	0.196669462	-0.172130443	0.607937182	-0.28314	0.777070643	0.837269822	brown	-0.116411432	0.146524924	GO:0006468,GO:0004672	AT5G54380.1	THE1	protein kinase family protein	tyrosine kinase domain protein
Sapur.003G165500.1	140.8707724	0.022323759	0.079330875	0.281401	0.778403124	0.838204665	brown	0.010209065	0.8990193	GO:0005515	AT2G44130.1		Galactose oxidase/kelch repeat superfamily protein	F-box protein
Sapur.010G170900.1	2.245877338	0.063225771	0.225685891	0.280149	0.779362871	0.839070721	brown	0.012283692	0.87864272		AT3G55020.1		Ypt/Rab-GAP domain of gyp1p superfamily protein	RabGAP/TBC domain protein
Sapur.001G130300.2	0.188550179	-0.217536228	0.777667623	-0.27973	0.779685387	0.839308144	brown	-0.087797536	0.274208576	GO:0005515,GO:0055114,GO:0046872,GO:0016702	AT1G17420.1	LOX3	lipoxygenase 3	linoleate 13S-lipoxygenase
Sapur.016G119400.1	0.129836339	0.270444919	0.969185278	0.279044	0.780211389	0.839751097	brown	0.052355364	0.514907439		AT5G53530.1	VPS26A	vacuolar protein sorting 26A	vacuolar protein sorting-associated protein
Sapur.T004500.9	0.199135577	0.176334288	0.635986251	0.277261	0.781579577	0.840789195	brown	0.009998025	0.901096024	GO:0003676	AT3G07810.2		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 1 in heterogeneous nuclear ribonucleoprotein A subfamily protein
Sapur.010G054600.4	0.166766262	-0.152041004	0.551959251	-0.27546	0.782965207	0.84203002	brown	-0.21215638	0.007641665	GO:0018342,GO:0008318	AT4G24490.2	ATRGTA1,RGTA1	RAB geranylgeranyl transferase alpha subunit 1	NA
Sapur.013G078500.1	0.088701252	0.276151911	1.013013478	0.272604	0.785157344	0.843975885	brown	-0.052198208	0.516171641	GO:0003723	AT4G13070.1		RNA-binding CRS1 / YhbY (CRM) domain protein	NA
Sapur.019G001900.4	0.138209262	-0.222773571	0.82861299	-0.26885	0.788044216	0.846301905	brown	-0.156562193	0.050214168		AT5G23610.1			hypothetical protein
Sapur.018G119000.4	0.167813119	-0.226082002	0.845618205	-0.26736	0.789194253	0.847241324	brown	-0.067519948	0.400784337		AT5G53530.1	VPS26A	vacuolar protein sorting 26A	vacuolar protein sorting-associated protein
Sapur.016G190700.1	0.155114968	-0.224245025	0.839404641	-0.26715	0.789355437	0.847359355	brown	-0.089830391	0.263208126		AT1G15800.1			hypothetical protein
Sapur.008G090000.3	0.078782249	-0.286260713	1.075749234	-0.2661	0.790159444	0.848139858	brown	-0.092003815	0.251784893	GO:0008725,GO:0006284	AT1G13635.2		DNA glycosylase superfamily protein	DNA-3-methyladenine glycosylase I
Sapur.016G234600.1	0.089282635	-0.325356004	1.224365742	-0.26573	0.790443826	0.848390041	brown	-0.146571214	0.066986923	GO:0008168	AT4G26600.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NOL1/NOP2/sun family RNA methylase, putative
Sapur.005G063000.1	0.100013609	-0.254669234	0.965202966	-0.26385	0.79189516	0.849644473	brown	-0.164816294	0.039134664	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G77940.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L30
Sapur.002G087400.3	0.083254445	0.367297498	1.401541069	0.262067	0.793269879	0.850788248	brown	0.107360602	0.180783578		AT5G64460.2		Phosphoglycerate mutase family protein	phosphoglycerate mutase family protein
Sapur.004G136300.1	0.247054617	-0.168618697	0.645642703	-0.26116	0.79396596	0.851396338	brown	-0.059017514	0.462815694		AT1G47670.1		Transmembrane amino acid transporter family protein	NA
Sapur.002G096900.1	0.112610909	-0.423960182	1.624840943	-0.26092	0.794151029	0.851429581	brown	-0.083560069	0.298126799		AT2G26680.1			FkbM family methyltransferase

Sapur.016G080400.2	0.157827438	-0.194967707	0.750053066	-0.25994	0.794911174	0.852023598	brown	0.02646886	0.74210939		AT3G53470.2			transmembrane protein, putative
Sapur.006G200600.1	0.211150108	-0.139595657	0.537338052	-0.25979	0.795024897	0.852090264	brown	-0.081861714	0.308089289		AT1G12700.1		ATP binding;nucleic acid binding;helicases	NA
Sapur.T117800.1	0.156624236	-0.286952662	1.105801586	-0.2595	0.79525147	0.85230548	brown	-0.050039395	0.533697593					NA
Sapur.013G038700.2	0.077034588	-0.358916842	1.399518759	-0.25646	0.797597726	0.854321756	brown	-0.214950548	0.006861835	GO:0006355,GO:0005634	AT1G04240.1	IAA3,SHY2	AUX/IAA transcriptional regulator family protein	indole-3-acetic acid inducible protein
Sapur.005G020700.1	2.279453078	-0.046211045	0.183412061	-0.25195	0.801078127	0.857300048	brown	0.014061976	0.861239383		AT3G50700.1	AtIDD2,IDD2	indeterminate(ID)-domain 2	zinc finger protein
Sapur.012G057400.1	1.238337575	0.076266082	0.305505596	0.249639	0.80286661	0.858769453	brown	0.024186987	0.763655258	GO:0005515	AT5G40200.1	DegP9	DegP protease 9	serine endopeptidase degp2 protein, putative
Sapur.002G039600.1	0.095563179	-0.441921336	1.775344126	-0.24892	0.803421498	0.859307397	brown	-0.114230923	0.154290505		AT4G02715.1			hypothetical protein
Sapur.15WG151200.1	0.110903486	-0.438158645	1.763664736	-0.24844	0.803796717	0.859604915	brown	-0.069213483	0.389047632		AT5G23890.1			oxidoreductase/transition metal ion-binding protein, putative
Sapur.003G157600.3	0.19119753	0.138101617	0.559907966	0.246651	0.805178666	0.860677249	brown	-0.115732775	0.148909453	GO:0055085,GO:0046873,GO:0030001,GO:0016020	AT3G20870.1	ZTP29	ZIP metal ion transporter family	zinc transporter
Sapur.005G102500.1	0.102035463	0.262435668	1.069516002	0.245378	0.806163784	0.861376913	brown	-0.081608864	0.309590942	GO:0008270	AT4G36860.1	DAR1	LIM domain-containing protein	zinc ion-binding protein, putative
Sapur.005G041800.1	0.090366281	-0.433643315	1.76768145	-0.24532	0.80621055	0.861399054	brown	-0.154896971	0.052739049	GO:0016592,GO:0006357,GO:0001104	AT3G04740.1	ATMED14,MED14,SWP	RNA polymerase II transcription mediators	mediator of RNA polymerase II transcription subunit 14
Sapur.018G103300.1	0.102528616	0.250478594	1.021670736	0.245166	0.806328154	0.861496879	brown	0.068062657	0.397000464	GO:0055085,GO:0008324,GO:0006812	AT4G10310.1	ATHKT1,HKT1	high-affinity K+ transporter 1	sodium transporter HKT1
Sapur.018G116200.1	0.276449083	0.107985661	0.444487591	0.242944	0.808048662	0.862944832	brown	-0.027412593	0.733255588	GO:0030247,GO:0006468,GO:0005524,GO:0004672	AT1G16120.1	WAKL1	wall associated kinase-like 1	tyrosine kinase domain protein
Sapur.010G036100.1	0.135033398	-0.320540059	1.320436837	-0.24275	0.808196714	0.863075074	brown	-0.054193731	0.500238321	GO:0008289	AT4G14500.1		Polyketide cyclase/dehydrase and lipid transport superfamily protein	phosphatidylcholine transfer protein, putative
Sapur.006G150300.2	0.089992749	0.276318373	1.138816321	0.242636	0.808287026	0.863133765	brown	-0.084796066	0.291011963	GO:0016746,GO:0008152	AT4G30580.1	ATS2,EMB1995,LPAT1	Phospholipid/glycerol acyltransferase family protein	1-acyl-sn-glycerol-3-phosphate acyltransferase
Sapur.018G090500.1	212.2507985	-0.018487863	0.076659416	-0.24117	0.809424249	0.863828132	brown	-0.019399706	0.80943277		AT5G11090.1		serine-rich protein-related	hypothetical protein
Sapur.002G016600.1	0.107123104	-0.336993256	1.40961629	-0.23907	0.811053345	0.865203791	brown	-0.080507266	0.316188999					hypothetical protein
Sapur.006G084100.1	0.202224259	0.183481603	0.7709174	0.238004	0.811877813	0.865943654	brown	-0.029772504	0.711271163					transmembrane protein, putative
Sapur.004G170300.1	0.090988626	-0.3108003	1.310051247	-0.23724	0.81246839	0.866381808	brown	-0.134541126	0.092962933	GO:0008270,GO:0003677	AT4G32010.1	HSI2-L1,HSL1,VAL2	HSI2-like 1	transcription factor, putative
Sapur.002G127400.1	0.096877213	0.238675929	1.010855829	0.236113	0.813345196	0.867061371	brown	-0.257737126	0.001118578					transmembrane protein, putative
Sapur.012G085800.2	0.081358508	-0.308590397	1.307539441	-0.23601	0.81342609	0.867119657	brown	-0.164161779	0.039930873		AT5G61670.2			orange protein
Sapur.001G068500.2	0.445689238	0.081542533	0.346891961	0.235066	0.814157446	0.867619647	brown	-0.101476504	0.206013537	GO:0006468,GO:0005524,GO:0004672	AT4G10730.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.001G149900.3	14.23606758	0.020709819	0.088295699	0.234551	0.814557471	0.867926155	brown	-0.177701793	0.025976976	GO:0016787	AT1G72880.1		Survival protein SurE-like phosphatase/nucleotidase	acid phosphatase, putative
Sapur.008G031600.1	0.093076864	-0.352128384	1.506763296	-0.2337	0.81521902	0.86841516	brown	-0.142867068	0.0742642		AT3G52250.1		Duplicated homeodomain-like superfamily protein	nuclear receptor corepressor, putative
Sapur.005G186200.1	0.094027257	-0.325170041	1.394461667	-0.23319	0.815616363	0.868642588	brown	-0.142817054	0.07436667	GO:0005525,GO:0003924,GO:0000287	AT5G18570.1	ATOBGC,CPSAR1,EMB269	GTP1/OBG family protein	GTP-binding protein Obg2, putative
Sapur.017G067900.2	0.282868017	0.106547326	0.467295829	0.228008	0.81963979	0.871833629	brown	-0.009037343	0.91055781	GO:0003677,GO:0043565,GO:0006355,GO:0003700	AT1G69780.1	ATHB13	Homeobox-leucine zipper protein family	transcription factor, putative
Sapur.018G097600.2	1.802493851	0.058440523	0.257156217	0.227257	0.820223989	0.872229703	brown	0.038045359	0.636164025	GO:0016157,GO:0005985	AT5G20280.1	ATSPS1F,SPS1F	sucrose phosphate synthase 1F	sucrose phosphate synthase
Sapur.010G140700.1	0.076285023	0.260384365	1.14856013	0.226705	0.820653111	0.872629919	brown	0.070113071	0.38289837	GO:0006355,GO:0003700,GO:0007275	AT5G17430.1	BBM	Integrase-type DNA-binding superfamily protein	AP2-like ethylene-responsive transcription factor BBM2
Sapur.013G026400.3	0.184823921	-0.162489269	0.72110377	-0.22533	0.821719374	0.873426744	brown	-0.113721862	0.156147258	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT3G05030.1	ATNHX2,NHX2	sodium hydrogen exchanger 2	NA
Sapur.004G045600.1	0.269194514	-0.165025493	0.748360373	-0.22052	0.825469254	0.87656746	brown	-0.016350766	0.838938912	GO:0016491	AT4G18360.1		Aldolase-type TIM barrel family protein	peroxisomal (S)-2-hydroxy-acid oxidase, putative
Sapur.014G081800.1	0.072624018	-0.394304623	1.791571419	-0.22009	0.825802076	0.876765631	brown	-0.155160182	0.052333104		AT4G00850.1	GIF3	GRF1-interacting factor 3	NA
Sapur.016G184300.1	0.072092117	-0.431718642	1.966259468	-0.21956	0.826211187	0.87702202	brown	-0.17973899	0.024290516		AT1G76750.1		Protein of unknown function (DUF1278)	prolamin-like protein
Sapur.006G210900.1	0.272370851	-0.099922316	0.455555303	-0.21934	0.82638381	0.87708806	brown	-0.025644018	0.749875616	GO:0005543	AT2G25430.1		epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	clathrin assembly protein, putative
Sapur.001G140200.1	0.111785148	-0.274600925	1.267677381	-0.21662	0.828506558	0.87899011	brown	-0.121897816	0.128298203	GO:0016020,GO:0006810,GO:0005215	AT5G47450.1	ATTIP2:3.DELTA-TIP3.TIP2:	tonoplast intrinsic protein 2;3	aquaporin TIP-type protein, putative
Sapur.016G150200.2	0.091022358	-0.325079415	1.509934545	-0.21529	0.829538331	0.879814993	brown	-0.102533933	0.201302085	GO:0043531	AT3G14470.1		NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.011G050400.3	19.02088719	-0.017365279	0.081756786	-0.2124	0.831793668	0.881359126	brown	-0.152563263	0.056453515		AT1G78700.1	BEH4	BES1/BZR1 homolog 4	brassinosteroid signaling positive regulator-like protein, putative
Sapur.15WG116100.2	0.108652034	-0.202944796	0.96095037	-0.21119	0.832737644	0.881992021	brown	-0.149301217	0.062004468	GO:0046872,GO:0030001	AT5G50740.1		Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.004G095900.1	0.081780494	-0.34601333	1.642408064	-0.21067	0.833141354	0.882391352	brown	-0.12591537	0.116097163	GO:0016758,GO:0005789	AT5G38460.2		ALG6, ALG8 glycosyltransferase family	ALG6, ALG8 glycosyltransferase family protein
Sapur.009G098900.1	64.4142282	-0.02406235	0.116316574	-0.20687	0.836111785	0.885055567	brown	-0.019299147	0.810401912		AT4G34700.1		LYR family of Fe/S cluster biogenesis protein	NADH ubiquinone oxidoreductase B22-like subunit
Sapur.003G018100.2	0.136837161	-0.171059883	0.828520515	-0.20646	0.836428272	0.885229555	brown	-0.10138602	0.206420347	GO:0016887,GO:0005524,GO:0016020	AT1G31770.1	ABCG14	ATP-binding cassette 14	white-brown-complex ABC transporter family protein, putative
Sapur.019G019800.2	0.08024978	0.265979606	1.2926234	0.205767	0.836972698	0.885570076	brown	0.077663816	0.333639181	GO:0006468,GO:0004672	AT1G07650.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.016G039200.3	0.08690036	-0.39796066	1.955158602	-0.20354	0.838709915	0.886888055	brown	-0.089406142	0.265478599		AT2G41430.5	CID1,ERD15,LSR1	dehydration-induced protein (ERD15)	polyadenylate-binding protein interacting protein, putative
Sapur.016G173700.2	0.105704738	-0.220716617	1.092178871	-0.20209	0.839847662	0.887914407	brown	-0.081608864	0.309590942	GO:0006508,GO:0004185	AT1G33540.1	scpl18	serine carboxypeptidase-like 18	serine carboxypeptidase, putative
Sapur.005G087900.4	1.339040572	0.046492428	0.230064488	0.202084	0.839850796	0.887914407	brown	-0.081608864	0.309590942		AT4G35920.3	MCA1	PLAC8 family protein	MID1-complementing activity protein
Sapur.010G203100.2	0.100154174	-0.216919116	1.075802902	-0.20163	0.840202373	0.888191686	brown	-0.122460437	0.126532445	GO:0016020,GO:0005509,GO:0004571	AT1G51590.1	MANIB,MNS1	alpha-mannosidase 1	mannosyl-oligosaccharide 1%2C2-alpha-mannosidase, putative
Sapur.006G066600.1	0.100087765	-0.252184083	1.297050073	-0.19443	0.845840024	0.893294791	brown	-0.079850745	0.320164402		AT5G24710.1		Transducin/WD40 repeat-like superfamily protein	peptidase S8 and S53, subtilisin%2C kexin, sedolisin; WD40-like protein
Sapur.002G113000.2	0.087227246	-0.235879207	1.219009429	-0.1935	0.846566839	0.893805518	brown	-0.138692506	0.083218868		AT4G17520.1		Hyaluronan / mRNA binding family	NA
Sapur.008G148700.3	0.061310937	-0.319419958	1.653692284	-0.19316	0.846837094	0.894033773	brown	-0.21246202	0.007552692		AT1G24560.1			paramyosin, putative
Sapur.010G124700.8	0.758164451	-0.055714406	0.288798774	-0.19292	0.847023394	0.894201913	brown	-0.115430784	0.149979911	GO:0005515,GO:0003677	AT2G03390.2		uvrB/uvrC motif-containing protein	hemimethylated DNA-binding domain protein
Sapur.T117000.1	4.139782351	0.030735883	0.159767469	0.192379	0.847445454	0.894590372	brown	-0.07774424	0.333137324	GO:0005524,GO:0005515	AT4G27220.1		NB-ARC domain-containing disease resistance protein	BED finger NBS-LRR resistance protein
Sapur.T005100.2	0.085207849	-0.252166384	1.312949094	-0.19206	0.847694383	0.89479603	brown	-0.108798626	0.174978594		AT1G55930.1		CBS domain-containing protein / transporter associated domain-containing protein	magnesium and cobalt efflux protein CorC, putative
Sapur.006G062500.2	0.076379164	-0.233665928	1.220244684	-0.19149	0.848140897	0.895181644	brown	-0.217780183	0.006145071		AT2G19080.1		metaxin-related	outer membrane import complex protein metaxin, putative
Sapur.002G072200.1	0.090569407	-0.287611654	1.503180496	-0.19134	0.848262822	0.895281762	brown	-0.124432844	0.12048985	GO:0051087,GO:0042803,GO:0006457,GO:0000774	AT1G36390.1		Co-chaperone GrpE family protein	co-chaperone GrpE
Sapur.008G165100.3	0.269077318	-0.094898402	0.499756559	-0.18989	0.84939591	0.896163084	brown	-0.040088311	0.618137595	GO:0046872	AT2G47850.1		Zinc finger C-x8-C-x5-C-x3-H type family protein	zinc finger CCCH domain protein, putative
Sapur.008G106400.1	0.189239683	0.13702987	0.724242777	0.189204	0.849932674	0.896586395	brown	0.013645421	0.865310383		AT5G28010.1		Polyketide cyclase/dehydrase and lipid transport superfamily protein	pathogenesis-related protein Bet V I family protein
Sapur.004G119700.1	0.065745243	-0.341567658	1.806792862	-0.18905	0.850056463	0.896602591	brown	-0.138470719	0.083717848	GO:0006355,GO:0003677	AT4G34610.2	BLH6	BEL1-like homeodomain 6	BEL1-related homeotic protein
Sapur.T118100.1	0.071834714	-0.283887602	1.511674712	-0.1878	0.851035981	0.897263757	brown	-0.178085606	0.025651789					hypothetical protein
Sapur.012G073500.1	0.087396369	0.189411535	1.012413299	0.187089	0.851590742	0.897791412	brown	0.055811253	0.487515333		AT3G48550.1			nucleic acid-binding protein, putative
Sapur.005G192500.1	31.09885907	-0.013447535	0.072316365	-0.18595	0.852480642	0.898557739	brown	-0.063922497	0.426404114		AT5G42470.1			brain and reproductive organ-expressed protein
Sapur.006G066100.2	0.062541965	-0.282023589	1.518820011	-0.18569	0.85269102	0.898722205	brown	-0.085667566	0.286063832	GO:0005515	AT1G62440.1	LRX2	leucine-rich repeat/extensin 2	LRR amino-terminal domain protein
Sapur.010G002600.2	0.107587545	-0.215497324	1.166140293	-0.1848	0.853389541	0.899315141	brown	-0.083402183	0.299043864					transmembrane protein, putative
Sapur.003G095000.1	0.087814887	-0.397907409	2.15830669	-0.18436	0.853730325	0.899566821	brown	-0.085341881	0.28790635	GO:0016757,GO:0016020	AT5G41460.1		Protein of unknown function (DUF604)	transferring glycosyl group transferase, putative
Sapur.018G092200.1	0.273394396	-0.079437956	0.430903207	-0.18435	0.853737164	0.899566821	brown	-0.040124013	0.617824545	GO:0005515	AT1G74190.1	AtRLP15,RLP15	receptor like protein 15	NA
Sapur.013G086300.2	2.82367313	-0.044685267	0.245260698	-0.18219	0.855429715	0.900891017	brown	-0.033422457	0.677738012	GO:0003723	AT4G13070.1		RNA-binding CRS1 / YhbY (CRM) domain protein	NA
Sapur.007G025500.4	0.085994669	-0.235857003	1.302829852	-0.18103	0.856340585	0.90162062	brown	-0.125476029	0.117385725	GO:0003676	AT4G36690.4	ATU2AF65A	U2 snRNP auxilliary factor, large subunit, splicing factor	U2 snRNP auxilliary factor, large subunit%2C splicing factor
Sapur.004G040000.1	0.077160522	-0.321222856	1.775555813	-0.18091	0.856435101	0.901691429	brown	-0.180309038	0.023835782		AT2G38300.1		myb-like HTH transcriptional regulator family protein	myb transcription factor, putative
Sapur.004G133300.3	0.080372301	-0.221624652	1.227975481	-0.18048	0.856775986	0.901992104	brown	-0.1308845	0.102277877	GO:0005515	AT1G12970.1	PIRL3	plant intracellular ras group-related LRR 3	plant/F13K23-18 protein
Sapur.018G036100.1	0.117979902	-0.18285117	1.018208285	-0.17958	0.857481284	0.90259177	brown	-0.08581729	0.285219443		AT1G15215.2			hypothetical protein
Sapur.016G060900.1	0.115688817	0.189543124	1.056746692	0.179365	0.857651295	0.902684538	brown	-0.05054954	0.529529354		AT3G24255.1		RNA-directed DNA polymerase (reverse transcriptase)-related family protein	NA
Sapur.005G113500.1	0.111258059	-0.18283571	1.023933145	-0.17856	0.858281512	0.903204134	brown	-0.106263679	0.185305921		AT5G49980.1	AFB5	auxin F-box protein 5	transport inhibitor response 1 protein, putative
Sapur.001G131100.1	0.063430779	-0.319357045	1.798751106	-0.17754	0.859081291	0.90379842	brown	-0.198186335	0.012840771		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.001G131200.1	0.063430779	-0.319357045	1.798751106	-0.17754	0.859081291	0.90379842	brown	-0.198186335	0.012840771		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.004G080800.2	0.468586376	-0.071960335	0.407101455	-0.17676	0.859694823	0.904259845	brown	-0.007869196	0.922079733	GO:0016021	AT3G02420.1			NA
Sapur.005G156500.1	0.079605972	0.189600897	1.078301694	0.175833	0.860425234	0.904740389	brown	-0.073895347	0.357695429	GO:0009058,GO:0008676,GO:0008152,GO:0005737	AT1G79500.1	AtkdsA1	Aldolase-type TIM barrel family protein	NA
Sapur.003G105700.1	0.064348021	-0.266644761	1.518192884	-0.17563	0.86058228	0.904847989	brown	-0.219973019	0.005636353	GO:0005515	AT4G24020.1	NLP7	NIN like protein 7	transcription factor, putative
Sapur.005G072900.3	0.06952094	0.228526237	1.30702328	0.174845	0.861201578	0.905326457	brown	-0.115272829	0.150542122		AT5G23200.1			NA
Sapur.T001600.2	0.112043464	-0.165479049	0.952287793	-0.17377	0.862046223	0.905897651	brown	-0.139718401	0.08094176	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT2G34660.1	ATMRP2,EST4,MRP2	multidrug resistance-associated protein 2	multidrug resistance protein ABC transporter family protein
Sapur.014G050000.4	0.725861409	-0.048397329	0.279693969	-0.17304	0.86262256	0.906361231	brown	-0.081608864	0.309590942		AT2G45320.1			hypothetical protein
Sapur.010G022500.1	4.319791534	-0.032492376	0.188366496	-0.1725	0.863047986	0.906604703	brown	-0.03449405	0.668008336		AT3G26380.1		Melibiase family protein	alpha-galactosidase
Sapur.008G007500.1	71.58693924	-0.012571917	0.07483754	-0.16799	0.866591582	0.909373259	brown	-0.028654234	0.72166039	GO:0016627,GO:0016021,GO:0006629,GO:0005737	AT5G16010.1		3-oxo-5-alpha-steroid 4-dehydrogenase family protein	3-oxo-5-alpha-steroid 4-dehydrogenase
Sapur.018G115700.1	1.359675819	-0.043095432	0.257625406	-0.16728	0.867150184	0.909793938	brown	-0.030144927	0.70782283	GO:0006468,GO:0005524,GO:0004672	AT1G69730.1		Wall-associated kinase family protein	NA
Sapur.001G096700.4	0.209620468	0.135666492	0.811057944	0.167271	0.867156803	0.909793938	brown	0.073053059	0.363216505	GO:0055114,GO:0048038,GO:0009308,GO:0008131,GO:0005507	AT1G62810.1		Copper amine oxidase family protein	amine oxidase [copper containing] protein, putative
Sapur.005G066900.1	0.27107783	0.071039328	0.427992509	0.165983	0.868170609	0.910395521	brown	0.052073242	0.517178038	GO:0007264,GO:0005525	AT5G64813.1	LIP1	Ras-related small GTP-binding family protein	Ras-related small GTP-binding family protein
Sapur.014G025700.2	0.083214364	-0.323017571	1.94969095	-0.16568	0.868411703	0.910599087	brown	-0.081608864	0.309590942	GO:0055085,GO:0016020,GO:0006810,GO:0005215	AT2G26510.1	PDE135	Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.008G081700.1	0.069818035	-0.321154602	1.974778335	-0.16263	0.8708112	0.912224565	brown	-0.114049607	0.154949924		AT4G21800.1	QQT2	P-loop containing nucleoside triphosphate hydrolases superfamily protein	GPN-loop GTPase-like protein
Sapur.012G079100.1	0.17308681	-0.115410588	0.711050908	-0.16231	0.871061834	0.91238031	brown	-0.11604045	0.147824797	GO:0006468,GO:0005524,GO:0004672	AT5G50860.1		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.016G236000.1	0.083025227	-0.469039512	2.904824395	-0.16147	0.871723911	0.912819245	brown	-0.116892682	0.144851611		AT1G55830.2			DUF812 family protein
Sapur.016G296900.1	0.059959474	-0.246405516	1.526353288	-0.16143	0.871751487	0.912819245	brown	-0.210118432	0.008259073	GO:0005525	AT1G56050.1		GTP-binding protein-related	NA
Sapur.016G159500.3	0.058447058	0.225134388	1.420089016	0.158535	0.874034924	0.914399667	brown	0.052895242	0.510576696		AT5G16950.1			plant/F2K13-100 protein, putative
Sapur.017G090500.1	0.093848273	-0.235819494	1.499324355	-0.15728	0.875021155	0.915195417	brown	-0.079989477	0.31932166					NA
Sapur.016G021800.2	0.064721758	-0.283739102	1.804377634	-0.15725	0.87504751	0.915195417	brown	-0.135687496	0.09018573	GO:0008168	AT3G57000.1		nucleolar essential protein-related	EMG1/NEP1 methyltransferase
Sapur.002G177500.1	0.136231931	-0.36443809	2.323682686	-0.15684	0.875373764	0.915323566	brown	-0.032987041	0.681706802	GO:0016020,GO:0004970	AT2G32400.1	ATGLR3.7,GLR3.7,GLR5	glutamate receptor 5	NA
Sapur.001G131000.1	0.058316295	-0.281881155	1.807970392	-0.15591	0.876103749	0.915810853	brown	-0.201710585	0.01129863		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.018G059900.2	11.53269823	0.024003879	0.156848702	0.153038	0.878367969	0.917452778	brown	0.005279551	0.947676852	GO:0055114,GO:0016491,GO:0006631,GO:0003857	AT4G29010.1	AIM1	Enoyl-CoA hydratase/isomerase family	peroxisomal fatty acid beta-oxidation protein
Sapur.002G170000.6	19.31066593	-0.014103483	0.092220502	-0.15293	0.878451755	0.917511316	brown	-0.112511804	0.160628137		AT3G27970.1		Exonuclease family protein	exonuclease domain protein
Sapur.016G164300.7	0.068345738	0.228741529	1.514201195	0.151064	0.879925105	0.918702031	brown	0.046828882	0.560300672		AT5G58575.1			Sgf11 (transcriptional regulation protein) protein
Sapur.005G157400.1	0.059726571	0.230087255	1.524172297	0.150959	0.880008198	0.918730781	brown	0.097905703	0.222508515	GO:0005507,GO:0055114,GO:0016491	AT5G09360.1	LAC14	laccase 14	laccase
Sapur.003G050100.2	0.070989277	-0.196172543	1.309202332	-0.14984	0.880889846	0.919390033	brown	-0.182721282	0.021991548		AT4G17520.1		Hyaluronan / mRNA binding family	nuclear RNA-binding protein, putative
Sapur.003G014300.1	0.072002554	-0.431567395	2.904824395	-0.14857	0.881893589	0.920091448	brown	-0.088211202	0.271945263	GO:0005525,GO:0003924	AT1G60500.1	DRP4C	Dynamin related protein 4C	interferon-induced GTP-binding protein mx protein, putative
Sapur.005G082300.5	0.058995813	-0.246330346	1.65881942	-0.1485	0.881950249	0.920091448	brown	-0.161550226	0.043244562	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	AT4G38380.1		MATE efflux family protein	MATE efflux family protein
Sapur.006G114200.2	0.098572462	-0.400003387	2.70547616	-0.14785	0.882461517	0.920351975	brown	-0.071715099	0.37209454	GO:0006355,GO:0005634,GO:0003677,GO:0009725	AT1G19220.1	ARF11,ARF19,IAA22	auxin response factor 19	auxin response factor, putative
Sapur.016G118200.2	0.070320846	-0.321102113	2.186452491	-0.14686	0.883242633	0.920944731	brown	-0.104051146	0.194678731	GO:0005515	AT2G26060.1	emb1345	Transducin/WD40 repeat-like superfamily protein	cytosolic iron-sulfur protein assembly protein, putative
Sapur.004G010900.2	0.061892981	-0.319244492	2.201425143	-0.14502	0.884697298	0.922141705	brown	-0.158930851	0.046796262		AT4G04860.1	DER2.2	DERLIN-2.2	derlin-2 protein
Sapur.005G182800.2	0.063828194	-0.356670798	2.472166583	-0.14427	0.88528365	0.922636566	brown	-0.111295887	0.16522695		AT1G19530.1			hypothetical protein
Sapur.019G006200.1	0.222228781	-0.06541716	0.453673083	-0.14419	0.885346889	0.9226734	brown	-0.088219067	0.271902355		AT5G63660.1	LCR74,PDF2.5	Scorpion toxin-like knottin superfamily protein	gamma-thionin family protein
Sapur.016G308800.1	0.109986112	-0.145375588	1.019325551	-0.14262	0.886590784	0.923678686	brown	-0.082362364	0.305130084		AT5G56170.1	LLG1	LORELEI-LIKE-GPI-ANCHORED PROTEIN 1	GPI-anchored protein, putative
Sapur.014G038000.1	0.744866066	0.052991115	0.373797838	0.141764	0.88726634	0.924207827	brown	0.003810194	0.962226104		AT2G44740.1	CYCP4;1	cyclin p4;1	cyclin-U4 protein
Sapur.008G154100.1	0.198295953	0.102248217	0.724434455	0.141142	0.887757667	0.924591521	brown	-0.009654151	0.904481319	GO:0016787	AT1G10430.1	PP2A-2	protein phosphatase 2A-2	serine/threonine-protein phosphatase PP2A catalytic subunit
Sapur.008G146800.1	0.056884373	-0.281820069	1.998503096	-0.14102	0.887857636	0.924644976	brown	-0.161030085	0.043931306		AT1G24440.1		RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.001G033100.1	0.129518274	-0.179121689	1.279337135	-0.14001	0.888651042	0.925183976	brown	-0.014799449	0.85404107		AT1G16000.1			GAG1At protein
Sapur.005G074900.3	0.089978979	-0.268835467	1.929527142	-0.13933	0.889191657	0.925581692	brown	-0.040946102	0.610635207		AT3G19800.1		Protein of unknown function (DUF177)	hypothetical protein
Sapur.013G011200.4	0.058030151	-0.208932359	1.527425715	-0.13679	0.891198964	0.926987095	brown	-0.197392659	0.013212499	GO:0003824,GO:0006470,GO:0004722	AT5G27930.2		Protein phosphatase 2C family protein	protein phosphatase 2C, putative
Sapur.016G096400.3	0.063332424	-0.24626807	1.800786496	-0.13676	0.89122379	0.926987095	brown	-0.147016381	0.066152879	GO:0055085,GO:0022857,GO:0016021	AT2G38060.1	PHT4;2	phosphate transporter 4;2	anion transporter, putative
Sapur.009G096200.1	0.059311553	-0.246263364	1.813116324	-0.13582	0.891961005	0.927287304	brown	-0.14068979	0.078832072	GO:0016787	AT2G16430.2	ATPAP10,PAP10	purple acid phosphatase 10	purple acid phosphatase
Sapur.018G115800.1	3.288883969	0.035018026	0.257962724	0.135748	0.892020187	0.92730876	brown	-0.000621809	0.993833224	GO:0030247,GO:0006468,GO:0005524,GO:0004672	AT1G16120.1	WAKL1	wall associated kinase-like 1	NA
Sapur.006G136800.4	0.080159939	-0.177228942	1.306083043	-0.1357	0.892062399	0.92730876	brown	-0.119384793	0.136417613	GO:0006468,GO:0005524,GO:0004672	AT2G18890.2		Protein kinase superfamily protein	receptor-like kinase
Sapur.010G185600.2	0.25026799	-0.056734846	0.420226476	-0.13501	0.892603838	0.927693157	brown	-0.319199557	4.61E-05		AT3G52170.2		DNA binding	plastid DNA-binding protein, putative
Sapur.019G030500.1	0.226667512	-0.078019733	0.582354221	-0.13397	0.893423938	0.928341292	brown	-0.095499633	0.234138313	GO:0016020,GO:0015696,GO:0008519,GO:0072488	AT1G64780.1	AMT1;2,ATAMT1;2	ammonium transporter 1;2	ammonium transporter 1 protein
Sapur.007G095200.2	0.056215729	-0.266613296	2.005478699	-0.13294	0.894238877	0.92877957	brown	-0.135367389	0.090954485	GO:0055114,GO:0016655,GO:0005886	AT1G74880.1	NDH-O	NAD(P)H:plastoquinone dehydrogenase complex subunit O	NAD(P)H-quinone oxidoreductase subunit, putative
Sapur.016G147600.2	0.088688258	0.151293508	1.141132348	0.132582	0.894524039	0.928959057	brown	0.037032416	0.645182592	GO:0055085,GO:0016021	AT5G12860.1	DiT1	dicarboxylate transporter 1	2-oxoglutarate/malate translocator
Sapur.006G014100.3	0.104194012	0.192568722	1.466639524	0.131299	0.895538557	0.929662342	brown	-0.049356474	0.539303103		AT4G16380.2		Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.012G027000.1	0.073454607	-0.23358255	1.794728286	-0.13015	0.896448341	0.930314793	brown	-0.094306582	0.240060461		AT1G73480.1		alpha/beta-Hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.002G174600.1	478.8953973	-0.004573718	0.035197677	-0.12994	0.896610922	0.93045432	brown	-0.032031718	0.690445015	GO:0005515	AT4G15410.1	PUX5	serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B prime gamma	plant UBX domain protein
Sapur.011G073300.2	0.078916266	-0.212584522	1.636881369	-0.12987	0.896667956	0.930484312	brown	-0.086094889	0.283658299		AT1G53300.1	TTL1	tetratricopetide-repeat thioredoxin-like 1	TPR repeat thioredoxin TTL4
Sapur.T112400.1	0.102944508	0.111107213	0.864836155	0.128472	0.897775472	0.931312171	brown	-0.025672803	0.749604164		AT4G17900.2		PLATZ transcription factor family protein	NA
Sapur.012G027700.1	0.054604862	0.192624444	1.537163103	0.125312	0.90027683	0.933350757	brown	0.04746833	0.55495168	GO:0016787	AT3G17790.1	ATACP5,ATPAP17,PAP17	purple acid phosphatase 17	purple acid phosphatase
Sapur.011G061500.1	0.094243277	-0.14185753	1.136437647	-0.12483	0.90066091	0.933661148	brown	-0.083374072	0.299207379		AT4G22320.1			hypothetical protein
Sapur.006G140400.1	0.084793383	-0.125757016	1.01345425	-0.12409	0.901245986	0.934033458	brown	-0.08545254	0.287279424	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G31500.1	ATR4.CYP83B1.RED1.RNT1.	cytochrome P450, family 83, subfamily B, polypeptide 1	NA
Sapur.003G041000.1	0.12789366	-0.120023351	0.971097349	-0.1236	0.901635483	0.934378567	brown	-0.076305583	0.342187672	GO:0006355,GO:0003700	AT1G53910.2	RAP2.12	related to AP2 12	ethylene-responsive-element-binding factor 2
Sapur.016G265000.1	0.16933583	-0.109847642	0.907716876	-0.12102	0.903678907	0.936176801	brown	-0.030047628	0.708723172	GO:0005096	AT5G54310.1	AGD5,NEV	ARF-GAP domain 5	ARF-GAP with coiled-coil, ANK repeat and PH domain protein, putative
Sapur.001G122500.1	0.07565125	-0.200522797	1.657058077	-0.12101	0.903682063	0.936176801	brown	-0.067535742	0.400673918	GO:0005525	AT2G44610.1	ATRAB6A.ATRABH1B.RAB6.	Ras-related small GTP-binding family protein	Ras-related protein Rab-6
Sapur.019G043400.1	0.097963558	-0.180685774	1.511914963	-0.11951	0.904872986	0.937146364	brown	-0.060471307	0.451848254		AT5G08630.1		DDT domain-containing protein	NA
Sapur.004G035500.1	0.189105205	0.081443823	0.682508008	0.11933	0.905013751	0.937233454	brown	-0.055539398	0.489641509		AT2G34040.1		Apoptosis inhibitory protein 5 (API5)	apoptosis inhibitory protein 5 (API5)
Sapur.012G056800.7	0.094276045	0.114279799	0.958736387	0.119198	0.905118211	0.937312283	brown	-0.094401937	0.23958332	GO:0055085,GO:0016020,GO:0006810,GO:0005215	AT5G62890.1		Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.010G087600.2	0.105946531	-0.108259734	0.910459285	-0.11891	0.905349252	0.937463484	brown	-0.073826226	0.358146527	GO:0016887,GO:0005524,GO:0016020	AT2G01320.4		ABC-2 type transporter family protein	ABC transporter family protein
Sapur.012G075200.2	0.089932792	-0.127924864	1.077590573	-0.11871	0.905502109	0.937565754	brown	-0.10975961	0.171176851	GO:0016788	AT3G48610.1	NPC6	non-specific phospholipase C6	phospholipase C
Sapur.010G091800.1	0.069580172	-0.285435549	2.457738477	-0.11614	0.907543587	0.93905946	brown	-0.081608864	0.309590942		AT2G01260.1		Protein of unknown function (DUF789)	DUF789 family protein
Sapur.019G045800.4	0.065122011	-0.175180239	1.523575189	-0.11498	0.908461202	0.939803127	brown	-0.109918638	0.170553676	GO:0016987,GO:0006355,GO:0006352,GO:0003700,GO:0003677	AT1G08540.1	ABC1.ATSIG1.ATSIG2.SIG1.S	RNApolymerase sigma subunit 2	NA
Sapur.004G002100.2	0.06808608	-0.321013863	2.794001387	-0.11489	0.908529178	0.939814658	brown	-0.080598284	0.315640405	GO:0006096,GO:0003872	AT1G12000.1		Phosphofructokinase family protein	pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit beta
Sapur.016G174900.5	0.552479379	-0.037967299	0.331832071	-0.11442	0.908907073	0.94017616	brown	-0.115274554	0.150535973	GO:0006281,GO:0003684	AT1G49980.1		DNA/RNA polymerases superfamily protein	DNA polymerase kappa subunit
Sapur.009G059900.3	0.059223754	-0.283576872	2.493501062	-0.11373	0.909454693	0.940594044	brown	-0.092089419	0.25134209	GO:0008270	AT5G58470.2	TAF15b	TBP-associated factor 15B	RNA recognition motif protein
Sapur.001G105800.1	0.08020016	-0.149266886	1.315761112	-0.11345	0.909677544	0.940737762	brown	-0.090584715	0.25920403	GO:0006468,GO:0005524,GO:0004672	AT1G31420.2	FEI1	Leucine-rich repeat protein kinase family protein	LRR receptor-like Serine/Threonine-kinase FEI
Sapur.007G050000.1	0.065787419	-0.158681584	1.408190885	-0.11268	0.910280522	0.941196989	brown	-0.16808158	0.035359208					NA
Sapur.15WG073700.1	0.061691224	-0.158680282	1.416116987	-0.11205	0.910781313	0.941437671	brown	-0.148668743	0.063130878	GO:0016747	AT5G48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	NA
Sapur.011G070200.2	0.531781595	0.039866305	0.363014499	0.10982	0.912552013	0.942844126	brown	-0.206089596	0.009610999	GO:0055114,GO:0016616,GO:0006694,GO:0003854,GO:0019752	AT1G53240.1	mMDH1	Lactate/malate dehydrogenase family protein	malate dehydrogenase
Sapur.019G041900.1	0.546748337	-0.042979982	0.392248023	-0.10957	0.912747642	0.942969186	brown	-0.011963402	0.881783699	GO:0005515	AT5G60570.1		Galactose oxidase/kelch repeat superfamily protein	kelch repeat F-box protein
Sapur.004G049100.1	0.078992677	0.130707561	1.217362939	0.107369	0.914495908	0.944307913	brown	0.04118546	0.608548906		AT1G21280.1			NA
Sapur.003G114700.3	0.056653058	-0.193897281	1.816528228	-0.10674	0.914994787	0.944612091	brown	-0.149730228	0.061249833	GO:0005515	AT4G20130.1	PTAC14	plastid transcriptionally active 14	ribulose-1%2C5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, putative
Sapur.006G063400.1	0.065744202	-0.210591072	1.980963762	-0.10631	0.915338474	0.944841672	brown	-0.102737506	0.200404057	GO:0005524,GO:0003676	AT2G06990.1	HEN2	RNA helicase, ATP-dependent, SK12/DOB1 protein	DEAD-box-like helicase superfamily protein
Sapur.008G158800.2	0.064728103	-0.210590878	1.981631819	-0.10627	0.915366986	0.944841672	brown	-0.094737939	0.237907309	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT3G06740.1	GATA15	GATA transcription factor 15	GATA transcription factor, putative
Sapur.010G189400.1	0.123916901	-0.095961073	0.911750231	-0.10525	0.916177993	0.945420453	brown	-0.100492072	0.210470563	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G27690.1	CYP94C1	cytochrome P450, family 94, subfamily C, polypeptide 1	cytochrome P450 family protein
Sapur.005G185100.2	0.115961648	-0.114356024	1.092908701	-0.10463	0.916665788	0.945717271	brown	-0.069591842	0.386454083	GO:0016021	AT1G35180.1		TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain protein, putative
Sapur.007G046100.4	16.6692064	0.008038067	0.076950106	0.104458	0.916805761	0.945832176	brown	-0.18952833	0.017435394	GO:0046872,GO:0000166	AT4G37270.1	ATHMA1,HMA1	heavy metal atpase 1	heavy metal ATPase, putative
Sapur.008G022200.1	0.05642712	-0.208730309	2.000032649	-0.10436	0.916880926	0.945880217	brown	-0.119567133	0.135815577					hypothetical protein
Sapur.010G010000.6	0.055566497	-0.208730054	2.000951993	-0.10432	0.916919078	0.945890072	brown	-0.081608864	0.309590942	GO:0008152,GO:0003824,GO:0016114,GO:0008661	AT4G15560.1	CLA,CLA1,DEF,DXPS2,DXS	Deoxyxylulose-5-phosphate synthase	1-deoxy-D-xylulose-5-phosphate synthase
Sapur.T117100.1	0.075471585	-0.283545807	2.752920955	-0.103	0.917964427	0.946496102	brown	-0.063446924	0.429860344		AT4G38620.1	ATMYB4,MYB4	myb domain protein 4	NA
Sapur.008G166200.3	0.068402342	-0.285394742	2.791570908	-0.10223	0.918570577	0.946884938	brown	-0.088012611	0.27303024	GO:0046872,GO:0008270,GO:0016567	AT5G18650.1		CHY-type/CTCHY-type/RING-type Zinc finger protein	CHY zinc finger protein
Sapur.006G047500.4	0.062774558	0.155141953	1.52368917	0.10182	0.918899591	0.946960931	brown	0.025261167	0.753488924	GO:0055114,GO:0050661,GO:0050660,GO:0004499	AT1G19250.1	FMO1	flavin-dependent monooxygenase 1	flavin containing monooxygenase, putative
Sapur.019G065000.3	0.10763448	-0.137838412	1.361047736	-0.10127	0.919333151	0.947228182	brown	-0.12681603	0.113490016	GO:0006415,GO:0003747	AT1G33330.1		Class I peptide chain release factor	peptide chain release factor, putative
Sapur.006G050500.1	0.063767758	-0.283539938	2.812397195	-0.10082	0.919695029	0.947512487	brown	-0.085646694	0.286181673	GO:0016758,GO:0009247	AT5G20410.1	ATMGD2,MGD2	monogalactosyldiacylglycerol synthase 2	monogalactosyldiacylglycerol synthase
Sapur.016G093300.1	0.12404863	0.087088321	0.867379743	0.100404	0.920023663	0.9476363	brown	-0.04734324	0.55599611					NA
Sapur.018G012800.1	0.060965189	-0.283538379	2.828900117	-0.10023	0.920162369	0.947698757	brown	-0.084736475	0.291352371	GO:0055085,GO:0016021	AT5G25050.1		Major facilitator superfamily protein	folate/biopterin transporter
Sapur.016G290600.1	0.060161758	0.223161397	2.232630431	0.099954	0.92038047	0.947834838	brown	0.050959039	0.526195375		AT1G11925.1		Stigma-specific Stig1 family protein	Stig1 stigma-specific protein
Sapur.017G120300.2	0.063008562	-0.246108262	2.46788168	-0.09972	0.920563051	0.947993347	brown	-0.113500689	0.156959174		AT5G52760.1		Copper transport protein family	hypothetical protein
Sapur.008G145700.1	0.075306399	-0.176894252	1.795873456	-0.0985	0.921534955	0.948513286	brown	-0.063527017	0.429277141	GO:0008601,GO:0007165,GO:0000159	AT3G26020.1		Protein phosphatase 2A regulatory B subunit family protein	serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' protein
Sapur.012G089100.1	0.052856444	-0.281681664	2.872858235	-0.09805	0.921893167	0.948801799	brown	-0.103928287	0.195209103	GO:0046872,GO:0016567,GO:0004842	AT4G19670.2		RING/U-box superfamily protein	zinc finger protein, putative
Sapur.003G013500.1	0.10064935	-0.094313395	0.965566077	-0.09768	0.922188946	0.948946874	brown	-0.13900758	0.082514119	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G33430.1	ATBAK1.ATSERK3.BAK1.ELG	BRI1-associated receptor kinase	somatic embryogenesis receptor kinase
Sapur.016G173100.1	0.178076532	0.068567238	0.705276696	0.09722	0.922551418	0.949213426	brown	0.017783199	0.825045933					NA
Sapur.15WG134800.1	0.067197198	-0.175035004	1.803424724	-0.09706	0.922681124	0.949314575	brown	-0.09026	0.260922526		AT2G35100.1	ARAD1	Exostosin family protein	exostosin family protein
Sapur.010G187200.1	0.055790201	-0.281678926	2.904824395	-0.09697	0.922750737	0.949329908	brown	-0.09705072	0.226593258	GO:0005524,GO:0003676	AT2G28600.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase, putative
Sapur.016G176500.1	0.11917321	-0.141463887	1.47043075	-0.09621	0.923357168	0.949730029	brown	-0.001320086	0.986908531	GO:0055085,GO:0016020,GO:0006810,GO:0015171,GO:0003333	AT3G19553.1		Amino acid permease family protein	neutral amino acid transporter, putative
Sapur.002G055800.3	0.064215633	-0.173179708	1.800818411	-0.09617	0.923387761	0.949730029	brown	-0.098144582	0.221376645	GO:0055114,GO:0016491,GO:0016209	AT1G21350.3		Thioredoxin superfamily protein	antioxidant, AhpC/TSA family protein
Sapur.016G147100.1	0.195895184	-0.049701405	0.520418264	-0.0955	0.923915461	0.950097182	brown	-0.086578002	0.280955094		AT5G19855.1		Chaperonin-like RbcX protein	chaperonin-like RbcX protein
Sapur.009G081400.1	0.104858044	-0.109464377	1.149401634	-0.09524	0.924127402	0.950194784	brown	-0.098378883	0.220270439	GO:0006508	AT1G49630.2	ATPREP2,PREP2	presequence protease 2	presequence protease
Sapur.008G137800.1	0.121410209	0.087225705	0.917542588	0.095064	0.924263614	0.950253343	brown	-0.083647775	0.297618172					hypothetical protein
Sapur.019G087100.1	0.070758526	-0.123438268	1.308035628	-0.09437	0.924815886	0.950632708	brown	-0.09297926	0.246771063		AT3G58110.2			hypothetical protein
Sapur.002G090700.1	0.101715528	-0.106181578	1.135537997	-0.09351	0.925500211	0.951063973	brown	-0.069960063	0.38394009	GO:0003723	AT5G64390.1	HEN4	RNA-binding KH domain-containing protein	K-like RNA-binding domain protein
Sapur.005G106200.4	0.052223906	-0.208674541	2.238644617	-0.09321	0.925733013	0.951214541	brown	-0.119867938	0.134826852	GO:0006457,GO:0003755,GO:0000413	AT2G15790.1	CYP40,SQN	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.019G078000.1	0.095272904	0.119294715	1.296363319	0.092023	0.926680089	0.951862395	brown	-0.000625523	0.993796392		AT4G03500.1		Ankyrin repeat family protein	ankyrin repeat protein
Sapur.006G033000.3	0.188008638	0.064243556	0.702086053	0.091504	0.927092271	0.952137926	brown	-0.083897255	0.296174522		AT2G41430.2	CID1,ERD15,LSR1	dehydration-induced protein (ERD15)	polyadenylate-binding protein interacting protein, putative
Sapur.016G303000.1	0.068411589	-0.179333114	1.969312779	-0.09106	0.927441893	0.95240827	brown	-0.076708751	0.339635848		AT4G03500.1		Ankyrin repeat family protein	NA
Sapur.019G066700.3	0.062646525	0.118911097	1.313248153	0.090547	0.927852295	0.952740975	brown	-0.11176627	0.163436377	GO:0008270,GO:0005515	AT1G21651.1		zinc ion binding	protein translocase subunit SECA2, putative
Sapur.002G188800.1	0.078293068	-0.176834341	1.963839737	-0.09005	0.928251297	0.952870107	brown	-0.05642601	0.482725594		AT3G07120.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.010G146900.3	0.641471474	-0.027893272	0.315299291	-0.08847	0.929506294	0.953758297	brown	-0.12853298	0.108646693	GO:0050826	AT3G55990.1	ESK1,TBL29	Plant protein of unknown function (DUF828)	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.012G025700.1	0.066662917	0.108450333	1.230823291	0.088112	0.929787639	0.953956952	brown	-0.082973788	0.30154154	GO:0005525	AT1G76810.1		eukaryotic translation initiation factor 2 (eIF-2) family protein	translation initiation factor IF-2
Sapur.004G155400.1	0.054991053	0.134522406	1.533656749	0.087714	0.930104387	0.954135185	brown	0.031761199	0.692926911	GO:0055085,GO:0016021	AT4G35300.1	TMT2	tonoplast monosaccharide transporter2	hexose transporter
Sapur.009G045900.2	0.659094998	-0.029900059	0.3453335	-0.08658	0.931002868	0.954731144	brown	-0.007685741	0.923890764		AT3G08020.1		PHD finger family protein	RING/FYVE/PHD zinc finger protein, putative
Sapur.004G110000.1	0.136588517	0.090219001	1.061416865	0.084999	0.932262464	0.955628568	brown	0.055515471	0.489828876	GO:0035091	AT2G15900.1		Phox-associated domain;Phox-like;Sorting nexin, C-terminal	sorting nexin-16 protein, putative
Sapur.010G060900.1	0.074363098	0.110533553	1.300801068	0.084973	0.932282499	0.955628568	brown	-0.073514053	0.360188246	GO:0005515	AT4G14920.1		Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein	acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein, putative
Sapur.013G069200.1	0.052314286	-0.206777032	2.506881129	-0.08248	0.934262016	0.957014118	brown	-0.144920885	0.070154002		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.003G009500.1	0.058820885	-0.135772433	1.655289935	-0.08202	0.934628142	0.957291232	brown	0.078548531	0.32814497	GO:0005622,GO:0003676,GO:0005524,GO:0043140,GO:0006281,GO:0006260	AT1G10930.1	ATRECQ4A.ATSGS1.RECQ4A	DNA helicase (RECQl4A)	ATP-dependent DNA helicase
Sapur.002G024900.10	0.511330318	0.029076318	0.355287698	0.081839	0.934774903	0.95739559	brown	-0.079502226	0.322287866		AT2G21520.1		Sec14p-like phosphatidylinositol transfer family protein	SEC14 cytosolic factor
Sapur.010G119300.5	0.053445369	-0.135765945	1.668167887	-0.08139	0.935134776	0.957656498	brown	-0.144209125	0.071556957	GO:0008168,GO:0008152	AT3G17365.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	thiopurine S-methyltransferase
Sapur.019G102500.1	0.068764537	-0.123398825	1.521291032	-0.08111	0.935350861	0.957764532	brown	-0.09863043	0.219087188		AT1G03670.1		ankyrin repeat family protein	NA
Sapur.003G092400.1	0.086514972	-0.104152883	1.29959092	-0.08014	0.936123666	0.958359624	brown	-0.079387513	0.322988778	GO:0016787,GO:0006541,GO:0006177,GO:0006164,GO:0005524,GO:0003922	AT1G63660.1		GMP synthase (glutamine-hydrolyzing), putative / glutamine amidotransferase, putative	GMP synthase (glutamine-hydrolyzing)
Sapur.006G083600.2	0.05965417	-0.121191799	1.526937479	-0.07937	0.93673897	0.958800009	brown	-0.144276816	0.071422559		AT3G51800.3	ATEBP1,ATG2,EBP1	metallopeptidase M24 family protein	proliferation-associated protein 2g4
Sapur.018G029100.1	0.059512697	-0.173061652	2.213121225	-0.0782	0.937670553	0.959426924	brown	-0.109009872	0.174137583		AT5G11460.1		Protein of unknown function (DUF581)	DUF581 family protein
Sapur.014G055900.5	0.070735626	-0.102280154	1.309508889	-0.07811	0.937743946	0.959435558	brown	-0.118392221	0.139730625	GO:0006355,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AT2G45650.1	AGL6	AGAMOUS-like 6	MADS-box transcription factor
Sapur.019G029700.1	0.059280535	-0.173061013	2.216226252	-0.07809	0.937757932	0.959435558	brown	-0.08872449	0.269154533	GO:0005515	AT4G33270.1	CDC20.1	Transducin family protein / WD-40 repeat family protein	cell division cycle 20, cofactor of APC complex protein
Sapur.012G009600.2	0.054733132	-0.141830317	1.823810317	-0.07777	0.938014332	0.959499745	brown	-0.117968622	0.141163042	GO:0006890	AT5G24350.1			neuroblastoma-amplified sequence protein
Sapur.T117500.1	0.077365613	0.108372474	1.397610283	0.077541	0.938192963	0.959570954	brown	0.014366244	0.858268071		AT1G14870.1	PCR2	PLANT CADMIUM RESISTANCE 2	NA
Sapur.016G102200.2	0.05288108	-0.171203315	2.233100221	-0.07667	0.938889091	0.959961391	brown	-0.108039091	0.178027265	GO:0055114,GO:0016491	AT5G05600.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	leucoanthocyanidin dioxygenase
Sapur.008G138600.2	0.055038702	0.127780576	1.684670059	0.075849	0.939539214	0.960474512	brown	-0.012092507	0.880517384		AT3G23510.1		Cyclopropane-fatty-acyl-phospholipid synthase	cyclopropane-fatty-acyl-phospholipid synthase
Sapur.004G075100.1	0.056999091	-0.135702594	1.81293331	-0.07485	0.940332069	0.961139219	brown	-0.115585857	0.149429504	GO:0046983	AT1G69010.1	BIM2	BES1-interacting Myc-like protein 2	transcription factor BIM1, putative
Sapur.005G131600.6	0.051222401	-0.133842289	1.823397718	-0.0734	0.941485681	0.961842757	brown	-0.030529363	0.704269476	GO:0006633,GO:0005524,GO:0003989	AT1G36160.1	ACC1.AT-ACC1.EMB22.GK.P	acetyl-CoA carboxylase 1	acetyl-CoA carboxylase
Sapur.018G113300.3	0.067640385	-0.102183281	1.408152187	-0.07257	0.942151874	0.962255847	brown	-0.095336019	0.234944348	GO:0030170,GO:0009058,GO:0003824				orn/lys/arg decarboxylase
Sapur.15WG073400.1	0.052107661	-0.121175232	1.677475871	-0.07224	0.942413581	0.962387497	brown	-0.12256138	0.126217632	GO:0016747	AT5G48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	NA
Sapur.012G028600.1	0.077307441	-0.137511215	1.949285633	-0.07054	0.94376035	0.963342072	brown	-0.039838286	0.620331849	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT1G05260.1	RCI3,RCI3A	Peroxidase superfamily protein	cationic peroxidase kDa protein
Sapur.T091400.4	0.236701797	-0.038985922	0.562460464	-0.06931	0.944740337	0.963976735	brown	-0.046287713	0.564846801		AT3G27470.1		Protein of unknown function (DUF707)	lysine ketoglutarate reductase trans-splicing-related protein
Sapur.001G103000.1	0.099880895	-0.068993966	1.007108571	-0.06851	0.945382065	0.964517527	brown	-0.092052394	0.251533541	GO:0051276,GO:0005694,GO:0005524,GO:0005515,GO:0007076,GO:0000796	AT5G62410.1	ATCAP-E1.ATSMC4.SMC2.T	structural maintenance of chromosomes 2	structural maintenance of chromosomes protein
Sapur.006G098200.3	0.064787136	-0.123367304	1.806823403	-0.06828	0.945563889	0.964568084	brown	-0.07620521	0.342824858		AT1G32700.1		PLATZ transcription factor family protein	PLATZ transcription factor
Sapur.016G150800.1	0.060362799	-0.135644483	1.987308936	-0.06826	0.94558236	0.964568084	brown	-0.075493075	0.347367181		AT3G63490.1		Ribosomal protein L1p/L10e family	50S ribosomal protein L1
Sapur.006G003800.6	0.058050528	-0.135642375	1.994659806	-0.068	0.945783436	0.964708646	brown	-0.08100376	0.313203997		AT5G47690.1		binding	androgen induced inhibitor of proliferation (As3)/PDS5 protein, putative
Sapur.005G154500.1	0.063614694	0.119255955	1.800083784	0.06625	0.947178611	0.965630522	brown	-0.000259327	0.997428114		AT4G09830.1		Uncharacterised conserved protein UCP009193	holocarboxylase synthetase
Sapur.013G035500.2	0.060753726	0.081192036	1.232443514	0.065879	0.947474231	0.965753289	brown	-0.115779006	0.148746091	GO:0008270	AT5G28050.2		Cytidine/deoxycytidylate deaminase family protein	deoxycytidylate deaminase (cytidine deaminase), putative
Sapur.008G109500.2	0.097701917	0.068987078	1.070184612	0.064463	0.948601741	0.966426009	brown	-0.02652309	0.741599697	GO:0070772,GO:0043550	AT2G01690.1		ARM repeat superfamily protein	VAC14-like protein
Sapur.012G064200.1	0.183876832	-0.040848119	0.647230846	-0.06311	0.949677214	0.967187681	brown	-0.053497475	0.505768098	GO:0006468,GO:0005524,GO:0004672	AT3G48260.1	WNK3	with no lysine (K) kinase 3	Serine/Threonine-kinase WNK2, putative
Sapur.009G126500.2	0.061199737	-0.135591192	2.204152043	-0.06152	0.950948065	0.967943213	brown	-0.064423513	0.422780406		AT2G27290.1		Protein of unknown function (DUF1279)	transmembrane protein C20orf108, putative
Sapur.004G045600.4	0.077243944	0.079983381	1.303152174	0.061377	0.951059085	0.967951726	brown	-0.019366105	0.809756573	GO:0016491	AT4G18360.1		Aldolase-type TIM barrel family protein	peroxisomal (S)-2-hydroxy-acid oxidase, putative
Sapur.010G027000.1	0.075942594	0.079986946	1.306054388	0.061243	0.951165528	0.967994359	brown	-0.08185274	0.308142506	GO:0003677,GO:0006355,GO:0005634	AT1G23380.1	KNAT6,KNAT6L,KNAT6S	KNOTTED1-like homeobox gene 6	homeobox knotted-like protein
Sapur.010G034200.2	0.093059637	0.068938923	1.140845331	0.060428	0.951814813	0.968476331	brown	-0.011407464	0.887239946	GO:0016020,GO:0006810,GO:0005215	AT1G69850.1	ATNRT1:2,NRT1:2,NTL1	nitrate transporter 1:2	nitrate transporter 1.2
Sapur.003G094200.2	0.051458074	-0.121151103	2.022410551	-0.0599	0.952231849	0.968721854	brown	-0.08649834	0.281399638	GO:0003676	AT4G35785.5		RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein G RNA recognition motif protein
Sapur.017G127600.1	0.141024044	-0.050134905	0.848927106	-0.05906	0.95290688	0.969050892	brown	-0.053005943	0.509691014	GO:0004866	AT1G17860.1		Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor
Sapur.005G191400.3	0.076189258	0.080090819	1.400573038	0.057184	0.954398367	0.970000971	brown	-0.03370651	0.675153641	GO:0016773,GO:0005975,GO:0005524,GO:0046835,GO:0005536,GO:0004396,GO:000167	AT1G47840.1	HXK3	hexokinase 3	hexokinase
Sapur.008G006500.1	0.50638484	-0.019489842	0.352072211	-0.05536	0.955853643	0.97103191	brown	-0.079468341	0.322494805		AT3G20770.1	AtEIN3,EIN3	Ethylene insensitive 3 family protein	ethylene insensitive 3 class transcription factor
Sapur.001G051500.1	0.061095876	-0.100088188	1.808456771	-0.05534	0.955863987	0.97103191	brown	-0.082095329	0.306706122		AT1G28100.2			PPR containing protein, putative
Sapur.010G145500.1	0.058833656	-0.100085866	1.8143875	-0.05516	0.956009129	0.971130745	brown	-0.09189192	0.252364505	GO:0019867	AT5G05520.1		Outer membrane OMP85 family protein	sorting and assembly machinery component-like protein
Sapur.001G051500.4	0.056426207	-0.100083306	1.820997374	-0.05496	0.956169767	0.971211083	brown	-0.064928683	0.419144796		AT1G28100.2			PPR containing protein, putative
Sapur.002G034100.3	0.05792021	-0.121142534	2.219329029	-0.05459	0.956468925	0.97138897	brown	-0.071827323	0.371344799	GO:0006355,GO:0005634	AT5G43700.1	ATAUX2-11,IAA4	AUX/IAA transcriptional regulator family protein	indole-3-acetic acid inducible protein
Sapur.002G089600.1	0.097297536	0.052062376	0.95975001	0.054246	0.956739357	0.97153887	brown	-0.087945153	0.273399457	GO:0043565,GO:0008270,GO:0006355,GO:0003700,GO:0005515	AT4G24470.1	GATA25,TIFY1,ZIM	GATA-type zinc finger protein with TIFY domain	GATA transcription factor, putative
Sapur.008G129100.2	0.072012893	0.081465594	1.509528398	0.053968	0.956960994	0.971598035	brown	0.023870514	0.766658254					hypothetical protein
Sapur.004G101300.1	0.112112439	-0.056742242	1.075923048	-0.05274	0.957940505	0.972256552	brown	-0.003920814	0.961130275	GO:0006468,GO:0005524,GO:0004672	AT3G48750.1	CDC2.CDC2A.CDC2AAT.CDK	cell division control 2	cyclin-dependent kinase A
Sapur.008G027200.1	0.062407104	-0.100028404	1.983686986	-0.05043	0.959783318	0.973547719	brown	-0.088397078	0.270932405		AT5G04240.1	ELF6	Zinc finger (C2H2 type) family protein / transcription factor jumonji (jmj) family protein	jumonji domain protein, putative
Sapur.009G021300.1	0.07775624	0.057503264	1.144006896	0.050265	0.959911383	0.973599592	brown	-0.088558043	0.270057358	GO:0051205,GO:0016021	AT2G28800.1	ALB3	63 kDa inner membrane family protein	inner membrane protein
Sapur.002G203300.2	0.065795476	-0.064805339	1.311617521	-0.04941	0.960593582	0.974112283	brown	-0.114388133	0.153720465	GO:0046080,GO:0016787	AT3G46940.1	DUT1	DUTP-PYROPHOSPHATASE-LIKE 1	NA
Sapur.016G062400.1	0.054987059	-0.098168394	2.000334143	-0.04908	0.960858731	0.974317008	brown	-0.080300516	0.317437444	GO:0006760,GO:0004150	AT3G11750.1	FOLB1	Dihydroneopterin aldolase	dihydroneopterin aldolase
Sapur.012G072500.1	0.070665253	0.059499925	1.220637233	0.048745	0.961122538	0.974409674	brown	-0.081463422	0.310456874	GO:0006414,GO:0005853,GO:0003746	AT2G18110.1		Translation elongation factor EF1B/ribosomal protein S6 family protein	elongation factor 1-delta 1

Sapur.005G065700.2	0.103196372	-0.05491839	1.136215238	-0.04833	0.961449663	0.974651694	brown	-0.022092801	0.783590209		AT5G64930.1	CPR5,HYS1	CPR5 protein, putative	CPR-5, putative
Sapur.006G187400.1	0.129295545	0.03584012	0.75097567	0.047725	0.961935616	0.974835595	brown	-0.048078935	0.54986714		AT3G13790.1	ATBFRUCT1,ATCWINV1	Glycosyl hydrolases family 32 protein	fructan 1-exohydrolase
Sapur.013G105800.1	0.078028602	-0.066577879	1.400147553	-0.04755	0.96207439	0.974926416	brown	-0.066833118	0.405603679	GO:0016021,GO:0015693,GO:0015095	AT1G34470.1		Protein of unknown function (DUF803)	Non-imprinted in prader-willi/angelman syndrome region protein, putative
Sapur.006G172100.1	0.059655065	-0.085894049	1.817074652	-0.04727	0.96229763	0.974983584	brown	-0.059368944	0.460151106		AT5G06130.2		chaperone protein dnaJ-related	chaperone dnaJ-like protein
Sapur.019G106700.1	0.141447521	0.03750705	0.795923371	0.047124	0.962414443	0.974983584	brown	-0.037109348	0.6444958	GO:0030247,GO:0048544	AT4G03230.1		S-locus lectin protein kinase family protein	wall-associated receptor kinase galacturonan-binding protein
Sapur.004G021500.1	0.081899322	-0.052947494	1.144715624	-0.04625	0.96310793	0.975525424	brown	-0.05251653	0.513612638		AT1G61340.1		F-box family protein	F-box plant protein
Sapur.010G032300.3	0.161718301	0.031792566	0.698684913	0.045503	0.963706034	0.975892146	brown	-0.081608864	0.309590942	GO:0005515	AT1G70180.2		Sterile alpha motif (SAM) domain-containing protein	SAM domain (sterile alpha motif) protein
Sapur.016G093400.7	0.193790231	0.024900112	0.555930038	0.04479	0.964274688	0.976202476	brown	-0.036132092	0.653242148		AT3G54020.1	AtIPCS1	Arabidopsis Inositol phosphorylceramide synthase 1	phosphatidylinositol:ceramide inositolphosphotransferase
Sapur.003G070200.1	0.052728482	0.085483906	2.002608773	0.042686	0.965951622	0.977358172	brown	0.035606773	0.657963369	GO:0006351,GO:0005634,GO:0003700,GO:0043565,GO:0006355	AT2G38250.1		Homeodomain-like superfamily protein	transcription factor, putative
Sapur.005G000700.2	0.069192449	-0.064626768	1.515884899	-0.04263	0.965994064	0.977371216	brown	-0.186140388	0.019588811	GO:0016787	AT3G05910.1		Pectinacetylesterase family protein	pectin acetylesterase, putative
Sapur.016G057800.1	0.064002088	-0.062767849	1.51617842	-0.0414	0.966978032	0.978252068	brown	-0.093309407	0.245089891		AT3G58560.1		DNAse I-like superfamily protein	carbon catabolite repressor-like protein
Sapur.006G185300.7	0.082663209	0.041975017	1.014904331	0.041359	0.967010021	0.978252068	brown	-0.089789644	0.263425616	GO:0017069,GO:0000398	AT1G76940.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif, a.k.a. RRM%2C RBD protein
Sapur.002G093000.2	0.100850736	-0.034931735	0.865168969	-0.04038	0.967793666	0.978777989	brown	-0.090407214	0.260142459		AT1G44920.1			transmembrane protein, putative
Sapur.003G130700.1	0.078131753	-0.044650735	1.106592277	-0.04035	0.967814282	0.978777989	brown	-0.100724214	0.209413365	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G74110.1	CYP78A10	cytochrome P450, family 78, subfamily A, polypeptide 10	cytochrome P450 family protein
Sapur.016G309000.5	0.081480051	-0.06456194	1.619369384	-0.03987	0.96819791	0.978972108	brown	-0.016080811	0.841562887	GO:0005515	AT5G56180.1	ARP8,ATARP8	actin-related protein 8	actin-6
Sapur.004G135200.2	21.71802338	0.003807762	0.096334628	0.039526	0.968470699	0.979188062	brown	-0.008854428	0.912360802		AT2G17020.1		F-box/RNI-like superfamily protein	F-box/LRR protein
Sapur.004G120400.1	0.064455637	-0.064543313	1.653445935	-0.03904	0.968861977	0.979400322	brown	-0.054258742	0.499723619	GO:0033179,GO:0015991,GO:0015078	AT4G39080.1	VHA-A3	vacuolar proton ATPase A3	vacuolar proton ATPase a3
Sapur.006G223500.1	0.06297743	0.05957626	1.526567989	0.039026	0.968869441	0.979400322	brown	-0.013842798	0.863380966	GO:0006887,GO:0000145	AT4G31540.1	ATEXO70G1,EXO70G1	exocyst subunit exo70 family protein G1	plant/F3L17-110 protein
Sapur.008G169800.3	0.06071012	-0.062686565	1.652331653	-0.03794	0.969736919	0.9799804	brown	-0.072703851	0.365520922	GO:0006468,GO:0005524,GO:0004672	AT5G19010.1	MPK16	mitogen-activated protein kinase 16	MAP kinase
Sapur.014G031300.1	0.055285825	-0.062680755	1.663593958	-0.03768	0.969944483	0.980138828	brown	-0.087915801	0.273560208	GO:0008168,GO:0006139	AT1G19340.1		Methyltransferase MT-A70 family protein	methyltransferase-like protein
Sapur.003G062200.2	0.078643468	-0.066337888	1.784453977	-0.03718	0.970345109	0.980430903	brown	-0.02486995	0.757186717		AT5G46860.1	ATSYP22.ATVAM3.SGR3.SYF	Syntaxin/t-SNARE family protein	syntaxin
Sapur.017G062300.2	0.157478373	0.029478725	0.888696466	0.033171	0.973538426	0.982659685	brown	0.002291627	0.977275663	GO:0055085,GO:0042626,GO:0016021,GO:0006810,GO:0005524	AT1G27940.1	PGP13	P-glycoprotein 13	NA
Sapur.006G211000.2	0.062916624	-0.050650389	1.531394866	-0.03307	0.973615038	0.982671847	brown	-0.059395807	0.459947779	GO:0006355,GO:0005634	AT4G32280.1	IAA29	indole-3-acetic acid inducible 29	auxin-responsive protein IAA29
Sapur.008G132100.2	0.059165623	-0.064406804	1.998396275	-0.03223	0.974289234	0.98302752	brown	-0.055008361	0.493808957	GO:0008289	AT4G14500.1		Polyketide cyclase/dehydrase and lipid transport superfamily protein	phosphatidylcholine transfer protein, putative
Sapur.001G092500.3	0.098911371	-0.041473816	1.295899817	-0.032	0.974468961	0.983178866	brown	-0.049613061	0.537193578		AT4G22890.5	PGR5-LIKE A	PGR5-LIKE A	PGR5-like protein 1A
Sapur.007G009400.2	0.098637306	-0.039351631	1.292030459	-0.03046	0.975702426	0.983917502	brown	-0.00455954	0.95480439	GO:0006468,GO:0005524,GO:0004672	AT5G65530.1		Protein kinase superfamily protein	cysteine-rich receptor-like kinase
Sapur.011G049700.1	0.062901508	0.045936513	1.522172583	0.030178	0.97592489	0.984047432	brown	-0.007000855	0.930655186	GO:0005992,GO:0003824	AT1G06410.1	ATTPS7,ATTPSA,TPS7	trehalose-phosphatase/synthase 7	trehalose-6-phosphate synthase
Sapur.004G140500.2	0.059609475	0.045940826	1.528410681	0.030058	0.976020871	0.984081371	brown	-0.052442364	0.514208277	GO:0006470,GO:0004725	AT3G44620.2		protein tyrosine phosphatases;protein tyrosine phosphatases	Low molecular weight tyrosine-phosphatase, putative
Sapur.016G144600.2	0.131657095	-0.03582332	1.202544417	-0.02979	0.976234851	0.984239947	brown	0.016492045	0.837566378	GO:0006468,GO:0004672	AT5G12480.1	CPK7	calmodulin-domain protein kinase 7	calcium-dependent kinase
Sapur.001G137100.2	0.227804825	-0.015248491	0.523247168	-0.02914	0.976751305	0.984546635	brown	-0.097408502	0.224877532		AT1G30970.1	SUF4	zinc finger (C2H2 type) family protein	zinc finger protein
Sapur.006G132200.1	0.056028648	-0.064349189	2.231778465	-0.02883	0.976997667	0.984738856	brown	-0.054713784	0.496128798		AT3G24530.1		AAA-type ATPase family protein / ankyrin repeat family protein	NA
Sapur.014G044100.6	0.052241581	-0.060641356	2.229553641	-0.0272	0.978301111	0.985752222	brown	-0.089374388	0.265649075		AT4G00030.1		Plastid-lipid associated protein PAP / fibrillin family protein	plastid-lipid associated protein PAP
Sapur.008G079200.5	0.075516415	-0.031093568	1.223895675	-0.02541	0.979731598	0.986878379	brown	-0.077815323	0.332694153	GO:0016021,GO:0006820,GO:0016020,GO:0005452	AT2G47160.1	BOR1	HCO3- transporter family	boron transporter
Sapur.016G224000.1	0.055392346	-0.041594464	1.674386075	-0.02484	0.980181293	0.987165532	brown	-0.110731147	0.167395974	GO:0008270,GO:0005515	AT5G40250.1		RING/U-box superfamily protein	RING finger protein
Sapur.001G118100.1	0.122208178	-0.031030958	1.270192836	-0.02443	0.980509526	0.987405903	brown	0.019796396	0.805612504					hypothetical protein
Sapur.004G060600.2	0.082964455	-0.030891836	1.396904714	-0.02211	0.982356627	0.988754203	brown	-0.048803427	0.543863899	GO:0016787	AT1G14860.1	atnudt18,NUDT18	nudix hydrolase homolog 18	nudix hydrolase
Sapur.T012300.3	0.08924773	-0.030803027	1.502329429	-0.0205	0.983641712	0.989866914	brown	-0.004774084	0.952680171	GO:0008017,GO:0000910,GO:0000226	AT5G55230.1	ATMAP65-1,MAP65-1	microtubule-associated proteins 65-1	microtubule-associated protein MAP65-1a
Sapur.010G149300.1	0.537959673	-0.005720877	0.314158452	-0.01821	0.985471195	0.991074666	brown	-0.082097651	0.306692396	GO:0016598,GO:0004057	AT5G05700.1	ATATE1,ATE1,DLS1	arginine-tRNA protein transferase 1	arginyl-tRNA-protein transferase
Sapur.001G087400.3	0.073965737	-0.027163756	1.502450285	-0.01808	0.985575323	0.991078952	brown	-0.020455942	0.799271048	GO:0005524,GO:0003676	AT1G63250.1		DEA(D/H)-box RNA helicase family protein	DEAD-box ATP-dependent RNA helicase, putative
Sapur.003G116000.1	0.115999698	0.014853664	0.824387122	0.018018	0.985624632	0.991078952	brown	-0.093687432	0.243174705	GO:0051716,GO:0046658	AT4G20260.3	ATPCAP1,PCAP1	plasma-membrane associated cation-binding protein 1	DREPP plasma membrane protein
Sapur.018G048700.2	0.098982389	0.018148177	1.010079928	0.017967	0.985665123	0.991078952	brown	0.020796161	0.796004979		AT5G56750.1	NDL1	N-MYC downregulated-like 1	pollen specific protein SF21, putative
Sapur.016G144900.1	0.062529907	-0.027150404	1.521534145	-0.01784	0.985763226	0.991124862	brown	-0.070685361	0.379017267	GO:0006412,GO:0005840,GO:0003735	AT1G59359.1		Ribosomal protein S5 family protein	40S ribosomal protein S2
Sapur.016G024300.1	1.066804719	0.00499814	0.288767107	0.017309	0.986190466	0.99134592	brown	-0.063087233	0.432485067					NA
Sapur.002G131200.1	0.292673939	-0.008290945	0.491240843	-0.01688	0.986534298	0.991511174	brown	-0.030480955	0.704716571		AT1G63800.1	UBC5	ubiquitin-conjugating enzyme 5	ubiquitin-conjugating enzyme E2
Sapur.005G100400.4	0.082126426	-0.027090613	1.617383746	-0.01675	0.986636337	0.99156185	brown	0.004372474	0.9566568	GO:0003676	AT4G36690.2	ATU2AF65A	U2 snRNP auxilliary factor, large subunit, splicing factor	splicing factor U2af large protein
Sapur.017G051000.5	0.139239486	-0.013004795	0.787671545	-0.01651	0.986827183	0.99156185	brown	-0.05388536	0.502683528	GO:0008152,GO:0003824	AT3G23790.1	AAE16	AMP-dependent synthetase and ligase family protein	long-chain-fatty-acid-CoA ligase
Sapur.004G114100.1	0.050954827	0.026509714	1.671974451	0.015855	0.987349803	0.991867766	brown	-0.048388741	0.547296092	GO:0016773,GO:0048015,GO:0046854	AT1G49340.2	ATPI4K ALPHA	Phosphatidylinositol 3- and 4-kinase family protein	NA
Sapur.002G031800.1	0.08645519	-0.027021417	1.756117456	-0.01539	0.987723418	0.992042646	brown	0.005455561	0.945935109	GO:0046983,GO:0003677	AT2G03710.1	AGL3,SEP4	K-box region and MADS-box transcription factor family protein	NA
Sapur.007G067600.1	0.052292133	-0.02520585	1.66844606	-0.01511	0.987946513	0.9920597	brown	-0.059060632	0.462488309					NA
Sapur.15WG108900.3	0.054061236	-0.026930839	2.010795807	-0.01339	0.989314152	0.993117042	brown	-0.057097959	0.477519345	GO:0055114,GO:0016620	AT1G13440.1	GAPC-2,GAPC2	glyceraldehyde-3-phosphate dehydrogenase C2	glyceraldehyde-3-phosphate dehydrogenase
Sapur.009G031700.1	0.05475404	-0.025078584	2.001143208	-0.01253	0.99000107	0.993606099	brown	-0.041020518	0.609986243	GO:0005975,GO:0004553	AT3G47000.1		Glycosyl hydrolase family protein	glycoside hydrolase family 3 protein
Sapur.006G202600.1	0.149450054	0.007966592	0.643210456	0.012386	0.990117918	0.993663067	brown	-0.008393989	0.916901325	GO:0005515	AT5G41840.1		F-box/RNI-like superfamily protein	F-box protein
Sapur.013G124900.1	0.137840229	-0.009118771	0.744115294	-0.01225	0.990222557	0.993737927	brown	-0.084561249	0.292354874		AT4G28260.1			NA
Sapur.009G093800.3	0.172637104	-0.007383635	0.619681748	-0.01192	0.990493267	0.99394928	brown	-0.056989923	0.47835435	GO:0016779,GO:0009058	AT4G39210.1	APL3	Glucose-1-phosphate adenylyltransferase family protein	glucose-1-phosphate adenylyltransferase
Sapur.016G140100.2	0.056325467	0.016820193	1.537638497	0.010939	0.991272133	0.994640329	brown	-0.084009119	0.29552871	GO:0055085,GO:0016021	AT2G29650.1	ANTR1,PHT4;1	phosphate transporter 4;1	sodium-dependent phosphate transporter
Sapur.005G034400.1	0.23744786	0.004218301	0.475341175	0.008874	0.992919458	0.995870274	brown	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004672	AT1G54610.3		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.002G137200.2	0.055586289	-0.021233223	2.830652038	-0.0075	0.994014982	0.996688599	brown	0.018910688	0.814148373	GO:0016787,GO:0005524,GO:0003677,GO:0016891,GO:0005515,GO:0006396,GO:000452	AT1G01040.1	ASU1.ATDCL1.CAF.DCL1.EM	dicer-like 1	endoribonuclease dicer-like protein
Sapur.002G088600.1	0.050786883	0.012335371	1.824773635	0.00676	0.994606385	0.996843814	brown	-0.038875956	0.628808509		AT1G09920.1		TRAF-type zinc finger-related	TRAF-type zinc finger protein
Sapur.003G063800.2	0.052380287	0.010334056	1.53934273	0.006713	0.994643609	0.996843814	brown	-0.065104152	0.417886249	GO:0043565,GO:0006355,GO:0003700	AT2G35530.1	AtbZIP16,bZIP16	basic region/leucine zipper transcription factor 16	BZIP transcription factor
Sapur.004G133500.4	0.072725628	0.008268381	1.302883778	0.006346	0.994936487	0.996967005	brown	-0.060156058	0.454214063	GO:0003824,GO:0006470,GO:0004722	AT4G38520.2		Protein phosphatase 2C family protein	protein phosphatase 2C, putative
Sapur.T171000.1	0.208710591	0.004045453	0.651550724	0.006209	0.995045998	0.9969752	brown	-0.026892177	0.738133705		AT1G40390.1		DNAse I-like superfamily protein	NA
Sapur.006G083200.4	0.052056202	0.010481057	1.829223457	0.00573	0.995428318	0.997120491	brown	-0.052375213	0.514747884	GO:0006629,GO:0055114,GO:0016717	AT5G05580.1	FAD8	fatty acid desaturase 8	omega-3 fatty acid desaturase
Sapur.004G030800.2	0.055662885	0.010538587	2.000619377	0.005268	0.995797033	0.99718568	brown	-0.033483742	0.677180108	GO:0006355,GO:0003677	AT1G28310.2		Dof-type zinc finger DNA-binding family protein	Dof zinc finger protein
Sapur.007G060000.1	0.091224354	0.005402907	1.02883533	0.005251	0.995809945	0.99718568	brown	-0.049796256	0.535689962		AT4G35510.1			hypothetical protein
Sapur.003G082300.1	0.064787539	-0.006953551	1.418413066	-0.0049	0.99608851	0.997204086	brown	-0.098421767	0.2200684	GO:0030170,GO:0009058	AT1G62960.1	ACS10	ACC synthase 10	1-aminocyclopropane-1-carboxylate synthase, putative
Sapur.003G063700.1	0.055748223	0.008686305	2.009650233	0.004322	0.996551317	0.997546632	brown	-0.045789224	0.569049874		AT1G32160.1		Protein of unknown function (DUF760)	plant/F3C3-6 protein
Sapur.017G068000.1	0.152982435	-0.002732851	0.865010281	-0.00316	0.997479225	0.998263976	brown	0.036565607	0.64935631	GO:0016817	AT5G39840.1		ATP-dependent RNA helicase, mitochondrial, putative	ATP-dependent RNA helicase
Sapur.009G008400.5	0.115203593	0.001863388	0.959059112	0.001943	0.998449765	0.998850173	brown	-0.061672361	0.442898348	GO:0055114,GO:0046429,GO:0016114	AT5G60600.1	CLB4,CSB3,GCPE,HDS,ISPG	4-hydroxy-3-methylbut-2-enyl diphosphate synthase	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
Sapur.014G080200.3	0.039007172	0.282514811	1.868412361	0.151206	0.879813365	NA	brown	-0.093780512	0.242704738	GO:0046872,GO:0000166	AT4G00900.1	ATECA2,ECA2	ER-type Ca2+-ATPase 2	endoplasmic reticulum-type calcium-transporting ATPase
Sapur.004G054900.1	0.048983638	-0.244399481	1.833287449	-0.13331	0.893946524	NA	brown	-0.201663579	0.011318076		AT1G17880.1	ATBTF3,BTF3	basic transcription factor 3	transcription factor-BTF3-like protein
Sapur.004G177300.2	0.035747657	0.269076331	2.077521254	0.129518	0.896947809	NA	brown	-0.068533868	0.39373247		AT1G33400.1		Tetratricopeptide repeat (TPR)-like superfamily protein	heat shock protein 70 (HSP70)-interacting protein, putative
Sapur.012G003400.1	0.027619823	0.246986125	1.925807342	0.128251	0.897950584	NA	brown	0.127840483	0.110580293	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT1G05260.1	RCI3,RCI3A	Peroxidase superfamily protein	NA
Sapur.012G029600.1	0.045530008	-0.206987636	1.684996277	-0.12284	0.902232533	NA	brown	-0.081608864	0.309590942		AT4G37110.1		Zinc-finger domain of monoamine-oxidase A repressor R1	monoamine-oxidase A repressor R1 zf-4CXXC-R1: zinc-finger protein
Sapur.019G074900.1	0.043705349	-0.206985026	1.690637486	-0.12243	0.90255835	NA	brown	-0.23333694	0.00327103	GO:0046983,GO:0003677,GO:0006355,GO:0005634,GO:0003700	AT4G09960.3	AGL11,STK	K-box region and MADS-box transcription factor family protein	agamous MADS box factor transcription factor
Sapur.014G119300.2	0.046738353	0.194145867	1.683926787	0.115294	0.908212465	NA	brown	-0.037496486	0.641044299		AT5G16490.1	RIC4	ROP-interactive CRIB motif-containing protein 4	wiscott-aldrich syndrome, carboxy-terminal protein%2C putative
Sapur.016G275600.1	0.038138813	0.233535012	2.061563019	0.113281	0.909808129	NA	brown	-0.057124784	0.477312141		AT5G54730.1	ATATG18F,ATG18F,G18F	homolog of yeast autophagy 18 (ATG18) F	breast carcinoma amplified sequence protein, putative
Sapur.15WG101100.2	0.049776679	0.156501528	1.430974608	0.109367	0.912911336	NA	brown	-0.140954332	0.078265271	GO:0006950	AT5G47740.1		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.002G088000.1	0.04363067	0.194222059	1.852367462	0.104851	0.916494265	NA	brown	0.049519676	0.537960868	GO:0055085	AT1G09930.1	ATOPT2,OPT2	oligopeptide transporter 2	oligopeptide transporter OPT family protein
Sapur.019G050100.1	0.031862381	0.196013467	1.900507308	0.103137	0.917853887	NA	brown	0.060211619	0.453796597		AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO	exportin 1A	NA
Sapur.014G124700.1	0.033226636	0.27111279	2.639616925	0.102709	0.918193818	NA	brown	0.139845908	0.080662276					NA
Sapur.003G028500.3	0.049610834	-0.206871031	2.014405672	-0.1027	0.918204396	NA	brown	-0.086109756	0.283574858					hypothetical protein
Sapur.007G036700.2	0.043761731	0.17201802	1.693161191	0.101596	0.919077535	NA	brown	0.030268559	0.706679408		AT4G37180.2		Homeodomain-like superfamily protein	NA
Sapur.004G130400.3	0.050530453	-0.281678926	2.904824395	-0.09697	0.922750737	NA	brown	-0.089724663	0.263772711		AT2G17840.1	ERD7	Senescence/dehydration-associated protein-related	senescence-associated protein
Sapur.018G062300.1	0.04271765	-0.244240546	2.574509591	-0.09487	0.924419066	NA	brown	-0.129232903	0.106719375		AT5G19670.1		Exostosin family protein	exostosin family protein
Sapur.009G004500.1	0.045104939	-0.191667268	2.038808557	-0.09401	0.925101651	NA	brown	-0.150682475	0.059601714		AT3G45050.1			hypothetical protein
Sapur.009G064300.1	0.050301358	-0.17131264	1.8289785	-0.09367	0.92537468	NA	brown	-0.179682836	0.02433571		AT4G17000.1			hypothetical protein
Sapur.006G198300.3	0.040829437	0.158458156	1.700125076	0.093204	0.925741638	NA	brown	0.043959622	0.584601847		AT4G14740.1		Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region	auxin canalisation protein
Sapur.15WG093100.1	0.036849696	-0.169440124	1.875415559	-0.09035	0.928010644	NA	brown	-0.114599155	0.152957804		AT5G13700.1	APAO,ATPAO1,PAO1	polyamine oxidase 1	polyamine oxidase
Sapur.014G031200.2	0.045844743	-0.229126413	2.559577245	-0.08952	0.928670815	NA	brown	-0.098983376	0.2174346					NAC domain protein
Sapur.013G035300.1	0.038733453	0.158530075	1.869605041	0.084793	0.93242568	NA	brown	0.027066286	0.736500524	GO:0030127,GO:0008270,GO:0006888,GO:0006886	AT4G32640.2		Sec23/Sec24 protein transport family protein	protein transporter Sec24-like CEF protein
Sapur.012G003300.1	0.045337693	-0.191660086	2.269516111	-0.08445	0.932698847	NA	brown	-0.12864878	0.108325955	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT1G05260.1	RCI3,RCI3A	Peroxidase superfamily protein	NA
Sapur.005G162300.1	0.034332251	0.196121984	2.328991635	0.084209	0.932890287	NA	brown	0.068319088	0.395220029	GO:0005515	AT5G45110.1	ATNPR3,NPR3	NPR1-like protein 3	NPR1/NIM1-like regulatory protein, putative
Sapur.008G019500.1	0.046030362	-0.244206808	2.904824395	-0.08407	0.933001264	NA	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.010G063100.1	0.046030362	-0.244206808	2.904824395	-0.08407	0.933001264	NA	brown	-0.081608864	0.309590942		AT3G22600.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	alpha-amylase inhibitors, lipid transfer (LT) and seed storage (SS) family protein
Sapur.014G105300.2	0.047675509	-0.244206808	2.904824395	-0.08407	0.933001264	NA	brown	-0.103892473	0.195363909	GO:0016758,GO:0016021,GO:0005783	AT2G47760.3	ALG3,AtALG3	asparagine-linked glycosylation 3	dolichyl-P-Man:Man(5)GlcNAc(2)-PP-dolichyl mannosyltransferase, putative
Sapur.007G109000.1	0.026597321	0.19798647	2.391796689	0.082777	0.93402862	NA	brown	0.10704722	0.182067211	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT5G15180.1		Peroxidase superfamily protein	NA
Sapur.T159800.1	0.02610683	0.197987299	2.396844557	0.082603	0.934166968	NA	brown	0.107116019	0.181784833		AT5G24280.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.T079800.1	0.025200979	0.197988865	2.40648488	0.082273	0.93442958	NA	brown	-0.075102413	0.349875031					NA
Sapur.T079900.1	0.025200979	0.197988865	2.40648488	0.082273	0.93442958	NA	brown	-0.074144297	0.356073667					NA
Sapur.018G059300.1	0.019157992	0.235520464	2.904820075	0.081079	0.935378974	NA	brown	-0.076757111	0.339330567					NA
Sapur.010G136200.3	0.045047036	-0.206770695	2.555533233	-0.08091	0.935512749	NA	brown	-0.132554318	0.097936772		AT1G79270.1	ECT8	evolutionarily conserved C-terminal region 8	YTH domain protein
Sapur.001G181400.1	0.04421098	-0.20676997	2.561294706	-0.08073	0.935657719	NA	brown	-0.131697887	0.100144702	GO:0005515	AT1G58025.3		DNA-binding bromodomain-containing protein	bromodomain domain protein
Sapur.003G057000.2	0.043352299	-0.206769213	2.567353563	-0.08054	0.93580947	NA	brown	-0.129355928	0.106383403		AT1G32470.1		Single hybrid motif superfamily protein	glycine cleavage system H protein
Sapur.016G250200.1	0.042108541	-0.206768093	2.576396958	-0.08025	0.936034646	NA	brown	-0.127365428	0.11192224	GO:0008270,GO:0003677	AT3G14890.2		phosphoesterase	polynucleotide phosphatase/kinase
Sapur.013G069300.1	0.040697462	-0.169339106	2.28595327	-0.07408	0.94094823	NA	brown	-0.16165678	0.043104993		AT5G35405.1		Protein of unknown function (DUF784)	prolamin-like protein
Sapur.008G049300.2	0.038851206	-0.169336808	2.2988764	-0.07366	0.941280383	NA	brown	-0.166368575	0.037299575		AT2G39870.1			hypothetical protein
Sapur.010G162000.1	0.045719135	-0.133835536	1.841919108	-0.07266	0.942075948	NA	brown	-0.136549123	0.088142192	GO:0008270,GO:0005515	AT5G17600.1		RING/U-box superfamily protein	RING-H2 finger protein
Sapur.005G161900.1	0.040121719	-0.133827865	1.863684727	-0.07181	0.942754539	NA	brown	-0.13580341	0.089908636		AT1G06660.1			hypothetical protein
Sapur.016G168400.2	0.02219351	0.198036645	2.779507733	0.071249	0.943199728	NA	brown	0.082922749	0.301840023	GO:0005515	AT1G73150.1	GTE3	global transcription factor group E3	global transcription factor group protein
Sapur.001G160300.1	0.037294875	-0.206734691	2.904824395	-0.07117	0.943262913	NA	brown	-0.0977476	0.223259905		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.002G168600.1	0.038747901	-0.206734691	2.904824395	-0.07117	0.943262913	NA	brown	-0.102360415	0.202069824	GO:0005634,GO:0003677	AT2G47070.1	SPL1	squamosa promoter binding protein-like 1	squamosa promoter-binding protein
Sapur.003G090900.1	0.044087877	-0.206734691	2.904824395	-0.07117	0.943262913	NA	brown	-0.125536871	0.117206616	GO:0003677,GO:0005515,GO:0055114,GO:0016706	AT1G63490.1		transcription factor jumonji (jmjC) domain-containing protein	lysine-specific demethylase 5D
Sapur.007G024500.1	0.041875009	-0.206734691	2.904824395	-0.07117	0.943262913	NA	brown	-0.094532293	0.238932118		AT5G49610.1		F-box family protein	F-box protein interaction domain protein
Sapur.010G022800.2	0.040915878	-0.206734691	2.904824395	-0.07117	0.943262913	NA	brown	-0.081608864	0.309590942	GO:0016788	AT1G67830.1	ATFXG1,FXG1	alpha-fucosidase 1	NA
Sapur.016G195300.1	0.04169213	-0.206734691	2.904824395	-0.07117	0.943262913	NA	brown	-0.094186586	0.240661838	GO:0030870,GO:0016887,GO:0006281,GO:0005634,GO:0000723	AT2G31970.1	ATRAD50,RAD50	DNA repair-recombination protein (RAD50)	DNA repair protein Rad50
Sapur.016G229600.2	0.041981016	-0.206734691	2.904824395	-0.07117	0.943262913	NA	brown	-0.094713568	0.238028598	GO:0016020	AT1G30360.1	ERD4	Early-responsive to dehydration stress protein (ERD4)	early-responsive to dehydration protein
Sapur.018G070800.2	0.041738451	-0.206734691	2.904824395	-0.07117	0.943262913	NA	brown	-0.094341346	0.239886431	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	AT4G25810.1	XTH23,XTR6	xyloglucan endotransglycosylase 6	xyloglucan endotransglycosylase/hydrolase
Sapur.001G091900.3	0.041419064	0.158641516	2.285525766	0.069411	0.944662164	NA	brown	0.04123523	0.608115496	GO:0046983,GO:0003677,GO:0006355,GO:0005634,GO:0003700	AT4G22950.1	AGL19,GL19	AGAMOUS-like 19	MIKC MADS-box transcription factor
Sapur.002G106100.1	0.017109345	0.199900829	2.904821116	0.068817	0.945135353	NA	brown	-0.069932009	0.384131275	GO:0003677	AT4G33280.1		AP2/B3-like transcriptional factor family protein	NA
Sapur.013G031800.1	0.023689878	0.199900829	2.904821116	0.068817	0.945135353	NA	brown	0.078548531	0.32814497					transmembrane protein, putative
Sapur.011G107600.2	0.030480922	0.160508419	2.357555049	0.068083	0.945719901	NA	brown	-0.07619091	0.342915702	GO:0055085,GO:0016021	AT1G20925.1		Auxin efflux carrier family protein	auxin efflux carrier family protein
Sapur.008G137000.1	0.029851483	0.160509369	2.363077031	0.067924	0.945846226	NA	brown	0.049053047	0.541803015	GO:0051861,GO:0046836,GO:0017089,GO:0005737	AT2G33470.2	ATGLTP1,GLTP1	glycolipid transfer protein 1	glycolipid transfer protein, putative
Sapur.016G167800.2	0.047152423	-0.171153045	2.546264209	-0.06722	0.9464087	NA	brown	-0.098235935	0.220944875	GO:0006355,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AT2G14210.1	AGL44,ANR1	AGAMOUS-like 44	MADS-box transcription factor
Sapur.010G197800.1	0.044355202	0.122904024	1.844334891	0.066639	0.94686936	NA	brown	-0.077250676	0.336224854		AT5G22040.2			disease resistance protein, putative
Sapur.012G030400.2	0.04703916	0.12104654	1.839887428	0.06579	0.947544868	NA	brown	0.008163267	0.919177563	GO:0048500,GO:0008312,GO:0006614	AT1G48160.1		signal recognition particle 19 kDa protein, putative / SRP19, putative	signal recognition particle 19 kDa protein
Sapur.007G076100.3	0.037626779	0.122914115	1.871859445	0.065664	0.947645191	NA	brown	0.008846222	0.912441706		AT2G21940.4	ATSK1,SK1	shikimate kinase 1	shikimate kinase
Sapur.001G018000.1	0.037065004	0.122915028	1.874416558	0.065575	0.947716124	NA	brown	-0.018969462	0.813581262	GO:0005515	AT5G13460.1	IQD11	IQ-domain 11	IQ calmodulin-binding motif protein
Sapur.010G171300.2	0.049705714	-0.118951467	1.832260179	-0.06492	0.948237203	NA	brown	-0.105308303	0.189311746		AT3G55005.1	TON1B	tonneau 1b (TON1b)	FGFR1 oncogene partner, putative
Sapur.013G102500.4	0.036573688	-0.169291089	2.616334762	-0.06471	0.948408532	NA	brown	-0.133371676	0.095865662		AT1G35510.1		O-fucosyltransferase family protein	GDP-fucose protein O-fucosyltransferase
Sapur.002G111000.3	0.036525042	-0.116729487	1.876923815	-0.06219	0.950410001	NA	brown	-0.19558544	0.014094267	GO:0098599	AT3G60340.2		alpha/beta-Hydrolases superfamily protein	palmitoyl-protein thioesterase, putative
Sapur.016G059500.2	0.037697024	0.122973927	2.066586053	0.059506	0.952549219	NA	brown	-0.205452028	0.009841966	GO:0008168	AT3G58470.1		nucleic acid binding;methyltransferases	N6-adenine methyltransferase, putative
Sapur.006G150700.2	0.04749933	-0.171115219	2.904823275	-0.05891	0.953025965	NA	brown	-0.07300904	0.363506489	GO:0016021	AT2G24170.1		Endomembrane protein 70 protein family	endomembrane family protein
Sapur.002G200200.1	0.022828408	0.162415905	2.766664251	0.058705	0.953187399	NA	brown	-0.110576635	0.167993087	GO:0006810,GO:0005622	AT5G43960.1		Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain	Ras GTPase-activating protein-binding protein
Sapur.001G070500.2	0.037771266	-0.169262574	2.904824395	-0.05827	0.953533987	NA	brown	-0.114908768	0.151843983		AT5G49330.1	ATMYB111,MYB111,PFG3	myb domain protein 111	R2R3-MYB transcription factor, putative
Sapur.002G046600.3	0.035801393	-0.169262574	2.904824395	-0.05827	0.953533987	NA	brown	-0.081608864	0.309590942		AT3G59090.1			plant/F17J16-140 protein, putative
Sapur.006G027900.1	0.036852113	-0.169262574	2.904824395	-0.05827	0.953533987	NA	brown	-0.096520425	0.229153239		AT5G19400.3	SMG7	Telomerase activating protein Est1	Est1 DNA/RNA-binding domain protein
Sapur.007G052000.1	0.035801393	-0.169262574	2.904824395	-0.05827	0.953533987	NA	brown	-0.081608864	0.309590942	GO:0008168	AT5G66180.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase domain protein
Sapur.007G112400.1	0.035062145	-0.169262574	2.904824395	-0.05827	0.953533987	NA	brown	-0.108849011	0.174777731		AT1G05870.3		Protein of unknown function (DUF1685)	DUF1685 family protein
Sapur.010G090100.1	0.039319894	-0.169262574	2.904824395	-0.05827	0.953533987	NA	brown	-0.1179924	0.141082343	GO:0030247,GO:0006468,GO:0004672	AT1G66920.2		Protein kinase superfamily protein	NA
Sapur.010G155000.3	0.037115279	-0.169262574	2.904824395	-0.05827	0.953533987	NA	brown	-0.096996422	0.226854448		AT5G05987.1	PRA1.A2	prenylated RAB acceptor 1.A2	prenylated rab acceptor family protein, putative
Sapur.016G303300.1	0.035801393	-0.169262574	2.904824395	-0.05827	0.953533987	NA	brown	-0.081608864	0.309590942					NA
Sapur.001G082200.2	0.019837975	0.162420949	2.818384948	0.057629	0.954044081	NA	brown	0.076726347	0.339524746	GO:0016757,GO:0016020	AT5G41460.1		Protein of unknown function (DUF604)	transferring glycosyl group transferase, putative
Sapur.001G159100.1	0.038022438	-0.131864251	2.300354783	-0.05732	0.954287548	NA	brown	-0.161746404	0.042987892		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.005G112400.3	0.037944043	-0.131864159	2.300875365	-0.05731	0.954297911	NA	brown	-0.081608864	0.309590942	GO:0019904	AT5G65430.1	14-3-3KAPPA.GF14 KAPPA.G	general regulatory factor 8	14-3-3-like protein GF14 lambda protein
Sapur.014G027500.1	0.019033682	0.162422428	2.83419082	0.057308	0.954299673	NA	brown	0.073319992	0.361461113	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G31940.1	CYP82C4	cytochrome P450, family 82, subfamily C, polypeptide 4	NA
Sapur.013G069400.1	0.035582977	-0.131861326	2.317194609	-0.05691	0.954620401	NA	brown	-0.156084567	0.050927887		AT5G35405.1		Protein of unknown function (DUF784)	prolamin-like protein
Sapur.013G069700.1	0.035582977	-0.131861326	2.317194609	-0.05691	0.954620401	NA	brown	-0.156084567	0.050927887		AT5G35405.1		Protein of unknown function (DUF784)	prolamin-like protein
Sapur.005G052300.2	0.040594729	-0.116722078	2.051517354	-0.0569	0.95462845	NA	brown	-0.174453707	0.028872997		AT5G09220.1	AAP2	amino acid permease 2	amino acid permease
Sapur.019G015100.1	0.017360128	0.164281247	2.904822183	0.056555	0.954899948	NA	brown	-0.079774479	0.320628304					NA
Sapur.005G126700.2	0.01230166	0.164281247	2.904822183	0.056555	0.954899948	NA	brown	-0.081608864	0.309590942		AT3G28370.1			NA
Sapur.012G083100.2	0.011954249	0.164281246	2.904822183	0.056555	0.954899949	NA	brown	0.009727869	0.903755456		AT5G51050.1		Mitochondrial substrate carrier family protein	substrate carrier family protein
Sapur.006G059300.3	0.017216722	0.162425915	2.872654208	0.056542	0.954909954	NA	brown	0.063809465	0.427224123		AT2G44120.2		Ribosomal protein L30/L7 family protein	60S ribosomal protein L7
Sapur.002G096400.1	0.034171329	0.115341178	2.08952979	0.0552	0.955979459	NA	brown	0.021339384	0.790797424		AT5G67420.1	ASL39,LBD37	LOB domain-containing protein 37	LOB domain protein, putative
Sapur.004G046700.3	0.033145237	0.11534026	2.09591511	0.055031	0.956113784	NA	brown	-0.24320634	0.002146083		AT1G73350.2			hypothetical protein
Sapur.004G156400.4	0.01117195	0.157814843	2.904822379	0.054329	0.956673388	NA	brown	-0.102104766	0.203204799	GO:0032012,GO:0005086	AT4G38200.1		SEC7-like guanine nucleotide exchange family protein	brefeldin A-inhibited guanine nucleotide-exchange protein
Sapur.001G002200.1	0.032223663	0.124886841	2.340203519	0.053366	0.957440451	NA	brown	-0.034476928	0.668163363		AT5G56520.1			hypothetical protein
Sapur.012G085100.1	0.031376299	0.124888073	2.347311269	0.053205	0.957568783	NA	brown	0.04806752	0.549961985	GO:0003676	AT5G65260.1		RNA-binding (RRM/RBD/RNP motifs) family protein	type II polyadenylate-binding family RNA recognition motif protein
Sapur.002G162500.3	0.036572925	-0.154177938	2.904823918	-0.05308	0.957670941	NA	brown	-0.091103876	0.25647262	GO:0006950	AT3G62550.1		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.002G005700.2	0.027789953	0.124893517	2.379589188	0.052485	0.958141987	NA	brown	-0.077967807	0.331744766		AT1G20696.2	HMGB3,NFD03,NFD3	high mobility group B3	high mobility group box protein
Sapur.017G081100.2	0.027082836	0.124894719	2.386914187	0.052325	0.958269922	NA	brown	0.019915002	0.804471183	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT3G30180.1	BR6OX2,CYP85A2	brassinosteroid-6-oxidase 2	cytochrome P450 family protein
Sapur.15WG000900.1	0.026893305	0.124895028	2.388807598	0.052283	0.958302865	NA	brown	0.045046272	0.575341486		AT1G18000.1		Major facilitator superfamily protein	UNC93-like protein C922.05c
Sapur.T186200.1	0.026392859	0.124895853	2.393887972	0.052173	0.958391001	NA	brown	0.002289373	0.977298008		AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO	exportin 1A	NA
Sapur.002G162500.2	0.041601988	-0.133676754	2.578206885	-0.05185	0.958649226	NA	brown	-0.114721026	0.152518644	GO:0006950	AT3G62550.1		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.010G093200.1	0.041167071	-0.133676345	2.581496412	-0.05178	0.958701998	NA	brown	-0.109776359	0.171111139	GO:0008270,GO:0005515	AT3G18290.1	BTS,EMB2454	zinc finger protein-related	zinc finger protein, putative
Sapur.003G156600.5	0.034037904	-0.131816809	2.634301827	-0.05004	0.960091618	NA	brown	-0.154011695	0.054123565	GO:0046872,GO:0000166	AT2G41560.1	ACA4	autoinhibited Ca(2+)-ATPase, isoform 4	calcium-transporting ATPase 4, plasma membrane-type protein
Sapur.002G034100.2	0.033712661	-0.131816451	2.637451151	-0.04998	0.960139341	NA	brown	-0.157527654	0.048796813	GO:0006355,GO:0005634	AT5G43700.1	ATAUX2-11,IAA4	AUX/IAA transcriptional regulator family protein	indole-3-acetic acid inducible protein
Sapur.017G028800.3	0.033476828	-0.13181604	2.641074175	-0.04991	0.9601941	NA	brown	-0.148484694	0.06346179	GO:0005515	AT3G21820.1	ATXR2,SDG36	histone-lysine N-methyltransferase ATXR2	histone-lysine N-methyltransferase ATXR2
Sapur.006G179100.2	0.031872994	-0.131814221	2.657320446	-0.0496	0.96043781	NA	brown	-0.145548298	0.068935915	GO:0005515	AT2G45700.1		sterile alpha motif (SAM) domain-containing protein	DNA cross-link repair 1A protein
Sapur.008G021700.1	0.031689064	-0.131814007	2.659248483	-0.04957	0.960466534	NA	brown	-0.145294833	0.069425915					NA
Sapur.019G055100.1	0.006480264	0.143384081	2.904822821	0.049361	0.960631849	NA	brown	0.091897757	0.252334244					NA
Sapur.018G105100.1	0.007094491	0.143384081	2.904822821	0.049361	0.960631849	NA	brown	0.090817653	0.257976035	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT5G36110.1	CYP716A1	cytochrome P450, family 716, subfamily A, polypeptide 1	cytochrome P450 family 716 protein
Sapur.T129000.1	0.008986688	0.143384081	2.904822821	0.049361	0.960631849	NA	brown	-0.074820339	0.351692855					NA
Sapur.T054400.1	0.049792282	-0.135495692	2.904822183	-0.04665	0.962796094	NA	brown	-0.061867584	0.441453141					NA
Sapur.010G070900.1	0.028791823	0.124935376	2.687671098	0.046485	0.96292399	NA	brown	-0.088817185	0.268652634	GO:0005515,GO:0006468,GO:0004672	AT2G01820.1		Leucine-rich repeat protein kinase family protein	receptor kinase, putative
Sapur.019G100300.2	0.038658926	0.085441024	1.869931888	0.045692	0.963555699	NA	brown	-0.020391872	0.799886506		AT4G03320.1	tic20-IV	translocon at the inner envelope membrane of chloroplasts 20-IV	Tic20-IV, putative
Sapur.002G131100.3	0.034843087	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.136641527	0.087925249	GO:0016787,GO:0005524,GO:0003677,GO:0006355,GO:0005634	AT2G46020.2	ATBRM,BRM,CHA2,CHR2	transcription regulatory protein SNF2, putative	ATP-dependent helicase BRM
Sapur.006G207800.7	0.032291271	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.084530771	0.292529477		AT3G63400.3		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.007G102300.3	0.030686908	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.081608864	0.309590942		AT5G09520.1		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative
Sapur.010G071500.1	0.031758162	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.098905052	0.217800562	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	AT1G14720.1	ATXTH28.EXGT-A2.XTH28.X	xyloglucan endotransglucosylase/hydrolase 28	xyloglucan endotransglucosylase/hydrolase, putative
Sapur.010G197400.1	0.030664735	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.096488186	0.229309525	GO:0008253,GO:0005737,GO:0000287	AT2G38680.1		5\'-nucleotidases;magnesium ion binding	cytosolic 5'-nucleotidase III-like protein
Sapur.011G048200.1	0.028876407	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.091928207	0.252176439	GO:0006468,GO:0005524,GO:0004672	AT4G21410.1	CRK29	cysteine-rich RLK (RECEPTOR-like protein kinase) 29	tyrosine kinase domain protein
Sapur.011G082600.4	0.03424425	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.136935803	0.087237197	GO:0016020,GO:0008375	AT3G15350.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	core-2/I-branching beta-1%2C6-N-acetylglucosaminyltransferase family protein, putative
Sapur.013G112000.1	0.030686908	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.081608864	0.309590942		AT1G28520.1	ATVOZ1,VOZ1	vascular plant one zinc finger protein	transcription factor VOZ1
Sapur.014G013800.4	0.030686908	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.081608864	0.309590942		AT1G60060.1		Serine/threonine-protein kinase WNK (With No Lysine)-related	bHLH-MYC/R2R3-MYB transcription factor amino-terminal protein
Sapur.014G103100.1	0.030686908	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.081608864	0.309590942		AT3G62860.1		alpha/beta-Hydrolases superfamily protein	monoglyceride lipase
Sapur.016G058500.2	0.031772376	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.098763117	0.218464867	GO:0003676	AT1G55310.3	ATSCL33,SCL33,SR33	SC35-like splicing factor 33	serine/arginine-rich splicing factor 10 (SRSF10)-like RNA recognition motif protein
Sapur.T129100.1	0.030686908	-0.131790456	2.904824395	-0.04537	0.963812784	NA	brown	-0.081608864	0.309590942					NA
Sapur.009G130600.3	0.021200635	0.124946679	2.796283891	0.044683	0.964359891	NA	brown	0.005207813	0.948386828	GO:0016020,GO:0008158	AT4G38350.1		Patched family protein	niemann-pick C type family protein
Sapur.018G067300.2	0.014918953	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.206507948	0.009462058	GO:0006468,GO:0005524,GO:0004672	AT2G18890.1		Protein kinase superfamily protein	receptor-like kinase
Sapur.005G206200.2	0.010741554	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.081608864	0.309590942	GO:0003677	AT1G76510.1		ARID/BRIGHT DNA-binding domain-containing protein	ARID/bright DNA-binding domain protein
Sapur.012G036300.1	0.007980969	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497					hypothetical protein
Sapur.014G032800.3	0.00778933	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT2G38740.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	haloacid dehalogenase-like hydrolase family protein
Sapur.005G051800.5	0.00734023	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.001702542	0.983116162	GO:0070403	AT5G09230.7	AtSRT2,SRT2	sirtuin 2	NAD-dependent protein deacetylase
Sapur.008G038200.2	0.006454126	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0016021,GO:0015116,GO:0008272,GO:0055085,GO:0016020,GO:0008271	AT5G13550.1	SULTR4;1	sulfate transporter 4.1	sulfate/bicarbonate/oxalate exchanger and transporter sat-1, putative
Sapur.010G043200.2	0.006454126	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT4G28600.1	NPGR2	no pollen germination related 2	O-linked N-acetylglucosamine transferase, ogt protein%2C putative
Sapur.002G159200.1	0.006449611	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT2G47540.1		Pollen Ole e 1 allergen and extensin family protein	pollen protein Ole E I-like protein
Sapur.007G018800.2	0.006449611	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0008168	AT4G36470.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase, putative
Sapur.002G084200.1	0.00611461	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT4G24560.1	UBP16	ubiquitin-specific protease 16	ubiquitin carboxyl-terminal hydrolase
Sapur.004G158000.1	0.00611461	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT2G17390.1	AKR2B	ankyrin repeat-containing 2B	TGB12K interacting protein
Sapur.003G051100.1	0.006088772	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0006468,GO:0005524,GO:0004672	AT4G16970.1		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein, putative
Sapur.008G070900.3	0.006088772	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0015934,GO:0006412,GO:0003735	AT1G26740.1		Ribosomal L32p protein family	ribosomal protein L32
Sapur.010G090100.2	0.006088772	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0030247,GO:0006468,GO:0004672	AT1G66920.2		Protein kinase superfamily protein	NA
Sapur.010G108100.1	0.006088772	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT2G03810.1		18S pre-ribosomal assembly protein gar2-related	hypothetical protein
Sapur.014G017500.1	0.006088772	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497					NA
Sapur.016G181100.1	0.006088772	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0019441,GO:0004061	AT4G35220.1		Cyclase family protein	cyclase family protein
Sapur.003G071700.2	0.005967487	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT1G31500.1		DNAse I-like superfamily protein	carbon catabolite repressor-like protein
Sapur.014G003000.2	0.005967487	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0016757,GO:0016021	AT2G22900.1		Galactosyl transferase GMA12/MNN10 family protein	alpha galactosyltransferase, putative
Sapur.009G058300.1	0.005789239	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT5G58560.1		Phosphatidate cytidylyltransferase family protein	phytol kinase, putative
Sapur.010G139100.3	0.005789239	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0003676	AT5G16260.1	ELF9	RNA binding (RRM/RBD/RNP motifs) family protein	splicing factor U2AF 35 kDa subunit B RNA recognition motif protein, putative
Sapur.017G128200.2	0.005659149	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.00072186	0.992840993		AT1G73390.1		Endosomal targeting BRO1-like domain-containing protein	BRO1-like domain protein
Sapur.001G135500.1	0.005637254	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497					NA
Sapur.008G131400.1	0.005637254	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0003677	AT3G42170.1		BED zinc finger ;hAT family dimerisation domain	NA
Sapur.012G028200.1	0.005637254	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT1G05260.1	RCI3,RCI3A	Peroxidase superfamily protein	cationic peroxidase kDa protein
Sapur.014G094400.1	0.005637254	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT1G02380.1			transmembrane protein, putative
Sapur.016G118500.1	0.005637254	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497					NA
Sapur.016G302900.1	0.005637254	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.078477539	0.328583686		AT4G03500.1		Ankyrin repeat family protein	ankyrin repeat protein
Sapur.017G053400.1	0.005637254	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497					NA
Sapur.001G010500.1	0.005474546	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0016020,GO:0006810,GO:0005215	AT5G19640.1		Major facilitator superfamily protein	peptide transporter PTR1
Sapur.005G118800.2	0.005474546	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT4G38040.1		Exostosin family protein	exostosin family protein
Sapur.007G044300.2	0.005474546	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0055114,GO:0016491	AT3G50210.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate-Fe(II)-dependent oxygenase domain protein
Sapur.008G019400.2	0.005474546	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497					hypothetical protein
Sapur.008G048800.1	0.005474546	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497					hypothetical protein
Sapur.009G044400.1	0.005474546	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT5G13690.1	CYL1,NAGLU	alpha-N-acetylglucosaminidase family / NAGLU family	alpha-N-acetylglucosaminidase
Sapur.011G112300.3	0.005474546	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.081608864	0.309590942		AT3G15850.1	ADS3,FAD5,FADB,JB67	fatty acid desaturase 5	palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, putative
Sapur.009G097200.2	0.005161387	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.108970111	0.174295651	GO:0003723	AT2G21350.1		RNA-binding CRS1 / YhbY (CRM) domain protein	NA
Sapur.003G009500.2	0.004974636	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.144103906	0.071766275	GO:0005622,GO:0003676,GO:0005524,GO:0043140,GO:0006281,GO:0006260	AT1G10930.1	ATRECQ4A.ATSGS1.RECQ4A	DNA helicase (RECQl4A)	ATP-dependent DNA helicase
Sapur.004G147500.1	0.004974636	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0005515	AT3G62020.2	GLP10	germin-like protein 10	NA
Sapur.005G140800.1	0.004974636	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT3G49600.1	ATUBP26,SUP32,UBP26	ubiquitin-specific protease 26	ubiquitin carboxyl-terminal hydrolase
Sapur.008G017800.2	0.004974636	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT5G03760.1	ATCSLA09.ATCSLA9.CSLA09	Nucleotide-diphospho-sugar transferases superfamily protein	cellulose synthase-like protein
Sapur.012G067100.4	0.004974636	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0006464,GO:0004719	AT5G50240.1	PIMT2	protein-l-isoaspartate methyltransferase 2	L-isoaspartate O-methyltransferase
Sapur.014G008100.1	0.004974636	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497	GO:0005515	AT1G27752.1		Ubiquitin system component Cue protein	ubiquitin system component CUE protein, putative
Sapur.15WG124300.3	0.004974636	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT4G21340.1	B70	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	hypothetical protein
Sapur.T174200.2	0.004974636	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	0.078548531	0.32814497		AT3G24880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.016G100400.7	0.004856032	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.081608864	0.309590942		AT5G01520.1		RING/U-box superfamily protein	RING finger protein
Sapur.001G112200.3	0.004438202	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.109902768	0.170615866	GO:0034755,GO:0016021,GO:0005381	AT5G03570.1	ATIREG2,FPN2,IREG2	iron regulated 2	solute carrier family 40 protein
Sapur.005G179800.1	0.00430041	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.1612834	0.054359396	GO:0016567,GO:0004842,GO:0005515	AT3G54790.1		ARM repeat superfamily protein	ubiquitin-protein ligase, PUB2
Sapur.006G176300.5	0.004340041	0.128661719	2.904823276	0.044292	0.964671295	NA	brown	-0.15489623	0.057740196	GO:0008270,GO:0003676	AT3G53500.2	RSZ32	RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain	RNA recognition motif, a.k.a. RRM%2C RBD protein

Sapur.010G128600.4	0.003883051	0.128661719	2.904823276	0.044292	0.964671296	NA	brown	-0.081608864	0.309590942		AT5G64130.1		cAMP-regulated phosphoprotein 19-related protein	NA
Sapur.001G167300.2	0.00377543	0.128661719	2.904823276	0.044292	0.964671296	NA	brown	0.05320448	0.508104592		AT1G51710.1	ATUBP6,UBP6	ubiquitin-specific protease 6	ubiquitin carboxyl-terminal hydrolase
Sapur.005G153100.2	0.003577442	0.128661719	2.904823276	0.044292	0.964671296	NA	brown	-0.157663184	0.048600536		AT1G76730.1		NagB/RpiA/CoA transferase-like superfamily protein	NA
Sapur.006G055800.2	0.002869527	0.128661719	2.904823276	0.044292	0.964671296	NA	brown	-0.016056727	0.841797072		AT3G15760.1			transmembrane protein, putative
Sapur.016G245700.3	0.002731927	0.128661719	2.904823276	0.044292	0.964671296	NA	brown	-0.010073523	0.900353013	GO:0006468,GO:0004672	AT1G53440.1		Leucine-rich repeat transmembrane protein kinase	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.15WG110600.5	0.044067065	0.12680913	2.904822183	0.043655	0.965179652	NA	brown	-0.040502715	0.614508158	GO:0005515,GO:0006468,GO:0004672	AT5G14210.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.012G036800.6	0.027415712	0.12680913	2.904822183	0.043655	0.965179652	NA	brown	-0.061017889	0.447762781		AT1G15060.1		Uncharacterised conserved protein UCP031088, alpha/beta hydrolase	alpha/beta hydrolase family protein
Sapur.009G130100.2	0.017462463	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.056491496	0.482216866	GO:0005515	AT2G17200.1	DSK2	ubiquitin family protein	ubiquitin domain protein
Sapur.002G006600.1	0.015664048	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.003446978	0.965824693	GO:0005515	AT2G30600.1		BTB/POZ domain-containing protein	BTB/POZ domain protein
Sapur.005G167400.3	0.016851209	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.03785685	0.637838393	GO:0005515	AT3G63220.2		Galactose oxidase/kelch repeat superfamily protein	F-box/kelch-repeat protein SKIP30
Sapur.005G180600.1	0.015996415	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.04742922	0.555278126	GO:0072588,GO:0042254,GO:0030515,GO:0001522	AT2G20490.1	EDA27,NOP10	nucleolar RNA-binding Nop10p family protein	H/ACA ribonucleoprotein complex subunit-like protein
Sapur.014G137400.1	0.015657108	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.047572789	0.554080231	GO:0016747,GO:0008152	AT5G48230.2	ACAT2,EMB1276	acetoacetyl-CoA thiolase 2	NA
Sapur.017G103600.1	0.014698426	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.04260577	0.596234376		AT1G70780.1			NA
Sapur.003G089700.2	0.014612884	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.040535123	0.61422472	GO:0006468,GO:0004672	AT1G63430.2		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.008G022700.2	0.015112397	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.043440318	0.589051433		AT5G04410.1	anac078,NAC2	NAC domain containing protein 2	NAC transcription factor
Sapur.009G085300.2	0.019932624	0.126809129	2.904822183	0.043655	0.965179652	NA	brown	0.048818951	0.543735617	GO:0003677	AT3G18990.1	REM39,VRN1	AP2/B3-like transcriptional factor family protein	B3 domain transcription factor VRN1
Sapur.013G098800.1	0.047679246	-0.098108135	2.257640023	-0.04346	0.965337992	NA	brown	-0.089277238	0.266171101	GO:0055114,GO:0016616,GO:0006694,GO:0003854	AT1G75280.1		NmrA-like negative transcriptional regulator family protein	phenylcoumaran benzylic ether reductase-like protein
Sapur.004G096700.2	0.044220524	0.087347062	2.031720158	0.042992	0.965708166	NA	brown	-0.077994376	0.331579518		AT5G16110.1			hypothetical protein
Sapur.006G087000.1	0.044707994	-0.09625272	2.264150489	-0.04251	0.966090843	NA	brown	-0.117209794	0.143756961		AT2G38420.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.008G019200.1	0.021518901	0.103698156	2.450252727	0.042321	0.966242476	NA	brown	-0.018631208	0.816846408					hypothetical protein
Sapur.009G086500.1	0.03652975	0.087357304	2.070419341	0.042193	0.966344804	NA	brown	0.017346685	0.829274084		AT3G50830.1	ATCOR413-PM2,COR413-PI	cold-regulated 413-plasma membrane 2	cold acclimation protein COR413-PM1
Sapur.018G046300.1	0.042123546	0.085496265	2.046696739	0.041773	0.966679814	NA	brown	-0.03346279	0.677370824	GO:0003677	AT3G43240.1		ARID/BRIGHT DNA-binding domain-containing protein	ARID/bright DNA-binding domain protein
Sapur.010G167500.2	0.037694866	-0.09624499	2.30648289	-0.04173	0.966715508	NA	brown	-0.13006725	0.104457081	GO:0005975,GO:0004553	AT3G55260.1	ATHEX2,HEXO1	beta-hexosaminidase 1	beta-hexosaminidase
Sapur.014G000300.1	0.037105418	-0.096244285	2.310470774	-0.04166	0.966773167	NA	brown	-0.120413839	0.133046593	GO:0005515,GO:0008270,GO:0006355,GO:0005634,GO:0004402,GO:0003712,GO:001657	AT1G16710.1	HAC12	histone acetyltransferase of the CBP family 12	histone acetyltransferase HAC12
Sapur.007G026000.2	0.030494107	0.087366765	2.108313435	0.041439	0.966945784	NA	brown	-0.390499906	4.28E-07	GO:0045735	AT4G36700.1		RmlC-like cupins superfamily protein	cupin protein
Sapur.T186600.1	0.034363118	-0.094387953	2.323526839	-0.04062	0.96759668	NA	brown	-0.17793585	0.025778253					NA
Sapur.009G097900.1	0.043239251	-0.10446583	2.575406358	-0.04056	0.967644399	NA	brown	-0.080233326	0.317843859	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT5G66320.1	GATA5	GATA transcription factor 5	GATA transcription factor
Sapur.004G062000.3	0.048441709	-0.08146922	2.019016724	-0.04035	0.967813344	NA	brown	-0.09005458	0.262013698		AT1G23890.1		NHL domain-containing protein	NHL domain protein, putative
Sapur.016G137200.1	0.032245877	-0.09438518	2.340027568	-0.04034	0.967825993	NA	brown	-0.18291329	0.021850183	GO:0017025,GO:0008270,GO:0006355,GO:0006352,GO:0006384,GO:0000126	AT3G09360.1		Cyclin/Brf1-like TBP-binding protein	transcription factor, putative
Sapur.008G005700.3	0.031167864	-0.116705819	2.904823918	-0.04018	0.967952369	NA	brown	-0.156367673	0.050503831		AT1G16880.1		uridylyltransferase-related	DS12 from 2D-PAGE of leaf protein, putative
Sapur.013G044800.1	0.028530913	-0.094379897	2.372521763	-0.03978	0.968268191	NA	brown	-0.183803844	0.021204707	GO:0034968,GO:0018024,GO:0008270,GO:0005634,GO:0005515	AT3G04380.2	SDG31,SUVR4	SET-domain containing protein lysine methyltransferase family protein	histone-lysine N-methyltransferase SUVR4, putative
Sapur.004G160100.2	0.028075487	-0.094379212	2.376841188	-0.03971	0.968326057	NA	brown	-0.183659699	0.021308054		AT2G28305.1	ATLOG1,LOG1	Putative lysine decarboxylase family protein	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1
Sapur.013G137800.2	0.04754522	0.087396877	2.245296795	0.038924	0.968950646	NA	brown	0.025615566	0.75014396		AT1G16870.1		mitochondrial 28S ribosomal protein S29-related	28S ribosomal protein S29
Sapur.016G080100.1	0.048565699	-0.098063102	2.537326538	-0.03865	0.969170873	NA	brown	-0.065882186	0.41233246		AT5G02790.1	GSTL3	Glutathione S-transferase family protein	NA
Sapur.005G070500.1	0.04670293	-0.098061533	2.549174474	-0.03847	0.96931458	NA	brown	-0.070357031	0.381240962	GO:0016021,GO:0006481,GO:0004671	AT5G08335.1	ATICMTB,ATSTE14B,ICMTB	Isoprenylcysteine carboxyl methyltransferase (ICMT) family	S-isoprenylcysteine O-methyltransferase
Sapur.T114100.1	0.022494034	0.103704107	2.774616817	0.037376	0.9701852	NA	brown	0.011471894	0.886607323		AT4G34990.1	AtMYB32,MYB32	myb domain protein 32	NA
Sapur.005G176500.6	0.001005719	0.108126894	2.904823918	0.037223	0.970307026	NA	brown	-0.163772258	0.040411148	GO:0006629	AT2G42450.1		alpha/beta-Hydrolases superfamily protein	NA
Sapur.008G105000.2	0.001005719	0.108126894	2.904823918	0.037223	0.970307026	NA	brown	0.008772239	0.913171092		AT1G14990.2			transmembrane protein, putative
Sapur.016G075100.2	0.001005719	0.108126894	2.904823918	0.037223	0.970307026	NA	brown	-0.057035529	0.478001764		AT3G55140.1		Pectin lyase-like superfamily protein	pectate lyase
Sapur.007G130400.1	0.035479215	-0.096198741	2.626187088	-0.03663	0.970779565	NA	brown	-0.101944723	0.203917658		AT2G44100.1	AT-GDI1,ATGDI1,GDI1	guanosine nucleotide diphosphate dissociation inhibitor 1	Rab GDP dissociation inhibitor
Sapur.010G077600.2	0.035170928	-0.096198409	2.629030159	-0.03659	0.970811251	NA	brown	-0.103552652	0.196837198	GO:0005634	AT1G70210.1	ATCYCD1;1,CYCD1;1	CYCLIN D1;1	cyclin-D1-1 protein
Sapur.011G054900.6	0.019145878	0.103704869	2.834364291	0.036588	0.970813189	NA	brown	-0.114798493	0.152239988	GO:0016020	AT5G46150.1		LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein	LEM3/CDC50 family protein
Sapur.001G028000.2	0.034680147	-0.096197874	2.633620018	-0.03653	0.97086276	NA	brown	-0.103521761	0.196971521	GO:0006355,GO:0005739,GO:0003690	AT5G07900.1		Mitochondrial transcription termination factor family protein	mTERF protein
Sapur.002G164500.3	0.009590219	0.105911962	2.904822821	0.036461	0.97091499	NA	brown	-0.008419291	0.91665175	GO:0006396,GO:0004526	AT2G47300.2		ribonuclease Ps	ribonuclease P/MRP protein subunit POP1, putative
Sapur.006G095500.1	0.010584001	0.105911962	2.904822821	0.036461	0.97091499	NA	brown	0.005081244	0.949639547	GO:0046872,GO:0005634,GO:0003723	AT5G42820.1	ATU2AF35B,U2AF35B	Zinc finger C-x8-C-x5-C-x3-H type family protein	splicing factor U2af subunit
Sapur.004G135800.1	0.012569815	0.105911962	2.904822821	0.036461	0.97091499	NA	brown	0.022416021	0.780503861		AT5G39130.1		RmlC-like cupins superfamily protein	rhicadhesin receptor, putative
Sapur.003G023600.2	0.01343399	0.105911962	2.904822821	0.036461	0.97091499	NA	brown	0.027541209	0.732051634	GO:0006334,GO:0005634	AT2G19480.3	NAP1;2,NFA02,NFA2	nucleosome assembly protein 1;2	NA
Sapur.002G173400.1	0.030776856	-0.094341169	2.665102049	-0.0354	0.971761815	NA	brown	-0.162061789	0.04257793		AT1G05000.1		Phosphotyrosine protein phosphatases superfamily protein	tyrosine phosphatase family protein, putative
Sapur.004G138800.3	0.028199644	-0.094337976	2.694786846	-0.03501	0.972073694	NA	brown	-0.159062696	0.046611854	GO:0009378,GO:0006310,GO:0006281	AT1G27600.1	ATSKD1,SKD1,VPS4	AAA-type ATPase family protein	vacuolar sorting protein 4b
Sapur.008G005700.4	0.025615205	-0.094334519	2.728164172	-0.03458	0.972416227	NA	brown	-0.091991429	0.251849008		AT1G16880.1		uridylyltransferase-related	DS12 from 2D-PAGE of leaf protein, putative
Sapur.15WG106900.2	0.032067966	0.080369697	2.346707021	0.034248	0.972679501	NA	brown	-0.141657552	0.076774537	GO:0016020,GO:0006075,GO:0003843,GO:0000148	AT2G36850.1	ATGSL08,ATGSL8,CHOR,GSL	glucan synthase-like 8	1%2C3-beta-glucan synthase
Sapur.016G056100.2	0.049559367	-0.062604756	1.837168315	-0.03408	0.972815935	NA	brown	-0.076509582	0.340894959	GO:0045454,GO:0015035,GO:0006662	AT5G06690.2	WCRKC1	WCRKC thioredoxin 1	thioredoxin-like protein
Sapur.016G228600.1	0.050155235	-0.060752514	1.826800674	-0.03326	0.973470253	NA	brown	-0.101608867	0.205419477	GO:0005515	AT1G30440.1		Phototropic-responsive NPH3 family protein	phototropic-responsive NPH3 family protein
Sapur.006G153400.1	0.033418836	-0.096170985	2.904823276	-0.03311	0.973588986	NA	brown	-0.074061582	0.356611991	GO:0000160	AT2G25180.1	ARR12,RR12	response regulator 12	type-B response regulator
Sapur.15WG027300.1	0.034156924	-0.096170985	2.904823276	-0.03311	0.973588986	NA	brown	-0.072035438	0.369956897	GO:0008270,GO:0006355,GO:0005634,GO:0003700	AT1G10170.1	ATNFXL1,NFXL1	NF-X-like 1	NA
Sapur.013G088100.2	0.046440166	-0.060747864	1.839346773	-0.03303	0.973653161	NA	brown	-0.113329359	0.157590298		AT1G65230.1		Uncharacterized conserved protein (DUF2358)	thioredoxin F, putative
Sapur.018G091900.1	0.02521435	0.089320755	2.731109885	0.032705	0.973909893	NA	brown	0.025822957	0.748188673	GO:0031515,GO:0030488,GO:0016429	AT5G14600.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NA
Sapur.002G101600.4	0.025572424	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.081608864	0.309590942		AT1G45688.1			late embryogenesis abundant protein
Sapur.002G193200.3	0.02501269	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.123045121	0.124717357		AT3G07370.1	ATCHIP,CHIP	carboxyl terminus of HSC70-interacting protein	NA
Sapur.002G201500.2	0.026365264	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.101396337	0.206373933		AT1G04030.1			hypothetical protein
Sapur.003G039600.5	0.026643677	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.102193443	0.20281059	GO:0016491	AT3G14130.1		Aldolase-type TIM barrel family protein	peroxisomal (S)-2-hydroxy-acid oxidase
Sapur.004G121500.1	0.025411094	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.099240611	0.216235759	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT5G66320.2	GATA5	GATA transcription factor 5	GATA transcription factor
Sapur.004G135500.3	0.025572424	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.081608864	0.309590942	GO:0005089	AT4G38430.1	ATROPGEF1,ROPGEF1	rho guanyl-nucleotide exchange factor 1	Rop guanine nucleotide exchange factor, putative
Sapur.005G093300.1	0.026053335	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.125744812	0.116596087	GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT3G51150.2		ATP binding microtubule motor family protein	kinesin motor domain protein
Sapur.005G163400.1	0.02769774	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.129073551	0.107155794	GO:0046983	AT3G59060.4	PIF5,PIL6	phytochrome interacting factor 3-like 6	helix loop helix DNA-binding domain protein
Sapur.006G139400.2	0.026602861	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.102149732	0.203004834	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G07210.1		Ribosomal protein S18	structural constituent of ribosome protein, putative
Sapur.008G083200.4	0.028123362	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.129822626	0.105116425	GO:0006355,GO:0006468,GO:0004672	AT3G06620.1		PAS domain-containing protein tyrosine kinase family protein	tyrosine kinase domain protein
Sapur.009G042300.2	0.025223114	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.098435559	0.220003449	GO:0008168,GO:0008152	AT3G60910.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase domain protein
Sapur.010G059900.1	0.025572424	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.081608864	0.309590942		AT2G32150.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	phosphatase, putative
Sapur.012G107800.2	0.025411094	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.099240611	0.216235759	GO:0006378,GO:0005849,GO:0003729	AT4G25550.1		Cleavage/polyadenylation specificity factor, 25kDa subunit	cleavage and polyadenylation specificity factor 5
Sapur.013G011400.1	0.025572424	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.081608864	0.309590942		AT3G05625.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR repeat protein
Sapur.016G048200.1	0.02555025	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.099501084	0.215026636		AT3G20898.1			hypothetical protein
Sapur.016G073900.1	0.026348676	-0.094318339	2.904824395	-0.03247	0.974097599	NA	brown	-0.101608081	0.205423001		AT2G37400.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR protein
Sapur.15WG140200.2	0.022812093	0.089324389	2.766924068	0.032283	0.97424643	NA	brown	-0.004716117	0.953254076	GO:0008017,GO:0000910,GO:0000226	AT5G51600.1	ATMAP65-3,MAP65-3,PLE	Microtubule associated protein (MAP65/ASE1) family protein	protein regulator of cytokinesis protein
Sapur.005G086900.2	0.022175285	0.089325403	2.777206387	0.032164	0.974341456	NA	brown	0.034593505	0.667108081		AT1G63855.3		Putative methyltransferase family protein	methyltransferase, putative
Sapur.011G115100.1	0.021216378	0.089326976	2.79340942	0.031978	0.974489787	NA	brown	-0.027051488	0.736639286	GO:0006508,GO:0004252	AT4G20430.1		Subtilase family protein	subtilisin-like protease
Sapur.017G057600.2	0.020795419	0.089327686	2.800815747	0.031893	0.97455702	NA	brown	-0.009608869	0.904927233		AT3G27100.1			enhancer of yellow 2 transcription factor-like protein
Sapur.T128300.1	0.020792694	0.08932769	2.800864304	0.031893	0.974557459	NA	brown	0.024619562	0.759556282					NA
Sapur.019G005400.1	0.020630512	0.089327967	2.803768635	0.03186	0.974583727	NA	brown	-0.027941972	0.728304377					NA
Sapur.014G082600.2	0.019009049	0.089330849	2.834681889	0.031514	0.974859997	NA	brown	-0.007597811	0.924758925	GO:0019205,GO:0006139,GO:0005524	AT5G26667.2	PYR6	P-loop containing nucleoside triphosphate hydrolases superfamily protein	adenylate kinase
Sapur.014G031100.5	0.022409295	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.114846535	0.152067369		AT1G75060.1			histone deacetylase complex subunit SAP30 Sin3-binding protein
Sapur.011G052400.2	0.019548011	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.225162003	0.004579305	GO:0046983,GO:0003677,GO:0006355,GO:0005634,GO:0003700	AT4G18960.1	AG	K-box region and MADS-box transcription factor family protein	MADS-box transcription factor
Sapur.15WG006600.3	0.017729487	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.156176775	0.050789448	GO:0016021,GO:0015689,GO:0015098	AT4G27720.1		Major facilitator superfamily protein	MFS transporter
Sapur.017G118700.1	0.013642903	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.026340003	0.74332094	GO:0003677,GO:0046983	AT3G42170.1		BED zinc finger ;hAT family dimerisation domain	BED zinc finger protein
Sapur.002G165100.1	0.012266991	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.028095007	0.726875137					NA
Sapur.003G057800.1	0.013095454	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.022181399	0.782743872		AT2G35330.1		RING/U-box superfamily protein	synaptonemal complex protein, putative
Sapur.005G117800.2	0.013095454	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.022181399	0.782743872		AT2G34320.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	ribonuclease HI
Sapur.016G001100.1	0.012903815	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.021942346	0.785028019		AT3G13300.2	VCS	Transducin/WD40 repeat-like superfamily protein	peptidase S26A, signal peptidase I; WD40-like protein, putative
Sapur.001G175100.2	0.012714087	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.081608864	0.309590942		AT1G60995.1			S3 self-incompatibility locus-linked pollen 3.15 protein
Sapur.017G041000.3	0.012523554	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.020171654	0.802002862	GO:0006508,GO:0004197	AT1G02170.1	AMC1,ATMC1,ATMCPB1,LO	metacaspase 1	ICE-like protease (caspase) p20 domain protein
Sapur.016G218200.7	0.012428271	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.018369268	0.819377074					hypothetical protein
Sapur.007G130100.1	0.011774057	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.014727107	0.854746663		AT2G44060.1		Late embryogenesis abundant protein, group 2	late-embryogenesis abundant protein
Sapur.018G049400.1	0.011568611	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.011149897	0.889769642		AT5G20120.1			transmembrane protein, putative
Sapur.005G200000.2	0.011564096	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.012546957	0.876062381		AT1G42430.1			hypothetical protein
Sapur.007G021800.2	0.011229095	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.010180568	0.899299686		AT2G18360.1		alpha/beta-Hydrolases superfamily protein	epoxide hydrolase
Sapur.010G180800.3	0.011218833	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.006954198	0.931116185	GO:0005525	AT3G54840.1	ARA-6,ARA6,ATRAB5C,ATRA	Ras-related small GTP-binding family protein	small GTPase family Rab protein
Sapur.004G127200.3	0.011203257	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.008772239	0.913171092		AT3G19860.2	bHLH121	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	DNA-binding protein, putative
Sapur.007G007600.4	0.011710772	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.081608864	0.309590942	GO:0005975,GO:0004553,GO:0051015,GO:0007015				NA
Sapur.005G071000.2	0.011081971	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.007969154	0.921093135		AT1G05460.1	SDE3	P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.002G013900.3	0.010903724	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.006556545	0.935046189	GO:0055085,GO:0042626,GO:0016021,GO:0006810,GO:0005524,GO:0016887	AT1G27940.1	PGP13	P-glycoprotein 13	ABC transporter family B protein, group MDR/PGP protein PpABCB18 protein
Sapur.013G138200.1	0.010773633	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.00331438	0.967138596	GO:0009982,GO:0009451,GO:0003723,GO:0001522	AT2G30320.1		Pseudouridine synthase family protein	tRNA pseudouridine synthase, putative
Sapur.016G179000.6	0.010751738	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.003318844	0.967094359		AT4G34260.1	FUC95A	1,2-alpha-L-fucosidases	NA
Sapur.T145500.1	0.011608632	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.081608864	0.309590942		AT1G55000.3		peptidoglycan-binding LysM domain-containing protein	NA
Sapur.001G090700.2	0.010089121	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.000231945	0.99769967	GO:0055085	AT1G12600.1		UDP-N-acetylglucosamine (UAA) transporter family	adenosine 3'-phospho 5'-phosphosulfate transporter 2
Sapur.010G053200.3	0.010089121	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.000231945	0.99769967		AT1G67600.1		Acid phosphatase/vanadium-dependent haloperoxidase-related protein	acid phosphatase/vanadium-dependent haloperoxidase-like protein
Sapur.009G106700.4	0.009934049	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.002730798	0.972922257	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT4G35000.1	APX3	ascorbate peroxidase 3	L-ascorbate peroxidase 3, peroxisomal protein
Sapur.006G157100.2	0.009843971	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.004345567	0.956923261	GO:0016787	AT2G42070.1	ATNUDT23,ATNUDX23,NUI	nudix hydrolase homolog 23	nudix hydrolase
Sapur.016G140400.1	0.009843971	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	0.055370559	0.49096448		AT2G29670.1		Tetratricopeptide repeat (TPR)-like superfamily protein	plant/F22G5-32 protein, putative
Sapur.001G092800.7	0.009840551	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.004238737	0.957981268		AT4G11970.2		YTH family protein	splicing factor YT521-B, putative
Sapur.T128800.1	0.009578282	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.00697611	0.930899682					NA
Sapur.016G274400.2	0.012307605	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.081608864	0.309590942	GO:0050662,GO:0003824	AT4G27250.1		NAD(P)-binding Rossmann-fold superfamily protein	oxidoreductase, short chain dehydrogenase/reductase family protein
Sapur.008G047900.3	0.009552687	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.0065031	0.93557451		AT5G05987.1	PRA1.A2	prenylated RAB acceptor 1.A2	prenylated rab acceptor family protein
Sapur.016G119700.2	0.009331617	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.22916433	0.003889383	GO:0005975,GO:0004553	AT2G44480.1	BGLU17	beta glucosidase 17	glycoside hydrolase family 1 protein
Sapur.014G137800.2	0.009152712	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.014073346	0.861128318	GO:0005515	AT3G07670.1		Rubisco methyltransferase family protein	ribulose-1%2C5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I, putative
Sapur.014G117200.2	0.00892009	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.015859544	0.84371491		AT3G19340.1		Protein of unknown function (DUF3754)	NA
Sapur.018G039800.3	0.00892009	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.015859544	0.84371491	GO:0055085,GO:0046873,GO:0030001,GO:0016020	AT1G10970.1	ATZIP4,ZIP4	zinc transporter 4 precursor	ZIP-like zinc transporter
Sapur.017G100300.1	0.009976959	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.027403511	0.733340627		AT1G60640.2			C2H2 type zf-met: zinc-finger protein
Sapur.T140300.2	0.008911822	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.016085734	0.841515014	GO:0009086,GO:0008270,GO:0003871,GO:0008652	AT5G17920.2	ATCIMS,ATMETS,ATMS1	Cobalamin-independent synthase family protein	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase
Sapur.005G021600.2	0.008895934	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.016977253	0.832856309		AT1G09020.1	ATSNF4,SNF4	homolog of yeast sucrose nonfermenting 4	5'-AMP-activated kinase subunit gamma
Sapur.002G069000.1	0.008889915	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.016867407	0.833922108		AT1G21930.1			transmembrane protein, putative
Sapur.005G034100.2	0.008691927	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.019082061	0.812495058	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT3G05030.1	ATNHX2,NHX2	sodium hydrogen exchanger 2	sodium/hydrogen exchanger
Sapur.001G027600.1	0.00863665	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.021570425	0.788585369	GO:0042546,GO:0016020,GO:0008107	AT2G03220.1	ATFT1,ATFUT1,FT1,MUR2	fucosyltransferase 1	galactoside 2-alpha-L-fucosyltransferase, putative
Sapur.002G023700.3	0.00863665	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.114024224	0.155042406	GO:0016021	AT1G35180.1		TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain protein, putative
Sapur.007G037500.3	0.0085845	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.022011075	0.784371127	GO:0005515,GO:0006457,GO:0003755,GO:0000413	AT2G15790.1	CYP40,SQN	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase	cyclophilin-type peptidylprolyl cis-trans isomerase family protein
Sapur.019G029600.1	0.0085845	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.022011075	0.784371127	GO:0016787,GO:0005524,GO:0003677	AT1G08600.4	ATRX,CHR20	P-loop containing nucleoside triphosphate hydrolases superfamily protein	chromatin remodeling complex subunit
Sapur.011G044600.2	0.008452824	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.023056553	0.774397724		AT1G29050.1	TBL38	TRICHOME BIREFRINGENCE-LIKE 38	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.013G012800.2	0.008760264	0.091189602	2.904823276	0.031392	0.97495654	NA	brown	-0.03766135	0.639576796	GO:0003723	AT1G09150.1		pseudouridine synthase and archaeosine transglycosylase (PUA) domain-containing protein	pseudouridine synthase and archaeosine transglycosylase domain protein
Sapur.T050100.7	0.009300923	0.091189601	2.904823276	0.031392	0.97495654	NA	brown	-0.040918931	0.610872238		AT3G24870.1		Helicase/SANT-associated, DNA binding protein	helicase/SANT-associated, DNA-binding protein, putative
Sapur.012G096800.2	0.007846412	0.091189601	2.904823276	0.031392	0.97495654	NA	brown	-0.033275808	0.679073724	GO:0005992,GO:0003824	AT5G51460.2	ATTPPA	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	trehalose-phosphate phosphatase
Sapur.008G165600.1	0.018380274	0.089332011	2.84746766	0.031372	0.974972519	NA	brown	-0.067382325	0.401747272	GO:0005515	AT5G18590.1		Galactose oxidase/kelch repeat superfamily protein	acyl-CoA-binding domain protein
Sapur.016G142000.1	0.01793132	0.089332861	2.856940498	0.031269	0.975055239	NA	brown	-0.019669504	0.806834033		AT5G01450.1		RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.004G104100.3	0.041473548	0.064011049	2.051161124	0.031207	0.975104277	NA	brown	-0.003754575	0.962777104	GO:0055114,GO:0016702	AT5G39890.1		Protein of unknown function (DUF1637)	2-aminoethanethiol dioxygenase, putative
Sapur.008G148600.1	0.027669758	0.06621559	2.12926103	0.031098	0.975191448	NA	brown	-0.059275462	0.460859069		AT5G14420.4	RGLG2	RING domain ligase2	E3 ubiquitin-protein ligase RGLG2
Sapur.017G019500.4	0.049591092	-0.062544835	2.022844657	-0.03092	0.97533394	NA	brown	-0.08130332	0.311411914	GO:0005524,GO:0005515	AT1G05910.1		cell division cycle protein 48-related / CDC48-related	bromodomain protein with A AAA ATPase domain protein
Sapur.019G060200.4	0.023073428	0.089337012	2.904822183	0.030755	0.975465146	NA	brown	0.011851962	0.882876988	GO:0071805,GO:0016020,GO:0015079	AT2G40540.2	ATKT2,ATKUP2,KT2,KUP2,SH	potassium transporter 2	potassium transporter 2
Sapur.016G000400.1	0.021527804	0.089337012	2.904822183	0.030755	0.975465146	NA	brown	0.006275982	0.937819946					transmembrane protein, putative
Sapur.016G167400.2	0.019086657	0.089337012	2.904822183	0.030755	0.975465146	NA	brown	-0.007703152	0.923718866		AT2G02560.2	ATCAND1,CAND1,ETA2,HVE	cullin-associated and neddylation dissociated	NA
Sapur.007G079800.1	0.019065983	0.089337012	2.904822183	0.030755	0.975465146	NA	brown	-0.00933215	0.90765285					hypothetical protein
Sapur.15WG042900.1	0.018122954	0.089337012	2.904822183	0.030755	0.975465146	NA	brown	-0.016549074	0.83701248		AT3G18210.2		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.003G095200.2	0.038312349	0.056936921	1.875454255	0.030359	0.975780741	NA	brown	-0.061494039	0.44422077		AT5G41470.1		Nuclear transport factor 2 (NTF2) family protein	NA
Sapur.005G000200.1	0.047416505	-0.060689683	2.023206289	-0.03	0.976069618	NA	brown	-0.10119057	0.207301049		AT3G05940.1		Protein of unknown function (DUF300)	organic solute transporter ostalpha protein
Sapur.006G218500.3	0.042424674	-0.046242581	1.561804135	-0.02961	0.976379336	NA	brown	-0.059348307	0.460307346		AT4G31850.1	PGR3	proton gradient regulation 3	PPR containing plant protein
Sapur.011G091100.1	0.007902174	0.085433515	2.904823455	0.029411	0.976536868	NA	brown	-0.050985013	0.525984256	GO:0005515,GO:0016459,GO:0005524,GO:0003774	AT5G54280.2	ATM2,ATM4,ATMYOS1	myosin 2	NA
Sapur.018G068000.1	0.008534419	0.085433515	2.904823455	0.029411	0.976536868	NA	brown	-0.053462954	0.506043093		AT4G25845.1			DUF688 family protein
Sapur.017G039600.3	0.047469489	0.047888604	1.68179538	0.028475	0.977283553	NA	brown	-0.122087571	0.12770056		AT3G21110.2	ATPURC,PUR7,PURC	purin 7	phosphoribosylaminoimidazole-succinocarboxamide synthase
Sapur.018G042100.1	0.036226584	-0.058821913	2.072142458	-0.02839	0.977353491	NA	brown	-0.124830669	0.119298652	GO:0009626	AT1G23070.1		Protein of unknown function (DUF300)	organic solute transporter ostalpha protein
Sapur.006G101700.2	0.031597734	0.06622319	2.347961819	0.028205	0.977499014	NA	brown	-0.024652941	0.759240267	GO:0016567,GO:0004842	AT3G53690.1		RING/U-box superfamily protein	zinc finger protein, putative
Sapur.016G172300.3	0.025315327	0.066224832	2.40787767	0.027503	0.978058225	NA	brown	-0.073781691	0.35843736	GO:0008144,GO:0016773,GO:0005515	AT1G50030.1	TOR	target of rapamycin	Serine/Threonine-kinase TOR
Sapur.016G062400.2	0.049586285	-0.060638918	2.241799301	-0.02705	0.978420478	NA	brown	-0.067807227	0.398778705	GO:0006760,GO:0004150	AT3G11750.1	FOLB1	Dihydroneopterin aldolase	dihydroneopterin aldolase
Sapur.010G014900.1	0.049532247	-0.060638499	2.243926432	-0.02702	0.978441078	NA	brown	-0.07952322	0.322159701		AT5G18800.2		Cox19-like CHCH family protein	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex protein
Sapur.016G035000.1	0.047813394	-0.060637469	2.24918703	-0.02696	0.978491855	NA	brown	-0.120515451	0.132717222					hypothetical protein
Sapur.010G114000.3	0.043096889	0.049816877	1.84909365	0.026941	0.9785066	NA	brown	-0.081905797	0.307827974					hypothetical protein
Sapur.010G114000.4	0.037654961	0.049825016	1.871734003	0.02662	0.978763053	NA	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.005G053800.1	0.035942777	-0.058771261	2.314622803	-0.02539	0.979742858	NA	brown	-0.106425877	0.184632049		AT4G08330.1			hypothetical protein
Sapur.018G048700.4	0.026871348	0.068437766	2.708832111	0.025265	0.979843849	NA	brown	-0.115782905	0.148732318		AT5G56750.1	NDL1	N-MYC downregulated-like 1	pollen specific protein SF21, putative
Sapur.002G147500.3	0.044417266	-0.046216464	1.850675353	-0.02497	0.980076694	NA	brown	-0.077142294	0.336905284	GO:0016853,GO:0005975	AT3G61610.1		Galactose mutarotase-like superfamily protein	aldose 1-epimerase
Sapur.009G064900.2	0.029968981	-0.05876322	2.36203947	-0.02488	0.980152139	NA	brown	-0.081608864	0.309590942	GO:0008152,GO:0003824	AT1G50110.1		D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein	branched-chain-amino-acid aminotransferase
Sapur.009G108300.2	0.04087632	0.049879648	2.050117001	0.02433	0.980589266	NA	brown	-0.022014613	0.784337319		AT2G16920.1	PFU2,UBC23	ubiquitin-conjugating enzyme 23	ubiquitin-conjugating enzyme E2, putative
Sapur.002G179800.2	0.005958874	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.064087446	0.425209107	GO:0006886,GO:0008536	AT2G31660.1	SAD2,URM9	ARM repeat superfamily protein	importin-7 protein, putative
Sapur.003G041300.1	0.006120203	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.063922497	0.426404114	GO:0044237	AT1G53880.1		Eukaryotic translation initiation factor 2B (eIF-2B) family protein	translation initiation factor eIF-2B subunit alpha
Sapur.006G023200.1	0.007079334	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.067295305	0.402356848	GO:0005515	AT1G79590.2	ATSYP52,SYP52	syntaxin of plants 52	syntaxin-52 protein
Sapur.008G130800.2	0.006120203	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.110170366	0.16957068	GO:0006355,GO:0005634	AT5G43700.1	ATAUX2-11,IAA4	AUX/IAA transcriptional regulator family protein	indole-3-acetic acid inducible protein
Sapur.013G139600.1	0.007205671	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.067256072	0.402631859		AT2G30370.1	CHAL,EPFL6	allergen-related	epidermal patterning factor-like protein, putative
Sapur.016G127500.2	0.006942776	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.067037927	0.404162998	GO:0006468,GO:0005524,GO:0004672	AT1G07870.2		Protein kinase superfamily protein	Serine/Threonine kinase
Sapur.016G283000.1	0.007079334	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.067295305	0.402356848	GO:0005515	AT2G33060.1	AtRLP27,RLP27	receptor like protein 27	NA
Sapur.018G037600.2	0.006913044	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.066603996	0.407218976	GO:0005515	AT4G33210.1	SLOMO	F-box family protein	F-box/LRR protein
Sapur.15WG149900.1	0.005929524	0.070654775	2.904823918	0.024323	0.980594763	NA	brown	-0.063790949	0.427358531		AT5G23760.1		Copper transport protein family	heavy-metal-associated domain protein, putative
Sapur.004G064700.3	0.048256067	-0.060591237	2.534580357	-0.02391	0.980927727	NA	brown	-0.043999629	0.584259702		AT1G23170.2		Protein of unknown function DUF2359, transmembrane	DUF2359 family protein
Sapur.014G113300.2	0.034079916	0.049889276	2.087464023	0.023899	0.9809328	NA	brown	-0.037506934	0.64095126	GO:0016021,GO:0015693,GO:0015095	AT3G26670.1		Protein of unknown function (DUF803)	magnesium transporter NIPA protein
Sapur.018G063000.1	0.033223875	0.049890606	2.092792715	0.023839	0.980980833	NA	brown	-0.048149202	0.54928348	GO:0005515	AT5G19680.1		Leucine-rich repeat (LRR) family protein	protein phosphatase 1 regulatory subunit
Sapur.009G055200.2	0.016021615	0.06843981	2.900878619	0.023593	0.981177426	NA	brown	-0.064989651	0.418707252		AT5G12330.3	LRP1	Lateral root primordium (LRP) protein-related	short internode-related sequence protein, putative
Sapur.004G024500.4	0.015117739	0.068439844	2.904822821	0.023561	0.98120297	NA	brown	-0.03850726	0.632069124	GO:0006508,GO:0004185	AT1G11080.2	scpl31	serine carboxypeptidase-like 31	serine carboxypeptidase-like protein
Sapur.005G003400.2	0.015347223	0.068439844	2.904822821	0.023561	0.98120297	NA	brown	-0.037686308	0.639354756		AT4G10710.1	SPT16	global transcription factor C	global transcription factor group protein
Sapur.013G011500.3	0.040465863	-0.060584265	2.588559296	-0.0234	0.981327514	NA	brown	-0.063403266	0.430178433	GO:0003824	AT3G12070.1	AtRGTB2,RGTB2	RAB geranylgeranyl transferase beta subunit 2	RAB geranylgeranyl transferase type II beta subunit, putative
Sapur.009G116800.3	0.039392263	-0.060583206	2.597081805	-0.02333	0.981389103	NA	brown	-0.075419299	0.347839913		AT5G40270.1		HD domain-containing metal-dependent phosphohydrolase family protein	metal-dependent phosphohydrolase HD domain protein
Sapur.15WG027600.2	0.047454423	-0.046206049	2.028832382	-0.02277	0.981829989	NA	brown	-0.064127011	0.424922758	GO:0006807,GO:0004356	AT5G37600.1	ATGLN1:1,ATGSR1,GLN1:1,(	glutamine synthase clone R1	glutamine synthetase
Sapur.016G216100.1	0.042924904	-0.046205075	2.048663719	-0.02255	0.982006227	NA	brown	-0.061228834	0.446191638		AT3G27460.1		SGF29 tudor-like domain	SGF29 tudor-like domain protein
Sapur.013G143500.3	0.036023015	-0.058727595	2.617173632	-0.02244	0.982097516	NA	brown	-0.101938181	0.203946835		AT5G10860.1		Cystathionine beta-synthase (CBS) family protein	named after animal CBS
Sapur.005G206700.2	0.03206466	-0.058723339	2.65400961	-0.02213	0.98234723	NA	brown	-0.096176977	0.230822061	GO:0006096,GO:0003872	AT1G20950.1		Phosphofructokinase family protein	pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha subunit
Sapur.016G040700.1	0.03157691	-0.058722616	2.660429745	-0.02207	0.982390039	NA	brown	-0.091635103	0.253698284	GO:0055114,GO:0050660,GO:0016491,GO:0019139,GO:0009690	AT2G41510.1	ATCKX1,CKX1	cytokinin oxidase/dehydrogenase 1	cytokinin oxidase/dehydrogenase
Sapur.002G090600.2	0.030381326	-0.058721177	2.673369657	-0.02197	0.982475692	NA	brown	-0.106007023	0.186375913		AT5G49630.1	AAP6	amino acid permease 6	amino acid transporter
Sapur.003G041600.2	0.029788165	0.051799612	2.361019229	0.02194	0.982496206	NA	brown	-0.05016977	0.532630777		AT3G14280.1			hypothetical protein
Sapur.016G216700.2	0.02908762	0.051800663	2.367352084	0.021881	0.982542668	NA	brown	-0.041708601	0.604000061	GO:0016020,GO:0006487,GO:0003830	AT3G27540.1		beta-1,4-N-acetylglucosaminyltransferase family protein	beta-1%2C4-N-acetylglucosaminyltransferase family protein
Sapur.15WG076800.1	0.038126759	0.049935716	2.303605887	0.021677	0.982705455	NA	brown	-0.010882319	0.892398849		AT5G08050.1		Protein of unknown function (DUF1118)	plant/F13G24-250 protein, putative
Sapur.016G250000.2	0.024691834	0.051807841	2.412097152	0.021478	0.982864082	NA	brown	-0.033841108	0.673930363	GO:0043565	AT3G58680.1	ATMBF1B,MBF1B	multiprotein bridging factor 1B	multiprotein bridging factor 1
Sapur.010G122000.7	0.023605051	0.051809767	2.424567327	0.021369	0.98295157	NA	brown	-0.035600283	0.658021779		AT2G03510.1		SPFH/Band 7/PHB domain-containing membrane-associated protein family	SPFH domain/band 7 family protein
Sapur.014G011500.3	0.028900093	-0.056866958	2.683785726	-0.02119	0.983094823	NA	brown	-0.159205512	0.046412785		AT5G01450.1		RING/U-box superfamily protein	zinc finger, RING-type protein
Sapur.005G053900.4	0.035068845	-0.043994226	2.081505582	-0.02114	0.98313735	NA	brown	-0.130505748	0.103283325		AT5G08720.1			cyclase/dehydrase
Sapur.010G195100.1	0.02652052	-0.056863852	2.713404874	-0.02096	0.983280244	NA	brown	-0.163092255	0.041261209	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G04800.1		Ribosomal S17 family protein	40S ribosomal protein S17
Sapur.010G104200.1	0.039016576	-0.060551457	2.904822183	-0.02085	0.98336918	NA	brown	-0.058389069	0.467601816	GO:0016780,GO:0016020,GO:0008654	AT1G13560.1	AAPT1,ATAAPT1	aminoalcoholphosphotransferase 1	aminoalcoholphosphotransferase
Sapur.006G108800.2	0.023627395	-0.056859745	2.754275287	-0.02064	0.9835295	NA	brown	-0.163989577	0.040142602	GO:0006468,GO:0004672	AT2G37050.3		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.016G152100.4	0.020580461	-0.056854948	2.804673031	-0.02027	0.983826785	NA	brown	-0.161000866	0.043970152	GO:0006265,GO:0005524,GO:0003918,GO:0003677	AT3G23890.2	ATTOPII,TOPII	topoisomerase II	DNA topoisomerase
Sapur.007G117200.2	0.020212705	-0.056854331	2.811387081	-0.02022	0.98386558	NA	brown	-0.161507534	0.043300589		AT3G20320.1	TGD2	trigalactosyldiacylglycerol2	ABC-type transport system protein
Sapur.001G069000.5	0.03036492	-0.05869868	2.904823276	-0.02021	0.983877941	NA	brown	-0.085213816	0.288633027		AT4G27745.1		Yippee family putative zinc-binding protein	Fad NAD-binding oxidoreductase, putative
Sapur.013G137400.3	0.030692568	-0.058698867	2.904823276	-0.02021	0.983877941	NA	brown	-0.063930187	0.426348364	GO:0043565,GO:0006355,GO:0003700	AT2G38470.1	ATWRKY33,WRKY33	WRKY DNA-binding protein 33	WRKY transcription factor
Sapur.001G054000.1	0.031046969	-0.058698867	2.904823276	-0.02021	0.983877941	NA	brown	-0.062870203	0.434073206		AT5G13390.1	NEF1	no exine formation 1	No exine formation protein
Sapur.011G007300.1	0.037707821	-0.058698867	2.904823276	-0.02021	0.983877941	NA	brown	-0.052463236	0.514040611		AT1G11925.1		Stigma-specific Stig1 family protein	NA
Sapur.004G004200.1	0.019855485	-0.056853722	2.8180575	-0.02017	0.983903937	NA	brown	-0.159692525	0.045739265		AT1G11925.1		Stigma-specific Stig1 family protein	Stig1 stigma-specific protein
Sapur.016G001800.2	0.019086281	-0.056852362	2.833150625	-0.02007	0.983990058	NA	brown	-0.161871712	0.042824614		AT2G01060.1		myb-like HTH transcriptional regulator family protein	Myb family transcription factor, putative
Sapur.009G027800.2	0.033304309	0.051838427	2.638851047	0.019644	0.984327111	NA	brown	-0.005558305	0.944918495	GO:0016787	AT2G39840.1	TOPP4	type one serine/threonine protein phosphatase 4	serine/threonine-protein phosphatase
Sapur.001G025800.5	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942	GO:0051726,GO:0005634,GO:0006357,GO:0007049,GO:0006351	AT3G12280.1	ATRBR1,RB,RB1,RBR,RBR1	retinoblastoma-related 1	retinoblastoma-related protein
Sapur.001G122400.4	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942	GO:0005515,GO:0006468,GO:0004672	AT1G14390.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.001G185900.1	0.021866437	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.10740469	0.180603527		AT1G10310.1		NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase
Sapur.003G016000.1	0.022228333	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.108271905	0.177088647		AT1G15290.1		Tetratricopeptide repeat (TPR)-like superfamily protein	eukaryotic translation initiation factor 3 subunit, putative
Sapur.003G078100.3	0.018358213	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.12931693	0.106489813		AT1G12250.2		Pentapeptide repeat-containing protein	thylakoid lumenal protein
Sapur.004G081000.1	0.025925866	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.13913716	0.082225669					NA
Sapur.004G088100.5	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.005G048000.1	0.021197687	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.135859954	0.089773714		AT4G33440.1		Pectin lyase-like superfamily protein	glycoside hydrolase family 28 protein
Sapur.005G129300.3	0.020354716	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.103718669	0.196116427	GO:0003676	AT5G64200.1	ATSC35,SC35	ortholog of human splicing factor SC35	arginine/serine-rich splicing factor SC30 transcript protein
Sapur.006G066000.3	0.023340259	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.110278816	0.169148484	GO:0046872	AT1G75340.1		Zinc finger C-x8-C-x5-C-x3-H type family protein	zinc finger CCCH domain protein, putative
Sapur.006G079000.2	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942		AT3G09090.1	DEX1	defective in exine formation protein (DEX1)	defective in exine formation protein
Sapur.007G038100.8	0.021128523	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.105598514	0.188088286		AT4G37080.2		Protein of unknown function, DUF547	ternary complex factor MIP1 leucine-zipper protein
Sapur.007G084400.3	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942		AT4G39870.1		TLD-domain containing nucleolar protein	TLD family protein
Sapur.008G067500.6	0.021759911	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.136678295	0.087839046		AT3G19895.1		RING/U-box superfamily protein	hypothetical protein
Sapur.008G069100.1	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942					transmembrane protein, putative
Sapur.008G112700.1	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942		AT1G68080.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase domain protein
Sapur.010G019100.2	0.026365436	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.112836444	0.159416651		AT1G13195.1		RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.010G112900.3	0.021174758	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.105977688	0.186498496	GO:0006457,GO:0003755,GO:0000413	AT3G66654.1		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	NA
Sapur.010G162800.2	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942		AT3G55390.1		Uncharacterised protein family (UPF0497)	CASP-like protein POPTRDRAFT-822486 protein
Sapur.011G042700.6	0.026222579	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.113128144	0.158333937	GO:0019478,GO:0016788,GO:0005737	AT4G18460.1		D-Tyr-tRNA(Tyr) deacylase family protein	D-tyrosyl-tRNA(Tyr) deacylase
Sapur.012G089200.2	0.022108255	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.107737513	0.179248553		AT5G45100.1		SBP (S-ribonuclease binding protein) family protein	baculoviral IAP repeat protein, putative
Sapur.013G035100.1	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942	GO:0008270,GO:0003676,GO:0004527	AT1G54490.1	AIN1,ATXRN4,EIN5,XRN4	exoribonuclease 4	5'-3' exoribonuclease
Sapur.013G079700.1	0.025400055	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.105012054	0.190566643					NA
Sapur.013G099900.2	0.021941903	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.107478127	0.180303909	GO:0043039,GO:0005737,GO:0005524,GO:0004812,GO:0000049	AT3G58140.1		phenylalanyl-tRNA synthetase class IIc family protein	phenylalanyl-tRNA synthetase
Sapur.014G070900.3	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942		AT2G46170.1		Reticulon family protein	24 kDa seed maturation protein, putative
Sapur.016G174200.1	0.024204528	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.139061109	0.082394863	GO:0005634	AT1G70210.1	ATCYCD1;1,CYCD1;1	CYCLIN D1;1	D-type cyclin
Sapur.016G307800.1	0.021508659	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.10678713	0.183137633		AT1G10010.1	AAP8,ATAAP8	amino acid permease 8	amino acid permease
Sapur.017G082300.2	0.023197451	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.110221558	0.169371291		AT3G62870.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	NA
Sapur.018G052500.2	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942	GO:0008270	AT1G11020.1		RING/FYVE/PHD zinc finger superfamily protein	C3HC4-type zinc finger protein, putative
Sapur.018G053600.1	0.024831371	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.140277395	0.079722247	GO:0016021	AT5G19930.1		Protein of unknown function DUF92, transmembrane	integral membrane family protein
Sapur.018G086900.2	0.023340259	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.110278816	0.169148484	GO:0006468,GO:0004672,GO:0005975,GO:0004553	AT4G19810.1		Glycosyl hydrolase family protein with chitinase insertion domain	tyrosine kinase family protein
Sapur.018G118200.1	0.021941903	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.107478127	0.180303909		AT4G18240.1	ATSS4,SS4,SSIV	starch synthase 4	starch synthase
Sapur.019G012400.1	0.020457939	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016491,GO:0008270	AT5G63620.2		GroES-like zinc-binding alcohol dehydrogenase family protein	NA
Sapur.019G021900.3	0.021924083	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.137373899	0.086220856		AT5G28640.1	AN3,ATGIF1,GIF,GIF1	SSXT family protein	SSXT protein (amino-terminal region) protein
Sapur.15WG009000.2	0.019933177	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.102301584	0.202330601	GO:0005515	AT4G03220.1		Protein with RNI-like/FBD-like domains	F-box protein
Sapur.15WG111600.1	0.021655571	-0.056846222	2.904824395	-0.01957	0.984386723	NA	brown	-0.137184375	0.086659366	GO:0006414,GO:0005853,GO:0003746	AT2G18110.1		Translation elongation factor EF1B/ribosomal protein S6 family protein	elongation factor 1-beta, putative
Sapur.011G020600.3	0.029634676	0.051842861	2.677857956	0.01936	0.984554059	NA	brown	-0.006010505	0.94044524	GO:0048544,GO:0006468,GO:0004672	AT1G11340.1		S-locus lectin protein kinase family protein	Serine/Threonine kinase domain protein

Sapur.008G166200.4	0.03933537	0.049979566	2.591246917	0.019288	0.984611481	NA	brown	-0.007111965	0.929557429	GO:0046872,GO:0008270,GO:0016567	AT5G18650.1		CHY-type/CTCHY-type/RING-type Zinc finger protein	CHY zinc finger protein
Sapur.001G081800.1	0.038827273	-0.04398701	2.297701893	-0.01914	0.984726299	NA	brown	-0.089599614	0.264441534		AT1G69230.1	SP1L2	SPIRAL1-like2	hypothetical protein
Sapur.001G001000.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G55535.1			transmembrane protein, putative
Sapur.001G072500.2	0.004765175	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0003677,GO:0009725,GO:0006355,GO:0005634	AT4G23980.1	ARF9	auxin response factor 9	auxin response factor
Sapur.001G093600.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0060236,GO:0032147,GO:0005874,GO:0005819	AT4G22860.1		Cell cycle regulated microtubule associated protein	cell cycle regulated microtubule-associated protein
Sapur.001G107000.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.001G107800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G45410.2			transmembrane protein, putative
Sapur.001G115300.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515,GO:0016567,GO:0004842	AT1G32340.1	NHL8	NDR1/HIN1-like 8	E3 ubiquitin-protein ligase RNF14
Sapur.001G119600.2	0.005733648	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0003677	AT4G17980.1	anac071,NAC071	NAC domain containing protein 71	NAC transcription factor 045
Sapur.001G141600.1	0.005733648	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.1168153	0.145119686		AT4G19160.2			transglutaminase family protein
Sapur.001G145000.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT1G15420.1			ubiquitin-like Rad60 SUMO-like protein
Sapur.001G150000.2	0.006431396	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G13890.2	ATMYB26,MS35,MYB26	myb domain protein 26	R2R3-Myb transcription factor, putative
Sapur.001G152300.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.001G157800.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					NA
Sapur.001G158800.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					NA
Sapur.001G161500.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0005634	AT1G51950.1	IAA18	indole-3-acetic acid inducible 18	auxin-responsive protein IAA26
Sapur.001G165800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G79830.2	GC5	golgin candidate 5	coiled-coil vesicle tethering protein, putative
Sapur.001G174000.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G71240.1		Plant protein of unknown function (DUF639)	transmembrane protein, putative
Sapur.002G002300.1	0.005890737	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G76500.1	AHL29,SOB3	Predicted AT-hook DNA-binding family protein	DNA-binding protein, putative
Sapur.002G006500.6	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005634	AT1G76310.1	CYCB2;4	CYCLIN B2;4	NA
Sapur.002G023100.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0003677	AT1G75430.1	BLH11	BEL1-like homeodomain 11	BEL1 homeotic protein, putative
Sapur.002G039500.2	0.006428371	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.017065582	0.831999502		AT3G22550.1		Protein of unknown function (DUF581)	senescence-associated protein SAG102
Sapur.002G055000.5	0.007234977	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0017069,GO:0000398	AT1G21320.2		nucleotide binding;nucleic acid binding	RNA recognition motif, a.k.a. RRM%2C RBD protein
Sapur.002G061900.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016020,GO:0015171,GO:0003333	AT2G01170.1	BAT1	bidirectional amino acid transporter 1	amino acid permease
Sapur.002G061900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055085,GO:0016020,GO:0006810,GO:0015171,GO:0003333	AT2G01170.1	BAT1	bidirectional amino acid transporter 1	amino acid permease
Sapur.002G073400.4	0.005937058	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G02130.1	NDP1	Tetratricopeptide repeat (TPR)-like superfamily protein	transmembrane protein, putative
Sapur.002G087100.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0046983	AT5G65640.1	bHLH093	beta HLH protein 93	transcription factor BHLH protein
Sapur.002G087500.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G28670.1		oxidoreductase, zinc-binding dehydrogenase family protein	zinc-binding dehydrogenase, putative
Sapur.002G100600.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.055945801	0.486464866		AT3G57870.1	AHUS5.ATSCE1.EMB1637.S(	sumo conjugation enzyme 1	SUMO E2 conjugating enzyme SCE1
Sapur.002G102000.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G45207.2		Remorin family protein	remorin
Sapur.002G106600.1	0.006431396	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.114846535	0.152067369	GO:0006468,GO:0004672	AT3G13690.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	receptor tyrosine kinase
Sapur.002G106900.2	0.005890737	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004672	AT2G23450.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.002G118400.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016021,GO:0006888,GO:0005801,GO:0000139	AT2G45200.1	ATGOS12,GOS12	golgi snare 12	SNAP receptor complex protein
Sapur.002G133400.4	0.004880298	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055085,GO:0016021	AT2G48020.2		Major facilitator superfamily protein	sugar transporter ERD6-like protein
Sapur.002G156900.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G02425.1			hypothetical protein
Sapur.002G181500.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005737,GO:0005094	AT3G07880.1	SCN1	Immunoglobulin E-set superfamily protein	Rho GDP-dissociation inhibitor
Sapur.002G182600.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G23740.1			hypothetical protein
Sapur.002G188200.2	0.00651968	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.072876299	0.364381813		AT4G13630.2		Protein of unknown function, DUF593	zein-binding protein
Sapur.002G192000.6	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004672	AT4G13020.4	MHK	Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.002G199900.2	0.00593829	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0005634	AT4G28640.2	IAA11	indole-3-acetic acid inducible 11	indoleacetic acid-induced protein
Sapur.002G202600.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055085,GO:0016021	AT1G75220.1		Major facilitator superfamily protein	sugar transporter, putative
Sapur.003G026100.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008152,GO:0003824	AT3G16190.1		Isochorismatase family protein	isochorismatase hydrolase family protein
Sapur.003G028300.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008601,GO:0000159	AT1G17720.2	ATB BETA	Protein phosphatase 2A, regulatory subunit PR55	serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B beta
Sapur.003G051300.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT4G17570.3	GATA26	GATA transcription factor 26	GATA transcription factor, putative
Sapur.003G053500.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016788	AT4G17100.2			endoribonuclease XendoU protein
Sapur.003G057000.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G32470.1		Single hybrid motif superfamily protein	glycine cleavage system H protein
Sapur.003G057900.2	0.006073616	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT4G35470.1	PIRL4	plant intracellular ras group-related LRR 4	plant intracellular Ras-group-related LRR protein
Sapur.003G077000.5	0.005011262	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G22540.1	ORP2A	OSBP(oxysterol binding protein)-related protein 2A	oxysterol-binding protein-related protein
Sapur.003G152100.7	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.003G159600.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G73730.1	AtEIL3,ATSLIM,EIL3,SLIM1	ETHYLENE-INSENSITIVE3-like 3	ethylene insensitive (EIN3/EIL)-like transcription regulator
Sapur.004G001600.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016491	AT1G05010.1	ACO4,EAT1,EFE	ethylene-forming enzyme	1-aminocyclopropane-1-carboxylate oxidase
Sapur.004G010500.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT4G21820.1		binding;calmodulin binding	abnormal spindle-like microcephaly-associated-like protein, putative
Sapur.004G011000.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016780,GO:0016020,GO:0008654	AT4G04870.1	CLS	cardiolipin synthase	phosphatidylglycerotransferase, putative
Sapur.004G020400.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0046854	AT4G05090.1		Inositol monophosphatase family protein	inositol monophosphatase family protein
Sapur.004G021700.4	0.006179623	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT1G30410.1	ATMRP13,MRP13	multidrug resistance-associated protein 13	NA
Sapur.004G029300.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G32480.1		Protein of unknown function (DUF506)	plant/F8B4-180 protein, putative
Sapur.004G041900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G29270.1			hypothetical protein
Sapur.004G087800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G72160.1		Sec14p-like phosphatidylinositol transfer family protein	NA
Sapur.004G088800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT3G19270.1	CYP707A4	cytochrome P450, family 707, subfamily A, polypeptide 4	cytochrome P450 family 707 ABA 8'-hydroxylase
Sapur.004G091400.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G33945.1		ARM repeat superfamily protein	armadillo/beta-catenin-like repeat protein
Sapur.004G105100.2	0.005937058	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G28880.1		Ankyrin repeat family protein	NA
Sapur.004G105800.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G23610.2			DYAD protein, putative
Sapur.004G119900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005975,GO:0004553	AT4G36360.1	BGAL3	beta-galactosidase 3	beta-galactosidase
Sapur.004G133100.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0071949	AT5G05320.1		FAD/NAD(P)-binding oxidoreductase family protein	FAD-binding domain protein
Sapur.004G155800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G35360.1		Uncharacterised conserved protein (UCP030210)	pantothenate kinase
Sapur.004G162700.1	0.006085689	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					NA
Sapur.005G020500.9	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G09060.3		Zinc finger, RING-type;Transcription factor jumonji/aspartyl beta-hydroxylase	transcription factor jumonji domain protein
Sapur.005G034400.2	0.00602393	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.038330437	0.633635406	GO:0006468,GO:0005524,GO:0004672	AT1G54610.1		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.005G045100.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016773,GO:0048015,GO:0046854,GO:0006661,GO:0004430	AT5G64070.1	PI-4KBETA1,PI4KBETA1	phosphatidylinositol 4-OH kinase beta1	phosphatidylinositol 4-kinase, putative
Sapur.005G045200.1	0.006444464	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					chitinase
Sapur.005G048600.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016624,GO:0008152	AT5G09300.1		Thiamin diphosphate-binding fold (THDP-binding) superfamily protein	2-oxoisovalerate dehydrogenase alpha subunit, putative
Sapur.005G052000.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006629	AT3G52430.1	ATPAD4,PAD4	alpha/beta-Hydrolases superfamily protein	NA
Sapur.005G070600.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0046872,GO:0006801,GO:0004784	AT5G23310.1	FSD3	Fe superoxide dismutase 3	iron superoxide dismutase
Sapur.005G088200.2	0.009759838	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008270,GO:0005515	AT2G26000.2	BRIZ2	zinc finger (C3HC4-type RING finger) family protein	ubiquitin carboxyl-terminal hydrolase
Sapur.005G114900.1	0.006083092	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0043565,GO:0006355,GO:0003700,GO:0003677	AT4G40060.1	ATHB-16,ATHB16,HB16	homeobox protein 16	homeobox leucine zipper protein
Sapur.005G124900.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016021	AT4G39220.1	ATRER1A	Rer1 family protein	RER1A protein
Sapur.005G126700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	0.107160336	0.181603109		AT3G28370.1			NA
Sapur.005G128900.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G34670.1	AtMYB93,MYB93	myb domain protein 93	transcription factor MYB39, putative
Sapur.005G137900.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G44780.2			histone chaperone domain CHZ protein
Sapur.005G140900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G63420.2	AGG1,ATAGG1,GG1	Ggamma-subunit 1	hypothetical protein
Sapur.005G144500.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT1G77250.1		RING/FYVE/PHD-type zinc finger family protein	PHD-finger protein
Sapur.005G161400.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0003723,GO:0008168	AT1G06560.1		NOL1/NOP2/sun family protein	ribosomal RNA small subunit methyltransferase B
Sapur.005G169700.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G14720.1	PPD2,TIFY4B	TIFY domain/Divergent CCT motif family protein	jasmonate ZIM domain protein K.2
Sapur.005G181300.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0007034	AT1G03950.1	VPS2.3	vacuolar protein sorting-associated protein 2.3	charged multivesicular body protein 2a, putative
Sapur.005G195200.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.105883216	0.186893673	GO:0043565,GO:0006355,GO:0003700	AT4G35900.1	atbzip14,FD,FD-1	Basic-leucine zipper (bZIP) transcription factor family protein	basic leucine zipper transcription factor
Sapur.005G202000.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004672	AT1G20650.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.006G008500.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G20130.1			transmembrane protein, putative
Sapur.006G008600.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT4G22360.1		SWIB complex BAF60b domain-containing protein	Brg-1 associated factor, putative
Sapur.006G028600.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008017,GO:0007010	AT1G24764.1	ATMAP70-2,MAP70-2	microtubule-associated proteins 70-2	microtubule-associated protein 70-2
Sapur.006G035300.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005509	AT3G10300.4		Calcium-binding EF-hand family protein	EF hand protein
Sapur.006G042500.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016746,GO:0008152	AT3G57650.1	LPAT2	lysophosphatidyl acyltransferase 2	1-acyl-sn-glycerol-3-phosphate acyltransferase
Sapur.006G043800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G12170.1		Chaperone DnaJ-domain superfamily protein	chaperone protein DnaJ
Sapur.006G070600.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G02250.1	ATMTRNASEII.EMB2730.RN	Ribonuclease II/R family protein	ribonuclease II
Sapur.006G073700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G31280.1	CPUORF7	conserved peptide upstream open reading frame 7	bHLH-MYC/R2R3-MYB transcription factor amino-terminal protein
Sapur.006G080400.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016020,GO:0006810,GO:0005215	AT4G00430.1	PIP1;4,PIP1E,TMP-C	plasma membrane intrinsic protein 1;4	plasma membrane intrinsic protein PIP1-1
Sapur.006G085800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G51670.1		SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	patellin-6 protein
Sapur.006G092300.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G54190.1		Transducin/WD40 repeat-like superfamily protein	plant/F24B22-150 protein
Sapur.006G092300.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G38630.1		Transducin/WD40 repeat-like superfamily protein	plant/F24B22-150 protein
Sapur.006G118400.7	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0032502,GO:0006351,GO:0005634	AT3G13960.1	AtGRF5,GRF5	growth-regulating factor 5	QLQ protein
Sapur.006G150100.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006508,GO:0004185	AT4G30610.1	BRS1,SCPL24	alpha/beta-Hydrolases superfamily protein	serine carboxypeptidase
Sapur.006G181100.1	0.006083092	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT2G26330.1	ER,QRP1	Leucine-rich receptor-like protein kinase family protein	LRR receptor-like Serine/Threonine-kinase
Sapur.006G200100.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0003723	AT4G32720.2	AtLa1,La1	La protein 1	lupus LA ribonucleoprotein, putative
Sapur.006G207700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G25480.1	AtDNMT2,DNMT2	DNA methyltransferase-2	DNA (cytosine-5)-methyltransferase
Sapur.006G228300.8	0.004953155	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G30650.1		ATP-dependent caseinolytic (Clp) protease/crotonase family protein	3-hydroxyisobutyryl-CoA hydrolase
Sapur.007G001900.4	0.006598449	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0003824	AT1G78950.1		Terpenoid cyclases family protein	beta-amyrin synthase
Sapur.007G015700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0050660,GO:0016491,GO:0003824	AT4G36400.1		FAD-linked oxidases family protein	NA
Sapur.007G031200.2	0.00602393	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G37235.1		Uncharacterised protein family (UPF0497)	transmembrane protein, putative
Sapur.007G032500.2	0.006085689	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G50380.1		Protein of unknown function (DUF1162)	Pol-like polyprotein/retrotransposon, putative
Sapur.007G071000.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0030244,GO:0016760,GO:0016020	AT5G64740.1	CESA6,E112,IXR2,PRC1	cellulose synthase 6	cellulose synthase A catalytic subunit 5 [UDP-forming] protein
Sapur.007G103700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G61000.1			NA
Sapur.007G106400.1	0.006444464	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					B3 DNA-binding domain protein
Sapur.007G108500.6	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G05270.1		TraB family protein	TraB family protein
Sapur.007G128600.1	0.004953155	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					NA
Sapur.008G006700.6	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008270,GO:0006355	AT2G27110.2	FRS3	FAR1-related sequence 3	FAR1-related sequence protein
Sapur.008G011800.2	0.006165205	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G04840.1		bZIP protein	BZIP protein, putative
Sapur.008G013100.2	0.006431396	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0004523,GO:0003723	AT2G25100.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	ribonuclease H
Sapur.008G017700.1	0.004953155	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G57810.3		Cysteine proteinases superfamily protein	OTU-like cysteine protease
Sapur.008G022500.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT5G04420.2		Galactose oxidase/kelch repeat superfamily protein	acyl-CoA-binding domain protein
Sapur.008G024500.2	0.005907325	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0007034	AT5G22950.1	VPS24.1	SNF7 family protein	charged multivesicular body protein
Sapur.008G033800.9	0.006073616	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G37060.1	NF-YB8	nuclear factor Y, subunit B8	nuclear transcription factor Y subunit B-1
Sapur.008G042700.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0003677	AT3G55370.2	OBP3	OBF-binding protein 3	Dof zinc finger protein
Sapur.008G044300.5	0.007810412	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0003676	AT3G13570.1	SCL30A	SC35-like splicing factor 30A	RNA recognition motif, a.k.a. RRM%2C RBD protein
Sapur.008G053100.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0005634,GO:0003682,GO:0003677	AT3G51880.2	HMGB1,NFD1	high mobility group B1	NA
Sapur.008G053100.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0005634,GO:0003682,GO:0003677	AT3G51880.2	HMGB1,NFD1	high mobility group B1	NA
Sapur.008G053800.3	0.005890737	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G55490.1		GINS complex protein	DNA replication complex GINS protein Psf3
Sapur.008G055000.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006629,GO:0055114,GO:0016717	AT5G05580.1	FAD8	fatty acid desaturase 8	omega-3 fatty acid desaturase
Sapur.008G067700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G69600.1	ATHB29,ZFHD1	zinc finger homeodomain 1	ZF-HD homeobox domain protein
Sapur.008G077700.8	0.006083092	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0005634,GO:0003700	AT1G69120.1	AGL7,AP1	K-box region and MADS-box transcription factor family protein	MADS-box transcription factor APETALA 1
Sapur.008G084900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008270,GO:0006351,GO:0003676	AT3G16980.1	NRPB9A,NRPD9A,NRPE9A	RNA polymerases M/15 Kd subunit	DNA-directed RNA polymerase subunit
Sapur.008G092600.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016021	AT1G26100.1		Cytochrome b561/ferric reductase transmembrane protein family	cytochrome protein b561, putative
Sapur.008G107100.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G23170.2		Protein of unknown function DUF2359, transmembrane	hypothetical protein
Sapur.008G119700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0043565,GO:0006355,GO:0003700,GO:0003677	AT1G69780.1	ATHB13	Homeobox-leucine zipper protein family	homeobox leucine zipper protein
Sapur.008G136200.4	0.00347127	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	0.078548531	0.32814497	GO:0006468,GO:0005524,GO:0004674,GO:0004672	AT3G23310.1		AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	AGC (cAMP-dependent, cGMP-dependent and kinase C) kinase family protein
Sapur.008G143900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0046872,GO:0016702	AT1G67560.1		PLAT/LH2 domain-containing lipoxygenase family protein	lipoxygenase
Sapur.008G152200.2	0.006910738	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.098639342	0.219045351	GO:0005975,GO:0004650	AT1G60590.1		Pectin lyase-like superfamily protein	polygalacturonase
Sapur.009G006900.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016021,GO:0008146	AT1G08030.1	TPST	tyrosylprotein sulfotransferase	tyrosine sulfotransferase
Sapur.009G028400.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G02020.2			hypothetical protein
Sapur.009G029200.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G59020.1		Protein of unknown function (DUF3527)	DUF3527 domain protein
Sapur.009G050000.2	0.005937058	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0046983	AT2G42280.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH122, putative
Sapur.009G050600.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0051082,GO:0031072	AT5G48030.1	GFA2	gametophytic factor 2	chaperone protein DnaJ
Sapur.009G058300.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G58560.1		Phosphatidate cytidylyltransferase family protein	phytol kinase, putative
Sapur.009G063000.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	0.051190765	0.524313464		AT5G64460.4		Phosphoglycerate mutase family protein	phosphoglycerate mutase-like protein
Sapur.009G064900.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.126802523	0.113528777	GO:0008152,GO:0003824	AT1G50110.1		D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein	branched-chain-amino-acid aminotransferase
Sapur.009G071100.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT3G43740.1		Leucine-rich repeat (LRR) family protein	somatic embryogenesis receptor kinase
Sapur.009G075200.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G15240.1		UNC-50 family protein	UNC-50
Sapur.009G076500.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT4G34150.1		Calcium-dependent lipid-binding (CaLB domain) family protein	C2 domain protein
Sapur.009G089300.2	0.005832192	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G36800.2	RCE1	RUB1 conjugating enzyme 1	ubiquitin-conjugating enzyme
Sapur.009G119000.3	0.007245688	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0030131,GO:0016192,GO:0006886,GO:0030117	AT5G22770.1	alpha-ADR	alpha-adaptin	AP-2 complex subunit alpha, putative
Sapur.009G126600.4	0.009759838	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0005667,GO:0003700	AT5G22220.2	ATE2FB,E2F1,E2FB	E2F transcription factor 1	transcription factor E2F
Sapur.010G002500.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G48320.1		Thioesterase superfamily protein	acyl-CoA thioesterase
Sapur.010G010000.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.149286102	0.062031195	GO:0008152,GO:0003824,GO:0016114,GO:0008661	AT4G15560.1	CLA,CLA1,DEF,DXPS2,DXS	Deoxyxylulose-5-phosphate synthase	1-deoxy-D-xylulose-5-phosphate synthase
Sapur.010G014700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005634,GO:0003677	AT5G18830.3	ATSPL7,SPL7	squamosa promoter binding protein-like 7	squamosa promoter-binding-like protein
Sapur.010G020300.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0034314,GO:0007015,GO:0005885,GO:0005524	AT1G13180.1	ARP3,ATARP3,DIS1	Actin-like ATPase superfamily protein	actin-related protein ARP3 subunit
Sapur.010G023100.2	0.005011262	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G67840.2	CSK	chloroplast sensor kinase	ATP-binding region, ATPase-like domain protein, putative
Sapur.010G024500.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G70630.1		Nucleotide-diphospho-sugar transferase family protein	NA
Sapur.010G031000.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G70070.1	EMB25,ISE2,PDE317	DEAD/DEAH box helicase, putative	DEAD-box ATP-dependent RNA helicase ISE2
Sapur.010G057000.7	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008601,GO:0007165,GO:0000159	AT3G26020.2		Protein phosphatase 2A regulatory B subunit family protein	serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' protein
Sapur.010G076900.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004672	AT1G24030.2		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.010G079600.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G02820.2	AtMYB88,MYB88	myb domain protein 88	Myb-like DNA-binding domain protein
Sapur.010G080900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016787	AT2G01670.1	atnudt17,NUDT17	nudix hydrolase homolog 17	nudix hydrolase
Sapur.010G091800.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.083293387	0.299676877		AT2G01260.2		Protein of unknown function (DUF789)	DUF789 family protein
Sapur.010G109500.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0032040	AT1G69070.1			Nop14 family protein
Sapur.010G114000.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081569362	0.309825971					hypothetical protein
Sapur.010G128200.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355	AT2G03150.1	emb1579	ATP/GTP-binding protein family	P30 dbc protein, putative
Sapur.010G136600.2	0.005011262	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016616,GO:0006102,GO:0004450	AT1G54340.1	ICDH	isocitrate dehydrogenase	isocitrate dehydrogenase [NADP] protein
Sapur.010G148700.1	0.004765175	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0033588	AT3G11220.1	ELO1	Paxneb protein-related	elongator component
Sapur.010G172300.6	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G37060.2	NF-YB8	nuclear factor Y, subunit B8	nuclear transcription factor Y subunit B-1
Sapur.010G195500.1	0.006444464	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0019538	AT3G52490.1		Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein	heat shock protein, putative
Sapur.011G002800.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016020,GO:0008378,GO:0006486	AT1G05170.1		Galactosyltransferase family protein	beta-1%2C3-galactosyltransferase, putative
Sapur.011G008700.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.103717051	0.196123443		AT4G04330.1		Chaperonin-like RbcX protein	RbcX protein
Sapur.011G030700.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515,GO:0006468,GO:0004672	AT4G03390.1	SRF3	STRUBBELIG-receptor family 3	LRR receptor-like kinase, putative
Sapur.011G056100.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006260,GO:0005664,GO:0003677	AT1G26840.1	ATORC6,ORC6	origin recognition complex protein 6	origin recognition complex subunit 6
Sapur.011G112300.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	0.078548531	0.32814497		AT3G15850.1	ADS3,FAD5,FADB,JB67	fatty acid desaturase 5	palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, putative
Sapur.011G115200.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0009052,GO:0004751	AT5G44520.1		NagB/RpiA/CoA transferase-like superfamily protein	ribose-5-phosphate isomerase A
Sapur.011G116200.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0042254,GO:0005622	AT1G25260.1		Ribosomal protein L10 family protein	ribosomal protein L10
Sapur.012G042700.4	0.005907325	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G18520.2	ATHDA15,HDA15	histone deacetylase 15	histone deacetylase family protein
Sapur.012G076300.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008641	AT4G24940.1	AT-SAE1-1,ATSAE1A,SAE1A	SUMO-activating enzyme 1A	SUMO-activating enzyme subunit 1A
Sapur.012G077100.1	0.006598449	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G50720.1	ATHVA22E,HVA22E	HVA22 homologue E	HVA22-like protein E
Sapur.012G077400.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G47350.2	ATHSD2,HSD2	hydroxysteroid dehydrogenase 2	short-chain dehydrogenase reductase
Sapur.013G008600.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006415,GO:0003747,GO:0016149,GO:0005737	AT1G56350.1		Peptide chain release factor 2	peptide chain release factor 2
Sapur.013G012400.1	0.006044912	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G64620.1	ATC/VIF2,C/VIF2	cell wall / vacuolar inhibitor of fructosidase 2	pectinesterase inhibitor domain protein
Sapur.013G041100.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G54650.2		Methyltransferase family protein	methyltransferase domain protein
Sapur.013G069500.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.013G069600.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.013G074200.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0051082,GO:0015631,GO:0007021	AT2G30410.2	KIS,TFCA	tubulin folding cofactor A (KIESEL)	tubulin folding cofactor A
Sapur.013G082400.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016987,GO:0006355,GO:0006352,GO:0003700,GO:0003677	AT1G64860.1	RPOD1.SIG1.SIG2.SIGA.SIGB	sigma factor A	RNA polymerase sigma factor
Sapur.013G091600.1	0.005907325	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008270,GO:0005515	AT4G10150.1		RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.013G131200.2	0.005890737	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016491	AT4G28220.1	NDB1	NAD(P)H dehydrogenase B1	external alternative NAD(P)H-ubiquinone oxidoreductase B1
Sapur.013G143300.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005622,GO:0003676,GO:0005524,GO:0043140,GO:0006281,GO:0006260	AT1G60930.1	ATRECQ4B.RECQ4B.RECQL	RECQ helicase L4B	ATP-dependent DNA helicase RecQ
Sapur.014G014600.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G57870.1	AHUS5.ATSCE1.EMB1637.S(	sumo conjugation enzyme 1	ubiquitin-conjugating enzyme E2
Sapur.014G069800.1	0.004923806	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008270,GO:0005515	AT4G01270.1		RING/U-box superfamily protein	RING zinc finger protein, putative
Sapur.014G090000.1	0.00527888	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT1G02520.1	PGP11	P-glycoprotein 11	NA
Sapur.014G099100.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G47900.1		Protein of unknown function (DUF1624)	heparan-alpha-glucosaminide N-acetyltransferase
Sapur.014G102700.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G47590.1	PHR2	photolyase/blue-light receptor 2	photolyase/blue-light receptor 2, putative
Sapur.014G121300.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006457	AT5G48570.1	ATFKBP65,FKBP65,ROF2	FKBP-type peptidyl-prolyl cis-trans isomerase family protein	peptidylprolyl isomerase, putative
Sapur.014G129600.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G05000.1		Phosphotyrosine protein phosphatases superfamily protein	tyrosine phosphatase family protein, putative
Sapur.014G129800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515,GO:0003676	AT2G32940.1	AGO6	Argonaute family protein	NA
Sapur.014G135700.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G07740.2	ADA2A.ATADA2A.HAC10.HX	homolog of yeast ADA2 2A	transcriptional adapter ADA2
Sapur.014G144200.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G07525.2	ATATG10,ATG10	autophagocytosis-associated family protein	autophagocytosis associated protein, active-site protein
Sapur.016G044800.1	0.005937058	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0009055	AT5G26330.1		Cupredoxin superfamily protein	NA
Sapur.016G048000.2	0.006179623	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0046872	AT2G41900.1		CCCH-type zinc finger protein with ARM repeat domain	zinc finger CCCH domain protein
Sapur.016G081800.2	0.006444464	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G37080.1	RIP3	ROP interactive partner 3	interactor of constitutive active ROPs protein, putative
Sapur.016G100000.3	0.006044912	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G40070.1			proteophosphoglycan protein, putative
Sapur.016G104900.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0033699,GO:0006281,GO:0003677	AT5G01310.1	APTX	APRATAXIN-like	transcription factor bHLH140
Sapur.016G106400.1	0.006044912	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0043565,GO:0006355,GO:0003700	AT2G42380.2	ATBZIP34,BZIP34	Basic-leucine zipper (bZIP) transcription factor family protein	BZIP transcription factor
Sapur.016G114700.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0003677	AT2G35940.1	BLH1,EDA29	BEL1-like homeodomain 1	BEL1-related homeotic protein, putative
Sapur.016G126500.4	0.005890737	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016491,GO:0008270	AT3G45770.1		Polyketide synthase, enoylreductase family protein	trans-2-enoyl-CoA reductase, putative
Sapur.016G143600.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G31530.1		NAD(P)-binding Rossmann-fold superfamily protein	NAD(P)H-binding family protein
Sapur.016G148900.1	0.005927541	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					NA
Sapur.016G157400.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016779,GO:0009058	AT5G19485.1		transferases;nucleotidyltransferases	translation initiation factor eIF-2B subunit gamma
Sapur.016G165100.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0005515	AT2G30105.1			ubiquitin-like protein
Sapur.016G176900.6	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G43740.1		Leucine-rich repeat (LRR) family protein	somatic embryogenesis receptor kinase
Sapur.016G189200.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G22310.1	ATMBD8,MBD8	methyl-CPG-binding domain 8	methyl-binding domain protein, putative
Sapur.016G220000.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G27770.1			plant/MGF10-16 protein, putative
Sapur.016G240800.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G73140.1	TBL31	Plant protein of unknown function (DUF828)	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.016G253800.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016757	AT1G16570.2		UDP-Glycosyltransferase superfamily protein	glycosyltransferase group 1 protein
Sapur.016G260500.5	0.006199952	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G15430.2		Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator repeat protein
Sapur.016G260700.4	0.006083092	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G27450.1		Aluminium induced protein with YGL and LRDR motifs	stem-specific protein tsjt1 protein, putative
Sapur.016G271100.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0048544,GO:0006468,GO:0005524,GO:0004672	AT4G21380.1	ARK3,RK3	receptor kinase 3	Serine/Threonine-kinase
Sapur.016G275400.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016757,GO:0047262	AT5G54690.1	GAUT12,IRX8,LGT6	galacturonosyltransferase 12	CAZy family GT8 glycosyltransferase
Sapur.016G290200.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016020,GO:0008378,GO:0006486	AT1G32930.1		Galactosyltransferase family protein	beta-1%2C3-galactosyltransferase, putative
Sapur.016G291300.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016491	AT4G10490.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase, putative
Sapur.016G292400.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016021,GO:0016020,GO:0022857	AT3G30340.1		nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4, putative
Sapur.016G292800.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016491,GO:0008152	AT5G15940.1		NAD(P)-binding Rossmann-fold superfamily protein	short chain dehydrogenase
Sapur.016G307900.3	0.006598449	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0003333	AT5G23810.2	AAP7	amino acid permease 7	transmembrane amino acid transporter protein
Sapur.017G022100.1	0.005011262	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G21280.1			NA
Sapur.017G037800.2	0.006083092	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016491	AT2G36690.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	flavonol synthase/flavanone 3-hydroxylase, putative
Sapur.017G070400.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G29010.1		Biotin/lipoate A/B protein ligase family	lipoate-protein ligase A
Sapur.017G078900.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G02160.1		Bromodomain transcription factor	Tbp-associated factor taf protein, putative
Sapur.017G084200.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0007165,GO:0005515,GO:0043531	AT5G17680.1		disease resistance protein (TIR-NBS-LRR class), putative	TIR-NBS-LRR TIR type disease resistance protein
Sapur.017G106900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G23890.2		NHL domain-containing protein	NA
Sapur.017G107700.1	0.005927541	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G16610.2			hypothetical protein
Sapur.017G107700.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G16610.2			hypothetical protein
Sapur.017G108000.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G54650.1	FBL17	RNI-like superfamily protein	hypothetical protein
Sapur.017G114300.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016740,GO:0009058	AT5G17230.1	PSY	PHYTOENE SYNTHASE	phytoene synthase
Sapur.018G000900.7	0.005907325	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0004672	AT2G24360.1		Protein kinase superfamily protein	Serine/Threonine/tyrosine kinase, putative
Sapur.018G016800.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0043531	AT3G14460.1		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein

Sapur.018G048500.2	0.005907325	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006334,GO:0005634	AT2G19480.3	NAP1;2,NFA02,NFA2	nucleosome assembly protein 1;2	nucleosome assembly protein
Sapur.018G050900.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0050113,GO:0019310,GO:0005737,GO:0005506	AT2G19800.1	MIOX2	myo-inositol oxygenase 2	Myo-inositol oxygenase
Sapur.018G055200.5	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016020	AT3G24460.1		Serinc-domain containing serine and sphingolipid biosynthesis protein	maternal effect embryo arrest protein 55-1
Sapur.018G060600.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016567,GO:0004842	AT3G06880.2		Transducin/WD40 repeat-like superfamily protein	E3 ubiquitin-protein ligase LIN, putative
Sapur.018G066100.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0003779	AT4G30160.1	ATVLN4,VLN4	villin 4	villin, putative
Sapur.018G071800.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G57630.1	CIPK21,SnRK3.4	CBL-interacting protein kinase 21	CBL-interacting kinase
Sapur.018G071800.7	0.006044912	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0007165	AT5G57630.1	CIPK21,SnRK3.4	CBL-interacting protein kinase 21	CBL-interacting kinase
Sapur.018G079600.3	0.005937058	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G17420.1	ATCESA7,CESA7,IRX3,MUR1	Cellulose synthase family protein	cellulose synthase A catalytic subunit 9 [UDP-forming] protein
Sapur.018G104900.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0004672	AT2G17220.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.019G015800.2	0.009759838	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016021,GO:0015693,GO:0015095	AT2G21120.1		Protein of unknown function (DUF803)	Non-imprinted in prader-willi/angelman syndrome region protein
Sapur.019G023900.2	0.006598449	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016491,GO:0050660,GO:0016021,GO:0004506	AT1G58440.1	SQE1,XF1	FAD/NAD(P)-binding oxidoreductase family protein	squalene monooxygenase
Sapur.019G024600.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006629	AT2G26560.1	PLA IIA,PLA2A,PLP2	phospholipase A 2A	NA
Sapur.019G030600.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G37360.1			ammonium transporter, putative
Sapur.019G046800.1	0.005011262	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.019G053900.4	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0051082,GO:0006457,GO:0005783,GO:0005509	AT1G08450.1	AtCRT3,CRT3,EBS2,PSL1	calreticulin 3	calreticulin, putative
Sapur.019G090200.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT4G28300.1		Protein of unknown function (DUF1421)	structural constituent of cell wall protein, putative
Sapur.019G111000.1	0.006522982	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G30370.2	CHAL,EPFL6	allergen-related	transmembrane protein, putative
Sapur.15WG009100.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G53050.2		alpha/beta-Hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.15WG010900.12	0.005907325	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G24270.2	ATSOS3,CBL4,SOS3	Calcium-binding EF-hand family protein	calcineurin B-like protein 4-1, putative
Sapur.15WG031300.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004672	AT3G18040.1	MPK9	MAP kinase 9	NA
Sapur.15WG033100.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT1G04420.1		NAD(P)-linked oxidoreductase superfamily protein	aldo-keto reductase family protein
Sapur.15WG098000.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016757,GO:0008152	AT5G17990.1	pat1,TRP1	tryptophan biosynthesis 1	anthranilate phosphoribosyltransferase
Sapur.15WG099800.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016491,GO:0008152	AT5G50130.2		NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase family protein
Sapur.15WG105700.1	0.00527888	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					hypothetical protein
Sapur.15WG108900.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016620	AT1G13440.1	GAPC-2,GAPC2	glyceraldehyde-3-phosphate dehydrogenase C2	glyceraldehyde-3-phosphate dehydrogenase
Sapur.15WG117600.2	0.005733648	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0009982,GO:0009451,GO:0003723,GO:0001522	AT5G51140.1		Pseudouridine synthase family protein	RNA pseudouridine synthase
Sapur.15WG117600.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0009982,GO:0009451,GO:0003723,GO:0001522	AT5G51140.1		Pseudouridine synthase family protein	RNA pseudouridine synthase
Sapur.15WG130200.1	0.00593829	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0016021	AT1G31300.2		TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	plant/T19E23-12 protein
Sapur.T026700.1	0.005937058	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					transmembrane protein, putative
Sapur.T046700.3	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0046872,GO:0030001	AT1G29000.1		Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.T048400.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G75130.1	CYP721A1	cytochrome P450, family 721, subfamily A, polypeptide 1	cytochrome P450 family protein
Sapur.T051600.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G44010.1			fanconi anemia group F protein (FANCF)
Sapur.T063500.2	0.00527888	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT2G43465.1		RNA-binding ASCH domain protein	NA
Sapur.T090200.2	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942	GO:0008270,GO:0005515	AT5G40250.1		RING/U-box superfamily protein	RING finger protein
Sapur.T128200.1	0.005114485	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942					NA
Sapur.T137000.1	0.00602393	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT5G24280.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.T174100.1	0.00602393	0.05557013	2.904824396	0.01913	0.984737169	NA	brown	-0.081608864	0.309590942		AT3G24880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.016G305500.1	0.025801812	0.051848008	2.725613373	0.019023	0.984823148	NA	brown	-0.048764172	0.544188343	GO:0005515,GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT3G44730.1	ATKP1,KP1	kinesin-like protein 1	kinesin heavy chain, putative
Sapur.014G101600.2	0.025427026	0.051848545	2.730755351	0.018987	0.984851566	NA	brown	-0.043986897	0.584368577	GO:0005975,GO:0004553	AT4G02290.1	AtGH9B13,GH9B13	glycosyl hydrolase 9B13	endo-1%2C4-beta-glucanase
Sapur.002G026400.2	0.034729625	0.049984705	2.633151294	0.018983	0.98485479	NA	brown	-0.02334408	0.771661217		AT1G19530.1			hypothetical protein
Sapur.005G049300.1	0.024353205	0.051850119	2.746029058	0.018882	0.984935356	NA	brown	-0.05399988	0.501774717		AT5G20680.3	TBL16	TRICHOME BIREFRINGENCE-LIKE 16	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.15WG088300.1	0.02191989	0.051853914	2.784037423	0.018625	0.985139911	NA	brown	-0.036842797	0.646876645		AT1G74850.1	PTAC2	plastid transcriptionally active 2	NA
Sapur.005G084400.2	0.028624143	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	0.025814703	0.748266456	GO:0006468,GO:0004672	AT4G35780.1		ACT-like protein tyrosine kinase family protein	tyrosine kinase family protein
Sapur.018G043800.6	0.025147923	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	0.018637658	0.816784116		AT4G32820.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR domain protein
Sapur.008G044200.2	0.021964599	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	0.002666115	0.973563397	GO:0051536,GO:0003824,GO:0008173,GO:0006364,GO:0005737	AT2G39670.1		Radical SAM superfamily protein	ribosomal RNA large subunit methyltransferase N
Sapur.009G067500.4	0.022074124	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.141729488	0.076623342	GO:0006629	AT5G14930.2	SAG101	senescence-associated gene 101	lipase
Sapur.003G169000.4	0.018209939	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.016056727	0.841797072	GO:0006468,GO:0004672	AT5G56460.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.017G029000.1	0.018187765	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.020342024	0.800365436	GO:0016021	AT5G35730.1		EXS (ERD1/XPR1/SYG1) family protein	small molecule transporter, putative
Sapur.004G057100.2	0.017828572	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.018053186	0.822433287	GO:0016157,GO:0005985	AT1G73370.1	ATSUS6,SUS6	sucrose synthase 6	sucrose synthase
Sapur.006G087600.3	0.017640885	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.0181084	0.82189923	GO:0030170,GO:0009058,GO:0008483,GO:0006520	AT2G30970.2	ASP1	aspartate aminotransferase 1	aspartate aminotransferase
Sapur.006G147300.2	0.019992137	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.035924095	0.655109856		AT3G58700.1		Ribosomal L5P family protein	NA
Sapur.018G119000.1	0.017640885	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.047045965	0.558481995		AT4G27690.1	VPS26B	vacuolar protein sorting 26B	vacuolar protein sorting-associated protein
Sapur.001G135300.1	0.020155691	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.034607615	0.6669804					NA
Sapur.016G250400.1	0.017187763	0.053717485	2.904823276	0.018493	0.98524595	NA	brown	-0.022104473	0.783478692	GO:0043087	AT3G14910.1			Rab3 GTPase-activating protein non-catalytic subunit, putative
Sapur.008G119000.1	0.019329767	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.040561716	0.613992169	GO:0071805,GO:0016020,GO:0015079	AT1G70300.1	KUP6	K+ uptake permease 6	high-affinity potassium transporter protein, putative
Sapur.004G132000.1	0.015676336	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.030860057	0.701217972	GO:0016780,GO:0016020,GO:0008654	AT1G68000.1	ATPIS,ATPIS1,PIS1	phosphatidylinositol synthase 1	CDP-diacylglycerol-inositol 3-phosphatidyltransferase
Sapur.010G123400.1	0.016537851	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.027932366	0.728394124	GO:0043565,GO:0006355,GO:0003700	AT1G69310.1	ATWRKY57,WRKY57	WRKY DNA-binding protein 57	WRKY transcription factor, putative
Sapur.003G114600.1	0.016649834	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.041631409	0.60467031		AT5G44710.1			ribosomal subunit S27
Sapur.013G054600.1	0.016161459	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.036776592	0.647468543		AT1G64770.1	NDF2,NDH45	NDH-dependent cyclic electron flow 1	NA
Sapur.013G028200.2	0.016206094	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.081608864	0.309590942	GO:0055085,GO:0016021	AT5G27360.1	SFP2	Major facilitator superfamily protein	sugar porter (SP) family MFS transporter
Sapur.012G073300.1	0.016840782	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.045413426	0.572228213	GO:0005524,GO:0003676,GO:0031204,GO:0008565	AT1G20960.2	emb1507	U5 small nuclear ribonucleoprotein helicase, putative	RNA helicase
Sapur.014G127700.2	0.017762838	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	0.005592399	0.944581172		AT1G05060.1			hypothetical protein
Sapur.012G000300.7	0.015866223	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.03367695	0.675422411		AT3G49590.3		Autophagy-related protein 13	autophagy-related protein
Sapur.001G165100.1	0.016452512	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.050615199	0.528994069	GO:0008152,GO:0003824	AT3G16170.1		AMP-dependent synthetase and ligase family protein	long-chain-fatty-acid-CoA ligase
Sapur.007G076100.1	0.015708968	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.03499378	0.663489665		AT2G21940.4	ATSK1,SK1	shikimate kinase 1	shikimate kinase
Sapur.013G141500.6	0.015349114	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.036132092	0.653242148		AT5G58320.2		Kinase interacting (KIP1-like) family protein	kinase interacting (KIP1-like) family protein
Sapur.016G099700.2	0.016752097	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.055043867	0.493529722	GO:0030132,GO:0030130,GO:0016192,GO:0006886,GO:0005198	AT3G51890.1		Clathrin light chain protein	clathrin light chain
Sapur.010G165900.3	0.016505156	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.05881906	0.464324153	GO:0019898,GO:0015979,GO:0009654,GO:0009523,GO:0005509	AT3G55330.1	PPL1	PsbP-like protein 1	thylakoid lumenal 25.6 kDa protein, putative
Sapur.016G299400.2	0.01723007	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.421685503	3.79E-08	GO:0043139,GO:0003697	AT1G30680.1		toprim domain-containing protein	DNA primase
Sapur.011G008500.4	0.015676162	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.056232252	0.48423248		AT1G62310.1		transcription factor jumonji (jmjC) domain-containing protein	lysine-specific demethylase 3A-B, putative
Sapur.15WG149700.3	0.014682578	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.042566126	0.59657657		AT5G52300.1	LTI65,RD29B	CAP160 protein	Low-temperature-induced protein, putative
Sapur.010G195700.3	0.014476493	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.053633855	0.504682437	GO:0006887,GO:0000145	AT5G03540.1	ATEXO70A1,EXO70A1	exocyst subunit exo70 family protein A1	exocyst subunit EXO70
Sapur.005G048600.4	0.017380362	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.075055914	0.350174282	GO:0016624,GO:0008152	AT5G09300.1		Thiamin diphosphate-binding fold (THDP-binding) superfamily protein	2-oxoisovalerate dehydrogenase alpha subunit, putative
Sapur.018G097400.3	0.014745053	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.300250459	0.000133128	GO:0055085,GO:0016020,GO:0006821,GO:0005247	AT5G33280.1		Voltage-gated chloride channel family protein	chloride channel ClC protein, putative
Sapur.006G005300.2	0.014010418	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.048158713	0.549204503	GO:0009058,GO:0003824	AT2G32260.1	ATCCT1,CCT1	phosphorylcholine cytidylyltransferase	choline-phosphate cytidylyltransferase
Sapur.003G057200.1	0.0140044	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.048089215	0.549781733	GO:0003824,GO:0006470,GO:0004722	AT2G35350.1	PLL1	poltergeist like 1	protein phosphatase 2C
Sapur.013G002900.1	0.014727222	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.085588434	0.286510781		AT1G28200.1	FIP1	FH interacting protein 1	GLABRA 2 expression modulator, putative
Sapur.005G114500.1	0.012922672	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.06570763	0.413574696					hypothetical protein
Sapur.013G052200.1	0.013594852	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.068833196	0.391664935		AT3G03810.1	EDA30	O-fucosyltransferase family protein	auxin-independent growth promoter protein
Sapur.001G144100.1	0.016052245	0.053717484	2.904823276	0.018493	0.98524595	NA	brown	-0.083916554	0.29606304	GO:0007031,GO:0005777,GO:0005524,GO:0042623,GO:0006625,GO:0005778	AT5G08470.1	PEX1	peroxisome 1	peroxisome biogenesis factor 1
Sapur.005G173800.2	0.02867901	0.051864895	2.904822183	0.017855	0.985754722	NA	brown	-0.011476295	0.886564112	GO:0016301,GO:0008152,GO:0005524	AT1G03030.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.016G123000.1	0.025323293	0.051864895	2.904822183	0.017855	0.985754722	NA	brown	-0.027245219	0.734823314					NA
Sapur.013G039700.2	0.023542955	0.051864895	2.904822183	0.017855	0.985754722	NA	brown	-0.035569932	0.658294983		AT1G54460.1		TPX2 (targeting protein for Xklp2) protein family	targeting protein for Xklp2 protein
Sapur.011G107700.2	0.022347928	0.051864895	2.904822183	0.017855	0.985754722	NA	brown	-0.041863195	0.602658729	GO:0055085,GO:0016021	AT1G76520.2		Auxin efflux carrier family protein	auxin efflux carrier family protein
Sapur.002G154500.8	0.024423984	-0.041767708	2.415108448	-0.01729	0.986201801	NA	brown	-0.106919253	0.182593296		AT1G02960.2			hypothetical protein
Sapur.002G092100.6	0.012049728	0.047961395	2.904823455	0.016511	0.986826766	NA	brown	-0.088835877	0.268551501	GO:0016020	AT1G58520.1	RXW8	lipases;hydrolases, acting on ester bonds	lipase/hydrolase
Sapur.018G076400.2	0.022797777	0.045407439	2.77235351	0.016379	0.986932303	NA	brown	-0.059549503	0.458785398	GO:0050662,GO:0003824	AT2G23910.1		NAD(P)-binding Rossmann-fold superfamily protein	cinnamoyl-CoA reductase
Sapur.002G128500.2	0.050281114	0.024297126	1.548228629	0.015694	0.987478912	NA	brown	-0.060993963	0.447941183		AT1G01770.1			propionyl-CoA carboxylase, putative
Sapur.008G012000.1	0.03555561	-0.029426488	1.884174535	-0.01562	0.987539378	NA	brown	-0.168029452	0.035416971	GO:0051082,GO:0031072	AT5G22060.1	ATJ2,J2	DNAJ homologue 2	chaperone protein DnaJ
Sapur.014G049300.3	0.023900332	-0.041762901	2.752765769	-0.01517	0.987895557	NA	brown	-0.132661124	0.097664142		AT2G45270.1	GCP1	glycoprotease 1	O-sialoglycoprotein endopeptidase, putative
Sapur.017G045900.2	0.043581466	0.026525963	1.852558939	0.014319	0.988575838	NA	brown	-0.050296216	0.531597139	GO:0034314,GO:0030041,GO:0015629,GO:0005885	AT4G14147.1	ARPC4	protein binding	actin-related protein 2/3 complex subunit 4
Sapur.15WG111700.5	0.032867694	0.028741779	2.095059171	0.013719	0.989054294	NA	brown	-0.065396218	0.415796316		AT5G63440.3		Protein of unknown function (DUF167)	plant/MLE2-7 protein
Sapur.004G143300.5	0.031398469	0.028742203	2.104723892	0.013656	0.989104391	NA	brown	-0.0815184	0.310129359		AT1G08200.1	AXS2	UDP-D-apiose/UDP-D-xylose synthase 2	UDP-D-apiose/UDP-D-xylose synthase
Sapur.001G060400.2	0.028457732	0.028743105	2.125797973	0.013521	0.98921206	NA	brown	-0.115365221	0.150213079					hypothetical protein
Sapur.001G063900.1	0.029734661	0.028751479	2.368062791	0.012141	0.990312842	NA	brown	-0.063155237	0.43198813		AT5G51180.2		alpha/beta-Hydrolases superfamily protein	serine esterase family protein
Sapur.006G209400.1	0.045320254	-0.023215617	2.029486509	-0.01144	0.990873071	NA	brown	-0.058050134	0.470194311	GO:0016787,GO:0005524,GO:0003677	AT5G11170.1		DEAD/DEAH box RNA helicase family protein	DEAD-box ATP-dependent RNA helicase
Sapur.003G020500.1	0.011131465	0.033182656	2.904823918	0.011423	0.990885729	NA	brown	-0.103290009	0.197981389	GO:0003824,GO:0006470,GO:0004722	AT1G72770.3	HAB1	homology to ABI1	protein phosphatase 2C
Sapur.006G181300.2	0.012996108	0.033182656	2.904823918	0.011423	0.990885729	NA	brown	-0.191031956	0.016547523	GO:0016020	AT5G21920.1	ATYLMG2,YLMG2	YGGT family protein	YGGT family protein
Sapur.008G007400.2	0.013030941	0.033182656	2.904823918	0.011423	0.990885729	NA	brown	-0.104022976	0.194800246	GO:0005515	AT5G06600.1	UBP12	ubiquitin-specific protease 12	ubiquitin carboxyl-terminal hydrolase
Sapur.006G133100.2	0.037782662	-0.023206018	2.066124028	-0.01123	0.991038614	NA	brown	-0.11646894	0.146324199		AT4G13270.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.002G024000.1	0.037312442	-0.023205365	2.068693024	-0.01122	0.991049995	NA	brown	-0.104524038	0.192647063		AT1G75400.1		RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.010G125900.5	0.022337797	0.030966428	2.777151243	0.01115	0.991103429	NA	brown	-0.048817514	0.543747491		AT1G26640.1		Amino acid kinase family protein	amino acid kinase family protein
Sapur.010G107600.1	0.021413285	0.030966604	2.792610943	0.011089	0.991152628	NA	brown	-0.071383339	0.374316374	GO:0016773	AT2G03890.1	ATPI4K GAMMA 7.PI4K GAM	phosphoinositide 4-kinase gamma 7	phosphatidylinositol 3- and 4-kinase
Sapur.018G048400.6	0.033231383	-0.023148731	2.338748785	-0.0099	0.992102737	NA	brown	-0.061840741	0.441651696	GO:0009432,GO:0006281,GO:0005524,GO:0003697	AT2G19490.1		recA DNA recombination family protein	DNA repair protein RecA
Sapur.004G081000.2	0.050073331	-0.024973145	2.528309973	-0.00988	0.992119098	NA	brown	-0.029394079	0.714781077					NA
Sapur.001G057600.2	0.048658824	-0.024972281	2.534654382	-0.00985	0.992139096	NA	brown	-0.043914983	0.584983726	GO:0006221,GO:0003883	AT1G30820.1		CTP synthase family protein	CTP synthase
Sapur.003G122300.5	0.030743401	-0.021292485	2.35267254	-0.00905	0.992778972	NA	brown	-0.106512245	0.184273955		AT5G13220.1	JAS1,JAZ10,TIFY9	jasmonate-zim-domain protein 10	ZIM motif protein
Sapur.016G145900.1	0.029717509	-0.021291004	2.361651025	-0.00902	0.992806925	NA	brown	-0.088741742	0.269061071	GO:0003676	AT3G51950.2		Zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	nucleic acid-binding protein, putative
Sapur.010G191900.8	0.028753553	-0.021289571	2.37043934	-0.00898	0.992834075	NA	brown	-0.114117458	0.15470291	GO:0055085,GO:0016021	AT2G16980.2		Major facilitator superfamily protein	hippocampus abundant transcript protein, putative
Sapur.013G080100.2	0.041164379	-0.023113255	2.578924658	-0.00896	0.992849166	NA	brown	-0.035351464	0.660262822	GO:0055085,GO:0016020	AT5G12080.2	ATMSL10,MSL10	mechanosensitive channel of small conductance-like 10	mechanosensitive ion channel domain protein, putative
Sapur.001G164800.4	0.025165507	-0.021283806	2.406875004	-0.00884	0.992944462	NA	brown	-0.399180318	2.23E-07		AT4G29100.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor, putative
Sapur.002G164000.1	0.036654375	-0.023108734	2.615620224	-0.00883	0.992950864	NA	brown	-0.066897456	0.405150779	GO:0006468,GO:0004672	AT4G02010.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.010G163600.2	0.024608205	-0.021282859	2.413033644	-0.00882	0.992962782	NA	brown	-0.12725527	0.112235226	GO:0016597,GO:0008152	AT2G39570.1		ACT domain-containing protein	ACT domain protein
Sapur.002G181000.1	0.032432266	-0.021251864	2.647620259	-0.00803	0.993595625	NA	brown	-0.104831229	0.191335585	GO:0016818,GO:0008270,GO:0003676,GO:0016788	AT1G48360.2		zinc ion binding;nucleic acid binding;hydrolases, acting on acid anhydrides, in phosphorus-containing anhydrides	fanconi-associated nuclease-like protein
Sapur.T190000.1	0.040554958	-0.02307934	2.904822183	-0.00795	0.993660729	NA	brown	-0.035132181	0.662240341	GO:0008270	AT1G48570.1		zinc finger (Ran-binding) family protein	Zn-finger in Ran-binding protein, putative
Sapur.013G070200.2	0.034998114	-0.02307934	2.904822183	-0.00795	0.993660729	NA	brown	-0.066651165	0.406886121		AT3G28910.1	ATMYB30,MYB30	myb domain protein 30	R2R3-MYB transcription factor, putative
Sapur.019G039000.3	0.028312057	-0.021246807	2.69342129	-0.00789	0.993706026	NA	brown	-0.096996409	0.226854512	GO:0016020,GO:0015171,GO:0003333	AT3G03720.1	CAT4	cationic amino acid transporter 4	NA
Sapur.013G126900.1	0.027960028	-0.021246347	2.697716621	-0.00788	0.993716183	NA	brown	-0.076927309	0.338257563		AT2G14830.1		Regulator of Vps4 activity in the MVB pathway protein	regulator of Vps4 activity in the MVB pathway protein
Sapur.016G123700.4	0.027658384	-0.021245949	2.70145119	-0.00786	0.993724988	NA	brown	-0.100308983	0.211307067	GO:0005515	AT2G44430.1		DNA-binding bromodomain-containing protein	bromodomain protein
Sapur.005G110000.2	0.027271622	-0.021245433	2.70631465	-0.00785	0.993736416	NA	brown	-0.096940737	0.227122531		AT4G36970.1		Remorin family protein	remorin
Sapur.014G004900.4	0.027105966	-0.021245211	2.70842414	-0.00784	0.99374136	NA	brown	-0.089676622	0.264029522	GO:0005515	AT1G44910.1	ATPRP40A,PRP40A	pre-mRNA-processing protein 40A	FF domain protein
Sapur.009G124500.2	0.026560042	-0.021244469	2.715491651	-0.00782	0.993757867	NA	brown	-0.108410838	0.176530267	GO:0005525	AT4G35860.1	ATGB2.ATRAB2C.ATRABB1E	GTP-binding 2	Ras small GTPase family Ras protein
Sapur.002G157500.1	0.023189866	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.070086478	0.383079297	GO:0032259,GO:0008168	AT4G02405.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	leucine carboxyl methyltransferase
Sapur.018G053800.3	0.023327466	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.069189664	0.389211252	GO:0016790,GO:0006633	AT1G08510.1	FATB	fatty acyl-ACP thioesterases B	acyl-ACP thioesterase B
Sapur.009G038700.2	0.024993092	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.088062602	0.272756841	GO:0016887,GO:0005524,GO:0016020	AT3G21090.1		ABC-2 type transporter family protein	white-brown-complex ABC transporter family protein
Sapur.008G035200.1	0.023782877	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.081147683	0.312342159	GO:0005515,GO:0000160	AT5G02810.1	APRR7,PRR7	pseudo-response regulator 7	two-component response regulator-like PRR73 protein
Sapur.006G207800.3	0.024972983	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.081608864	0.309590942	GO:0006457,GO:0003755,GO:0000413	AT4G32420.1		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.001G187500.2	0.024496166	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.113693096	0.156252676		AT5G49820.1	EMB1879,RUS6	Protein of unknown function, DUF647	DUF647 domain protein
Sapur.001G183100.1	0.024896141	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.061867584	0.441453141					NA
Sapur.008G018100.1	0.024083084	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.076190894	0.342915801		AT5G04550.1		Protein of unknown function (DUF668)	plant/T32M21-140 protein
Sapur.004G088700.2	0.026021949	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.067216155	0.402911776	GO:0055114,GO:0016491,GO:0051536,GO:0020037	AT2G15620.1	ATHNIR,NIR,NIR1	nitrite reductase 1	ferredoxin-nitrite reductase
Sapur.002G082300.3	0.028299979	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.066873694	0.405318015	GO:0010181,GO:0055114,GO:0016638	AT5G49970.1	ATPPOX,PDX3,PPOX	pyridoxin (pyrodoxamine) 5\'-phosphate oxidase	pyridoxamine 5'-phosphate oxidase
Sapur.002G161200.3	0.038218251	-0.02122675	2.904823276	-0.00731	0.994169578	NA	brown	-0.01034166	0.897714866	GO:0006420,GO:0005737,GO:0005524,GO:0004814,GO:0000166	AT4G26300.1	emb1027	Arginyl-tRNA synthetase, class Ic	arginyl-tRNA synthetase
Sapur.016G133700.1	0.041024673	0.012281821	1.699458714	0.007227	0.994233817	NA	brown	-0.06291224	0.433765333		AT5G59410.1		Rab5-interacting family protein	Rab5-interacting protein
Sapur.006G216600.1	0.038016774	0.014265342	2.062223267	0.006917	0.994480711	NA	brown	-0.087011438	0.27854464		AT1G13940.1		Plant protein of unknown function (DUF863)	hypothetical protein
Sapur.003G028500.1	0.033831686	0.01427141	2.086360985	0.00684	0.994542244	NA	brown	-0.195365654	0.014204935					hypothetical protein
Sapur.016G279600.2	0.031835542	0.01427454	2.099162176	0.0068	0.994574337	NA	brown	-0.091256519	0.255673311					NA
Sapur.001G009300.3	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942		AT1G51110.1		Plastid-lipid associated protein PAP / fibrillin family protein	plastid-lipid-associated protein, putative
Sapur.001G020500.2	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942	GO:0005516	AT2G38800.1		Plant calmodulin-binding protein-related	plant calmodulin-binding domain protein
Sapur.001G051600.1	0.01689596	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.10715922	0.181607687		AT5G13270.1	RARE1	Pentatricopeptide repeat (PPR) superfamily protein	NA
Sapur.001G099600.5	0.01370024	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.104765698	0.191614804		AT1G63370.1		Flavin-binding monooxygenase family protein	flavin containing monooxygenase FMO GS-OX protein
Sapur.001G147300.2	0.016200829	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.140923119	0.078331976	GO:0007034	AT2G06530.1	VPS2.1	SNF7 family protein	charged multivesicular body protein 2a
Sapur.001G187500.4	0.017139707	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.064493937	0.42227248		AT5G49820.1	EMB1879,RUS6	Protein of unknown function, DUF647	DUF647 domain protein
Sapur.002G041700.2	0.01636298	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.140373495	0.079514089		AT4G02800.1			hypothetical protein
Sapur.002G056400.2	0.01565997	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.110986343	0.166413222	GO:0006508,GO:0004185	AT5G42240.1	scpl42	serine carboxypeptidase-like 42	serine carboxypeptidase
Sapur.002G062000.1	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942	GO:0055085,GO:0016020,GO:0006810,GO:0015171,GO:0003333	AT2G01170.1	BAT1	bidirectional amino acid transporter 1	amino acid permease
Sapur.002G125700.2	0.0162402	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.085084984	0.289365288	GO:0016559,GO:0005779	AT2G45740.2	PEX11D	peroxin 11D	peroxisomal biogenesis factor 11
Sapur.003G002900.1	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.080726832	0.314866659		AT1G33980.1	ATUPF3,UPF3	Smg-4/UPF3 family protein	regulator of nonsense transcripts protein 3A, putative
Sapur.003G161700.2	0.014886943	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.108950416	0.174373986	GO:0005515	AT3G57980.1		DNA-binding bromodomain-containing protein	DNA-binding bromodomain protein
Sapur.004G007900.3	0.018711201	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.140855828	0.078475937	GO:0016020,GO:0008378,GO:0006486	AT1G05170.2		Galactosyltransferase family protein	beta-1%2C3-galactosyltransferase, putative
Sapur.004G038900.1	0.018828819	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.13971929	0.08093981		AT4G18593.1		dual specificity protein phosphatase-related	dual specificity protein phosphatase
Sapur.004G043500.2	0.015152775	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.109667403	0.171538952	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G23535.1		KOW domain-containing protein	ribosomal protein L24
Sapur.004G061600.3	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942		AT5G37690.1		SGNH hydrolase-type esterase superfamily protein	GDSL esterase/lipase
Sapur.004G082900.1	0.015743222	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.111059283	0.166133122		AT1G43760.1		DNAse I-like superfamily protein	NA
Sapur.004G126100.1	0.016905521	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.140559085	0.079113334		AT4G34830.1	MRL1	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.005G015700.3	0.01699377	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.11334257	0.157541566	GO:0005515	AT5G27030.1	TPR3	TOPLESS-related 3	topless-related protein
Sapur.005G069900.2	0.015743222	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.111059283	0.166133122		AT5G08350.1		GRAM domain-containing protein / ABA-responsive protein-related	PH-GRAM-GEM domain protein
Sapur.005G079500.4	0.016746437	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.113335126	0.157569023	GO:0005634	AT1G20610.1	CYCB2;3	Cyclin B2;3	cyclin B2
Sapur.005G135000.1	0.016066679	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.141288439	0.077554124	GO:0005515	AT2G17900.1	SDG37	SET domain group 37	histone-lysine N-methyltransferase ASHR1
Sapur.006G155200.1	0.017977277	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.105921399	0.186733877	GO:0005515,GO:0006468,GO:0004672	AT3G46920.1		Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain	tyrosine kinase domain protein
Sapur.006G189200.2	0.017910229	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.141909329	0.076246407	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT4G26150.1	CGA1,GATA22	cytokinin-responsive gata factor 1	GATA zinc finger protein
Sapur.006G196200.1	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT2G25790.1		Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.006G200000.4	0.01560465	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.141668786	0.076750909		AT4G32730.2	ATMYB3R-1.ATMYB3R1.MY	Homeodomain-like protein	Myb transcription factor
Sapur.006G217600.2	0.016302585	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.112511804	0.160628137	GO:0043565,GO:0006355,GO:0003700	AT1G80840.1	ATWRKY40,WRKY40	WRKY DNA-binding protein 40	WRKY transcription factor
Sapur.007G102300.1	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942		AT5G09520.1		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative
Sapur.007G103400.3	0.015946499	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.111674679	0.163783888		AT4G33625.1			COPI associated protein
Sapur.008G030400.4	0.021198105	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.135101632	0.091596671	GO:0009073,GO:0004107	AT1G48850.1	EMB1144	chorismate synthase, putative / 5-enolpyruvylshikimate-3-phosphate phospholyase, putative	chorismate synthase
Sapur.008G130800.3	0.015321281	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.063922497	0.426404114	GO:0006355,GO:0005634	AT5G43700.1	ATAUX2-11,IAA4	AUX/IAA transcriptional regulator family protein	indole-3-acetic acid inducible protein
Sapur.009G046800.5	0.01472906	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.108881201	0.174649489	GO:0006355,GO:0003700	AT5G12840.4	ATHAP2A.EMB2220.HAP2A.	nuclear factor Y, subunit A1	CCAAT-binding transcription factor
Sapur.009G070700.3	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016972	AT1G49880.1		Erv1/Alr family protein	FAD-linked sulfhydryl oxidase Alr protein, putative
Sapur.010G115300.1	0.019002027	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.139862023	0.080627008		AT3G06550.3		O-acetyltransferase family protein	Cas1p 10-TM acyl transferase domain protein
Sapur.011G008700.3	0.013532953	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942		AT4G04330.1		Chaperonin-like RbcX protein	RbcX protein
Sapur.012G009200.3	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942		AT4G27700.1		Rhodanese/Cell cycle control phosphatase superfamily protein	rhodanese-like domain protein
Sapur.012G020900.2	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942	GO:0033314,GO:0010212,GO:0006260,GO:0005634	AT5G52950.1			LRR receptor-like kinase PEPR2, putative
Sapur.012G065300.1	0.017139707	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.113693096	0.156252676		AT4G24680.1	MOS1	modifier of snc1	modifier OF SNC1 1, putative
Sapur.012G066400.14	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0004672	AT4G24740.1	AFC2,AME1,FC2	FUS3-complementing gene 2	Serine/Threonine kinase AFC2
Sapur.013G043100.6	0.016836611	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.141845144	0.076380763	GO:0016829,GO:0006520	AT1G08630.4	THA1	threonine aldolase 1	L-allo-threonine aldolase
Sapur.013G115400.2	0.018930546	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.108038452	0.178029846	GO:0005515	AT3G59660.1		C2 domain-containing protein / GRAM domain-containing protein	GRAM domain protein
Sapur.014G093000.1	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942		AT5G14670.1	ARFA1B,ATARFA1B	ADP-ribosylation factor A1B	ADP-ribosylation factor(Arf)/Arf-like (Arl) small GTPase family protein
Sapur.014G093800.1	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942	GO:0045892.GO:0005634.GO:0043968.GO:0043967.GO:0035267.GO:0006338.GO:000628	AT2G47210.1		myb-like transcription factor family protein	DNA methyltransferase 1-associated protein
Sapur.014G095500.3	0.016136294	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.111947836	0.162749112		AT2G47350.2		HIT zinc finger ;PAPA-1-like conserved region	INO80 complex subunit B, putative
Sapur.016G063400.3	0.012282353	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.114085747	0.154818319	GO:0016888	AT3G52390.2		TatD related DNase	deoxyribonuclease TATDN1-like protein
Sapur.016G091800.1	0.022147566	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.115431234	0.149978313					NA
Sapur.016G146000.1	0.01472906	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.108881201	0.174649489	GO:0003676,GO:0046872	AT5G12440.1		CCCH-type zinc fingerfamily protein with RNA-binding domain	zinc finger C-x8-C-x5-C-x3-H type protein, putative
Sapur.016G150600.2	0.016292485	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.141280927	0.077570056	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G59240.1		Ribosomal protein S8e family protein	40S ribosomal protein S8
Sapur.017G002700.1	0.015187171	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.109832681	0.170890301		AT2G31820.1		Ankyrin repeat family protein	ankyrin-like protein
Sapur.017G058900.1	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942	GO:0005524	AT5G20420.1	CHR42	chromatin remodeling 42	NA
Sapur.017G072000.2	0.015321281	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.110170366	0.16957068		AT5G39530.1		Protein of unknown function (DUF1997)	DUF1997 family protein
Sapur.019G062300.1	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942		AT1G43760.1		DNAse I-like superfamily protein	NA
Sapur.019G110100.1	0.016045318	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.141106831	0.077940028	GO:0016021,GO:0012511	AT3G18570.1		Oleosin family protein	oleosin protein
Sapur.15WG005000.1	0.018039382	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.114746599	0.152426615		AT5G53620.2			hypothetical protein
Sapur.15WG106900.4	0.016325699	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.005752765	0.942994639	GO:0016020,GO:0006075,GO:0003843,GO:0000148	AT2G36850.1	ATGSL08.ATGSL8.CHOR.GSL	glucan synthase-like 8	1%2C3-beta-glucan synthase
Sapur.T064500.2	0.015343454	-0.019374104	2.904824395	-0.00667	0.994678445	NA	brown	-0.081608864	0.309590942		AT5G08420.1		RNA-binding KH domain-containing protein	KRR1 small subunit processome component
Sapur.018G108700.1	0.042660772	0.012346061	1.853441671	0.006661	0.994685207	NA	brown	-0.055373128	0.490944336	GO:0006310,GO:0006281,GO:0003910,GO:0003677,GO:0005524	AT5G57160.1	ATLIG4,LIG4	DNA ligase IV	ATP-dependent DNA ligase
Sapur.013G001700.1	0.03772616	-0.015283561	2.312803794	-0.00661	0.994727426	NA	brown	-0.071439856	0.373937298		AT3G05858.1			hypothetical protein
Sapur.016G027500.1	0.011042025	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115376283	0.150173717		AT5G45790.2		Ubiquitin carboxyl-terminal hydrolase family protein	plant organelle RNA recognition domain protein
Sapur.001G000900.2	0.010393365	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115695728	0.149040462		AT4G26410.1		Uncharacterised conserved protein UCP022280	hypothetical protein
Sapur.001G009700.3	0.011558949	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.114951456	0.151690895		AT3G06880.2		Transducin/WD40 repeat-like superfamily protein	ubox-like protein, putative
Sapur.001G016200.2	0.011781475	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0046872,GO:0030001,GO:0000166	AT1G63440.1	HMA5	heavy metal atpase 5	heavy metal P-type ATPase
Sapur.001G041200.1	0.010022524	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0071949	AT3G24200.1		FAD/NAD(P)-binding oxidoreductase family protein	ubiquinone biosynthesis monooxygenase COQ6
Sapur.001G074300.5	0.009772458	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115740333	0.148882736		AT1G64430.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR domain protein
Sapur.001G093300.2	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0006355,GO:0005634,GO:0005524,GO:0032502,GO:0006351	AT4G37740.1	AtGRF2,GRF2	growth-regulating factor 2	NA
Sapur.001G162900.2	0.01003829	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115783338	0.148730788	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT4G32890.1	GATA9	GATA transcription factor 9	GATA transcription factor
Sapur.002G023700.4	0.012360172	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.021570425	0.788585369	GO:0016021	AT1G35180.1		TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain protein, putative
Sapur.002G044100.3	0.010852461	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115531724	0.149621469		AT3G10260.3		Reticulon family protein	reticulon protein
Sapur.002G106600.2	0.011712934	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0006468,GO:0004672	AT1G55200.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	receptor tyrosine kinase
Sapur.002G136500.2	0.011712934	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.114846535	0.152067369		AT1G02270.1		Calcium-binding endonuclease/exonuclease/phosphatase family	calcium-binding endonuclease/exonuclease/phosphatase family protein
Sapur.002G167500.4	0.01210369	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.114218666	0.154335013		AT1G02475.1		Polyketide cyclase/dehydrase and lipid transport superfamily protein	polyketide cyclase/dehydrase and lipid transporter
Sapur.002G189800.3	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0042765,GO:0016255	AT3G07180.1		GPI transamidase component PIG-S-related	phosphatidylinositol-glycan biosynthesis class S protein
Sapur.002G202900.1	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0032259,GO:0008168	AT5G42760.1		Leucine carboxyl methyltransferase	leucine carboxyl methyltransferase
Sapur.003G026700.1	0.01186289	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.114519661	0.15324477	GO:0005515	AT1G49450.1		Transducin/WD40 repeat-like superfamily protein	F-box and WD40 domain protein, putative
Sapur.003G072100.4	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0005089	AT1G31650.1	ATROPGEF14,ROPGEF14	RHO guanyl-nucleotide exchange factor 14	Rop guanine nucleotide exchange factor, putative
Sapur.003G095400.2	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0016491,GO:0006633,GO:0005506	AT4G25700.1	B1.BCH1.BETA-OHASE 1.chy	beta-hydroxylase 1	beta-carotene hydroxylase
Sapur.003G096400.1	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0003676	AT1G63980.2		D111/G-patch domain-containing protein	Pin2-interacting protein x1, putative
Sapur.003G111900.5	0.009879659	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115749337	0.148850914		AT5G51180.2		alpha/beta-Hydrolases superfamily protein	serine esterase family protein
Sapur.003G117500.1	0.011159397	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115228114	0.150701564		AT5G47900.1		Protein of unknown function (DUF1624)	transmembrane protein, putative
Sapur.003G152200.2	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0016787	AT3G55850.1	LAF3,LAF3 ISF1,LAF3 ISF2	Amidohydrolase family	amidohydrolase
Sapur.004G001200.3	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0055114,GO:0009916	AT4G22260.1	IM,IM1	Alternative oxidase family protein	ubiquinol oxidase
Sapur.004G011700.1	0.011649124	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.114798493	0.152239988	GO:0009982,GO:0009451,GO:0003723,GO:0001522	AT4G21770.1		Pseudouridine synthase family protein	RNA pseudouridine synthase
Sapur.004G012100.5	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0005975,GO:0004553	AT4G21760.1	BGLU47	beta-glucosidase 47	NA
Sapur.004G016000.3	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.07302262	0.363417017	GO:0006468,GO:0004672	AT4G05200.1	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	cysteine-rich receptor-like kinase
Sapur.004G034200.3	0.009970499	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.041134674	0.608991308	GO:0048193,GO:0016020,GO:0005515	AT1G28490.2	ATSYP61,OSM1,SYP61	syntaxin of plants 61	syntaxin-61 protein
Sapur.004G051700.2	0.009530349	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942		AT4G25700.1	B1.BCH1.BETA-OHASE 1.chy	beta-hydroxylase 1	beta-carotene hydroxylase
Sapur.004G062300.1	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942		AT1G70750.1		Protein of unknown function, DUF593	zein-binding protein
Sapur.004G115600.2	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0005975,GO:0004553	AT2G16230.1		O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase
Sapur.004G158700.1	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942		AT5G60550.1	ATSNAK1,GRIK2	geminivirus rep interacting kinase 2	calcium/calmodulin-dependent kinase kinase
Sapur.005G000800.2	0.011634165	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.114778505	0.152311849		AT1G09540.1	ATMYB61,MYB61	myb domain protein 61	R2R3-MYB transcription factor, putative
Sapur.005G053700.2	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0005515	AT3G52950.1		CBS / octicosapeptide/Phox/Bemp1 (PB1) domains-containing protein	meiotically up-regulated protein
Sapur.005G063400.2	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0008270,GO:0005515	AT1G15100.1	RHA2A	RING-H2 finger A2A	zinc finger, C3HC4 type (RING finger) protein
Sapur.005G141300.1	0.011052775	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115320782	0.150371276	GO:0006355,GO:0003677	AT1G01720.1	ANAC002,ATAF1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC transcription factor, putative
Sapur.005G142400.3	0.011649124	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.114798493	0.152239988	GO:0005524	AT1G21690.1	EMB1968,RFC4	ATPase family associated with various cellular activities (AAA)	replication factor C subunit 2/4
Sapur.005G162500.2	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT2G32060.2		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	40S ribosomal protein S12
Sapur.005G162800.8	0.012580222	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.113764496	0.155991112	GO:0005515	AT5G08560.1		transducin family protein / WD-40 repeat family protein	transducin/WD40 domain protein
Sapur.005G173300.2	0.011545881	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.114902006	0.151868242	GO:0006355,GO:0005634	AT5G43700.1	ATAUX2-11,IAA4	AUX/IAA transcriptional regulator family protein	indole-3-acetic acid inducible protein
Sapur.005G174700.1	0.010228969	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.081608864	0.309590942	GO:0043565,GO:0006355,GO:0003700	AT2G30590.1	WRKY21	WRKY DNA-binding protein 21	WRKY transcription factor, putative
Sapur.005G178300.2	0.011043891	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.1075461	0.180026907		AT4G14385.1			histone acetyltransferase subunit NuA4
Sapur.006G025200.2	0.011005222	0.018098013	2.904824395	0.00623	0.995028949	NA	brown	-0.115365221	0.150213079	GO:0005634	AT5G06150.1	CYC1BAT,CYCB1;2	Cyclin family protein	cyclin B

Sapur.006G069500.2	0.011206174	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114869942	0.151983321	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	AT5G02370.1		ATP binding microtubule motor family protein		kinesin motor domain protein
Sapur.006G081500.2	0.01655776	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G01510.1	RUSS	Protein of unknown function, DUF647		DUF647 domain protein
Sapur.006G098700.4	0.011637967	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114879715	0.151948238	GO:0005515;GO:0006468;GO:0005524;GO:0004672	AT5G01910.1		Leucine-rich repeat protein kinase family protein		LRR receptor-like kinase
Sapur.006G101900.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0017183	AT5G59630.1		diphthamide synthesis DPH2 family protein		diphthamide biosynthesis enzyme DPH2
Sapur.006G103100.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G60660.1	TK11	TSL kinase interacting protein 1		NPB DNA-binding domain protein, putative
Sapur.006G122300.4	0.011188101	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115220025	0.150796649	GO:0006468;GO:0005524;GO:0004672	AT4G26100.1	CK1;CKL1	casein kinase 1-like protein		casein kinase I-like protein
Sapur.006G129400.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0003244;GO:0016758;GO:0016020	AT5G17170.1	CESA8;CESA9	cellulose synthase A catalytic subunit 6 [UDP-forming] protein, putative		cellulose synthase A catalytic subunit 6 [UDP-forming] protein, putative
Sapur.006G147700.2	0.011005212	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115382121	0.150213079	GO:0003244;GO:0016758;GO:0016020	AT1G54270.1	AtCESA7;CESA7;RSW1	Cellulose synthase family protein		cellulose synthase A catalytic subunit 9 [UDP-forming] protein
Sapur.006G175800.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G07730.1		Ankyrin-repeat family protein		viral ankyrin protein
Sapur.006G179300.3	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT3G22620.1		Rhamnogalacturonase lyase family protein		rhamnogalacturonase lyase
Sapur.006G180900.2	0.010921843	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.143610377	0.072567512	GO:0044237	AT3G05830.4		N-acyl-PE/CoA transferase-like superfamily protein		methylthioribose-1-phosphate isomerase
Sapur.006G207800.5	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115108424	0.150424477	GO:0004671;GO:0003755;GO:0006413	AT3G12420.1		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein		peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.007G025500.5	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0003676	AT4G36690.4	ATU2AF65A	U2 snRNP auxiliary factor, large subunit,N;U2 snRNP auxiliary factor, large subunit,N;U2 splicing factor		U2 snRNP auxiliary factor, large subunit,N;U2 splicing factor
Sapur.007G204000.3	0.018846133	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115405588	0.149767465		AT1G21775.3	GATA24;TIFY28;ZML1	ZIM-like 1		CCT motif protein
Sapur.008G037700.2	0.011200174	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114869942	0.151983321		AT3G26420.1		alpha/beta-hydrolases superfamily protein		alpha/beta fold hydrolase
Sapur.008G086800.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.106245415	0.153323513		AT5G05180.1		Homeodomain-like superfamily protein		transcription factor, putative
Sapur.008G077300.1	0.011294107	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115107846	0.151313044	GO:0007275	AT5G59180.1	CRC	Plant-specific transcription factor YABBY family protein		YABBY-like transcription factor CRABS CLAW-like protein
Sapur.008G082700.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0003824;GO:0006470;GO:0004722	AT5G17060.1		Protein phosphatase 2C family protein		protein phosphatase 2C
Sapur.008G105100.3	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115382121	0.150213079	GO:0003824;GO:0051116;GO:0008272;GO:0055085;GO:0016020;GO:0008271	AST5L;SULTR3;3		sulfate transporter 3.1		sulfate/bicarbonate/oxalate exchanger and transporter sat-1
Sapur.008G146200.7	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT4G02730.1	PLP;PLPA;PLPB;PLPC	PAG1/LOV protein 9		TWIN LOV protein, putative
Sapur.009G051505.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114869942	0.151983321	GO:0005515	AT2G27980.1		Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain		chromodomain helicase DNA-binding protein, putative
Sapur.009G030800.1	0.013260172	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114024224	0.151924405	GO:0006468;GO:0005524;GO:0004672	AT5G58940.1	CRCK1	calmodulin-binding receptor-like cytoplasmic kinase 1		calmodulin-binding receptor-like cytoplasmic kinase
Sapur.009G050200.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G11481.1		basic helix-loop-helix (bHLH)2 DNA-binding superfamily protein		transcription factor bHLH122, putative
Sapur.009G090300.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G11750.2	CLPP6;NCLP1;NCLPP6	CLP protease proteolytic subunit 6		ATP-dependent Clp protease proteolytic subunit
Sapur.009G111600.4	0.011294107	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114869942	0.151983319		AT5G45570.1	ATL6;ATL4;TERP1;LATHCP	ZIM-like 4		expansin-like protein A1
Sapur.010G000500.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0043565;GO:0008270;GO:0006355;GO:0003700	AT5G06740.1	GATA15	GATA transcription factor 15		GATA transcription factor
Sapur.010G028000.9	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0005975;GO:0004650	AT5G05580.1		Pectin lyase-like superfamily protein		polygalacturonase
Sapur.010G043400.2	0.009400556	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115770053	0.149481983		AT1G52580.1		plastid development protein DAG, putative		plastid development protein DAG, putative
Sapur.010G055700.6	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0017069;GO:0000398					NA
Sapur.010G068700.2	0.011975777	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115219049	0.150881116	GO:0006355;GO:0005634	AT4G37030.1	ATAUX2-11;IAA4	AUX/IAA transcriptional regulator family protein		auxin inducible protein IAA3
Sapur.010G079400.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0071805;GO:0016020;GO:0015079	AT5G60160.1		Potassium transporter family protein		potassium transporter
Sapur.010G113600.4	0.00682575	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114869942	0.151931003						iron-sulfur-binding ERF-45 ferredoxin
Sapur.010G140000.3	0.011294107	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115107846	0.151313044		AT3G48480.1		Cysteine proteinases superfamily protein		sentrin/sumo-specific protease, putative
Sapur.010G161700.2	0.009876659	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115749317	0.148802664	GO:0005524	AT2G37262.1	RCA	rubisco activase		rubulose-1%2C5-bisphosphate carboxylase/oxygenase activase
Sapur.010G245900.7	0.011649124	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.014680064	0.855205564	GO:0016020	AT5G46150.1		LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein		LEM3/CDC50 family protein
Sapur.010G255700.3	0.013862791	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0005515;GO:0048544;GO:0006468;GO:0004672	AT5G11461.1		S-locus lectin protein kinase family protein		Serine/Threonine kinase
Sapur.010G257900.2	0.011188415	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115291976	0.15059079		AT2G34460.1		NAD(P)-binding Rossmann-fold superfamily protein		NAD-dependent epimerase/dehydratase family protein
Sapur.010G273800.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0016757	AT5G16900.1		Alg9-like mannosyltransferase family		alpha-1%2C2-mannosyltransferase ALG9
Sapur.010G285000.2	0.012142124	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114869942	0.154818319		AT4G29320.1		SWI/SNF-or-Chromodomain binding protein family protein		zinc ion-binding protein
Sapur.010G319300.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G47780.1	EMB3611;MEE22	maternal effect embryo arrest 22		EMB3611/MEE22 protein, putative
Sapur.010G328600.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0005515;GO:0016818;GO:0008270;GO:0003676;GO:0008381;GO:0006281;GO:0005634	AT5G07400.1		forkhead-associated domain-containing protein / FHA domain-containing protein		tyrosyl-DNA phosphodiesterase
Sapur.012G070000.1	0.012676308	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115764615	0.148867602	GO:0006355;GO:0003677	AT5G12260.1	ANAC007;EMB2749;NAC007	NAC 007		NAC transcription factor
Sapur.012G083300.3	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G57760.1		O-Glycosyl hydrolases family 17 protein		hydrolyzing O-glycosyl compounds hydrolase, putative
Sapur.013G039500.1	0.010849939	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115381542	0.150142305		AT5G09030.1	NF-YB4	nuclear factor Y, subunit B4		nuclear transcription factor protein
Sapur.013G083700.1	0.011541884	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114869006	0.151682042	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	AT5G27561.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein		kinesin motor domain protein
Sapur.013G069800.1	0.009400556	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115372053	0.149481983		AT5G35405.1		Protein of unknown function (DUF784)		NA
Sapur.013G098700.14	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT3G10840.1		alpha/beta-Hydrolases superfamily protein		alpha/beta hydrolase, putative
Sapur.014G088400.2	0.013399904	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G01060.3	LHY;LHY1	Homeodomain-like superfamily protein		late elongated hypocotyl and circadian clock associated-like protein
Sapur.014G091400.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G27460.1		O-Glycosyl hydrolases family 17 protein		NA
Sapur.014G129000.4	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT2G37570.2				rice genome annotation project protein, putative
Sapur.014G132800.3	0.010999636	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.113195656	0.158221001	GO:0043039;GO:0016878;GO:0005524;GO:0006418;GO:0004812;GO:0000166	AT4G08421.1	EMB2761	threonyl-tRNA synthetase, putative / threonine--tRNA ligase, putative		threonyl-tRNA synthetase/threonine-tRNA ligase, putative
Sapur.015G037000.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0005509;GO:0004185	AT5G15120.1	scpl46	serine carboxypeptidase-like 18		serine carboxypeptidase-like 18
Sapur.015G050000.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT4G31830.1		Protein of unknown function, DUF642		transmembrane protein, putative
Sapur.015G087200.2	0.010519677	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G25791.1		thylakoid lumen 15.4-kDa protein		thylakoid lumen 15.4-kDa protein, putative
Sapur.015G096500.5	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G37680.1				vacuolar import and degradation protein
Sapur.015G098200.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G38650.1		Uncharacterized protein family (UPF0497)		CASP-like protein D2Q08T4400
Sapur.015G129000.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G59770.1		Protein-tyrosine phosphatase-like, PTPLA		tyrosine phosphatase-like protein PTPLB protein, putative
Sapur.016G142700.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0016021;GO:0015693;GO:0015295	AT5G34470.1		Protein of unknown function (DUF803)		Non-imprinted in prader-willi/angelman syndrome region protein, putative
Sapur.016G168400.2	0.010451254	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115729935	0.148921509	GO:0005885;GO:0016020	AT5G64500.1		Major facilitator superfamily protein		NA
Sapur.016G173700.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115092516	0.059181848	GO:0006508;GO:0004185	AT5G35450.1	scpl18	serine carboxypeptidase-like 18		serine carboxypeptidase, putative
Sapur.016G203800.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0006412;GO:0005840;GO:0005622;GO:0003735	AT5G40650.1	RPL27	ribosomal protein L27 family protein		50S ribosomal protein L27
Sapur.016G261000.5	0.01169444	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114728667	0.152490423	GO:0016491;GO:0008152	AT5G54190.1	PORA	protochlorophyllide oxidoreductase A		NADPH-protochlorophyllide oxidoreductase
Sapur.016G278300.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT4G15120.1				hypothetical protein
Sapur.016G287100.1	0.01107595	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115274554	0.150153073	GO:0070184	AT5G44540.1	VPS2.2	SNF7 family protein		charged multivesicular body protein
Sapur.016G288200.3	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0016787;GO:0008378;GO:0006486	AT5G23230.1		Glycosyltransferase family protein		beta-1%2C3-galactosyltransferase, putative
Sapur.016G290400.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0006508;GO:0004252	AT5G23960.1	AT5BT3.3;5BT3.3	Subtilase family protein		subtilisin-like protease, putative
Sapur.016G306100.2	0.011862809	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114524661	0.15124477	GO:0016491;GO:0009055;GO:0009174	AT5G44030.1	ETFQO	electron transfer flavoprotein ubiquinone oxidoreductase		electron transfer flavoprotein ubiquinone oxidoreductase
Sapur.017G071600.2	0.009947783	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115780113	0.148747181	GO:0016021	AT3G29060.1		EXS (ERD1/PHO1/SPX1) family protein		phosphate transporter PHO1-like protein
Sapur.017G092500.5	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0044237	AT5G38640.1		N-acyl-PE/CoA transferase-like superfamily protein		translation initiation factor 2B, delta subunit%2C putative
Sapur.017G138800.2	0.010946777	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115431541	0.149977224	GO:0016787	AT5G02670.1	atnudt17;NUDT17	nudix hydrolase 17		nudix hydrolase
Sapur.018G031400.3	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT4G32330.1		TPX2 (targeting protein for Xklp2) protein family		targeting protein for Xklp2 protein
Sapur.018G048700.1	0.01006754	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.015631176	0.846937207		AT5G67520.1	NDL1	N-MYC downregulated-like 1		pollen specific protein SF21, putative
Sapur.018G060900.2	0.011051543	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115294919	0.150463403	GO:003676;GO:0006414;GO:0005622;GO:0003746	AT4G29060.1	emb2726	elongation factor Ts family protein		elongation factor Ts protein
Sapur.018G098500.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT4G28060.1				67.1 protein short-form protein, putative
Sapur.019G018500.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.015718223	0.845089993	GO:0005515;GO:0006468;GO:0004672	AT5G14840.2		Leucine-rich repeat transmembrane protein kinase		NA
Sapur.019G075600.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0016021;GO:0006665;GO:0004348	AT5G49600.1		Beta-glucosidase, GBA2 type family protein		NA
Sapur.019G086400.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT5G61600.1				transmembrane protein, putative
Sapur.019G107000.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0005515	AT5G41056.1		F-box/RNI-like superfamily protein		F-box protein
Sapur.019G109700.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0006810;GO:0005515	AT4G34120.1		Nucleoporin interacting component (Nup88/Nic96-like) family protein		nucleoporin interacting component, putative
Sapur.019G072900.1	0.012656334	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.113839493	0.151716725	GO:0016592;GO:0006357;GO:0001104	AT4G20170.1		RNA polymerase II transcription mediator family protein		mediator of RNA polymerase II transcription subunit 17
Sapur.019G128900.2	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0044477;GO:0006138	AT5G17130.1				NA
Sapur.T001300.3	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT4G26980.1		RNI-like superfamily protein		hypothetical protein
Sapur.T032600.1	0.013025212	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.114869006	0.151402381		AT4G14440.1		Calcium-binding EF-hand family protein		NA
Sapur.T053000.3	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT4G40070.1	ARA8;ATPCS1;CAD1;PCS1	phytochelatin synthase 1 (PCS1)		phytochelatin synthase
Sapur.T074100.5	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042		AT4G14640.1		ferredoxin hydrogenase		cytosolic Fe-S-cluster assembly factor nar5 protein
Sapur.T083000.1	0.013144437	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115216798	0.150741936	GO:0016787	AT4G19180.1		GDA1/CD39 nucleoside phosphatase family protein		nucleoside phosphatase family protein
Sapur.T090300.1	0.010228969	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.081608864	0.309509042	GO:0005634;GO:0003677;GO:0005515	AT5G60.61	ATMBD6;MBD9	methyl-CpG-binding domain 9		methyl-CpG-binding domain protein
Sapur.T117400.1	0.012596601	0.018088013	2.904824395	0.00623	0.995829949	NA	brown	-0.115761536	0.148795088						NA
Sapur.016G222500.1	0.084491131	0.0142212	3.325188287	0.006159	0.995825737	NA	brown	-0.045024967	0.575267665		AT5G74860.1				NA
Sapur.004G016000.2	0.084939897	0.014212128	3.329137872	0.006157	0.995825737	NA	brown	-0.081608864	0.309509042	GO:0006468;GO:0004672	AT4G26100.1	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25		cysteine-rich receptor-like kinase
Sapur.016G287000.3	0.035579612	0.014322408	2.332102795	0.006141	0.995809892	NA	brown	-0.071913933	0.362648776		AT4G20180.2	LSD1	LSD1 zinc finger family protein		zinc finger protein LSD1
Sapur.009G020400.2	0.033084873	0.014323074	2.310545886	0.006152	0.995807746	NA	brown	-0.101918225	0.188533692	GO:0005525	AT5G03150.1		Ras-related GTP-binding family protein		Ras small GTPase family Ras protein
Sapur.018G012000.1	0.03169956	0.014324567	2.344651233	0.006109	0.995125382	NA	brown	-0.047859525	0.551764653	GO:0006468;GO:0005524;GO:0004672	AT5G20050.1		Protein kinase superfamily protein		receptor-like kinase, putative
Sapur.009G091000.1	0.030742152	0.014326275	2.331366664	0.006083	0.995146822	NA	brown	-0.076163447	0.34295687						NA
Sapur.001G138400.2	0.046918227	0.014408284	2.051878366	0.006041	0.995179696	NA	brown	-0.067615298	0.40011593		AT5G46800.1	BOU	Mitochondrial substrate carrier family protein		carnitine/acylcarnitine carrier-like protein
Sapur.008G082000.1	0.032663011	0.014229114	2.720678489	0.006247	0.995232118	NA	brown	-0.060052208	0.352388178		AT4G22260.1				hypothetical protein
Sapur.015G084000.1	0.02300787	0.014232604	2.762839661	0.005873	0.995231888	NA	brown	-0.066934381	0.406581313	GO:0009607;GO:0006952	AT1G70890.1	MLP43	MLP-like protein 43		Bet v I allergen family protein
Sapur.014G077300.1	0.023997886	0.014232639	2.762689024	0.005873	0.995234141	NA	brown	-0.051237255	0.529372815		AT5G17750.1		Cytochrome b561/ferric reductase transmembrane with DOMON related domain		dopamine beta-monooxygenase
Sapur.015G183400.1	0.023344488	0.014233629	2.774386274	0.005851	0.995234191	NA	brown	-0.082428644	0.304740904						transmembrane protein, putative
Sapur.003G102900.2	0.025285649	0.014234949	2.788036405	0.005823	0.995235884	NA	brown	-0.101908324	0.203756782	GO:0008152;GO:0003824	AT4G23850.1	LAC54	AMP-dependent synthetase and ligase family protein		long-chain fatty acyl CoA ligase, putative
Sapur.009G132600.3	0.021493394	0.014235006	2.788641984	0.005822	0.995235876	NA	brown	-0.068891419	0.391188889	GO:0032012;GO:0005086	AT4G38200.1		SEC7-like guanine nucleotide exchange family protein		brefeldin A-inhibited guanine nucleotide-exchange protein
Sapur.018G031100.1	0.019958643	0.016237588	2.816116656	0.005766	0.995396946	NA	brown	-0.101113393	0.207649557		AT3MYB38-LATMYB38;LMY	Homeodomain-like protein		Myb-like DNA-binding protein
Sapur.003G115200.16	0.034918904	0.016238535	2.826455518	0.005745	0.995416024	NA	brown	-0.068236182	0.392461582	GO:0005801	AT5G12540.2		Phos-associated domain/Vps26-like/Sorting nexin, C-terminal		phos (PX) domain protein
Sapur.012G014400.1	0.018233271	0.016240702	2.85205386	0.005697	0.995456141	NA	brown	-0.112164538	0.161931676	GO:0005515	AT5G13430.1	ATXS;SDG29;SET29	SET domain group 29		histone-lysine N-methyltransferase ATXS
Sapur.005G039300.1	0.017593834	0.016243583	2.871175236	0.005679	0.995458928	NA	brown	-0.107334744	0.168838074		AT1T4A6-2;T4A6-2		nucleobase ion transmembrane subunit 4A-2		import inner membrane translocase subunit Tim44
Sapur.016G051200.1	0.033007636	0.016245388	2.934832276	0.005593	0.995537814	NA	brown	-0.033434219	0.968560157	GO:0055114;GO:0006457;GO:0051287;GO:0016616;GO:0008152	AT4G45430.2		D-isomer specific 2-hydroxyacid dehydrogenase family protein		D-isomer specific 2-hydroxyacid dehydrogenase-like protein
Sapur.017G135700.1	0.033007636	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.033183003	0.692303557		AT5G44640.4				D3ART-2 domain protein, putative
Sapur.019G164500.1	0.023086596	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.036434311	0.650523198	GO:0007165;GO:0005515;GO:0043531	AT5G63930.2		Disease resistance protein (TIR-NBS-LRR class) family		TIR-NBS-LRR disease resistance-like protein
Sapur.012G232600.3	0.023008326	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.042138652	0.599857698		AT5G28370.1				hypothetical protein
Sapur.006G211600.1	0.023581281	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.063378642	0.419322628		AT5G22150.1		Protein kinase superfamily protein		kinase, putative
Sapur.014G028100.1	0.023154885	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.078341173	0.371252336	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT5G19550.1	CYP82C3	cytochrome P450, family 82, subfamily C, polypeptide 3		NA
Sapur.007G024200.1	0.023008326	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.074577481	0.341098177	GO:0016021	AT5G27271.1		Sulfite exporter TauE/SafE		sulfite exporter TauE/SafE
Sapur.006G108700.3	0.020004841	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.051967637	0.518190593	GO:0004842	AT5G02880.1	UPL4	ubiquitin-protein ligase 4		E3 ubiquitin-protein ligase
Sapur.006G000400.1	0.020004841	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.074457417	0.35417051		AT4G27410.2	IQD12	IQ-domain 12		IQ calmodulin-binding protein family protein
Sapur.013G028300.1	0.021868125	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.075123651	0.349706238	GO:0055114;GO:0020037;GO:0004679;GO:0004601	AT5G05260.1	RC1;RC10A	Peroxidase superfamily protein		cationic peroxidase 60a protein
Sapur.006G088200.2	0.018822981	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.020320747	0.38123237		AT2G04430.1		Major facilitator superfamily protein		UNC93-like protein
Sapur.010G364000.11	0.018855032	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.070476763	0.38042829		AT3G32060.1		TPX2 (targeting protein for Xklp2) protein family		targeting protein for Xklp2 protein
Sapur.006G039300.1	0.018566588	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.056743426	0.480361685		AT5G54270.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein		alpha-amylase inhibitor, lipid transfer (LT) and seed storage (SS) family protein
Sapur.003G029000.2	0.020372223	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.081608864	0.309509042		AT3G19880.1	ATUPR1;UPR3	Smg-4/UPF3 family protein		regulator of nonsense transcripts protein 3A, putative
Sapur.012G009000.2	0.019560586	0.016245387	2.934832276	0.005593	0.995537815	NA	brown	-0.056743426	0.480361685		AT5G27600.1		MIBDAT (membrane bound O-acyl transferase) family protein		membrane bound-O-acyl transferase family protein

Sapur.01BG046700.1	1.96253813	1.80815876	0.34862609	8.05485	7.96E-16	2.10E-15	ppm	0.37463076	1.35E-06						NA
Sapur.00BG085800.1	2.88602336	2.93437274	0.36559763	8.026278	1.00E-15	2.64E-15	ppm	0.36089806	3.43E-06						NA
Sapur.00BG031400.1	381.1778669	0.76999930	0.09916558	7.960512	1.63E-15	4.26E-15	ppm	0.47834056	2.41E-10	GD:0055114,GO:0016491		ATLG15510.1	ATGA3OX1,GA3OX1,GA4	gibberellin 3-oxidase 1	gibberellin 3-beta-hydroxylase
Sapur.01BG094600.1	23.71390233	0.96645087	0.12469283	7.891392	2.99E-15	7.75E-15	ppm	0.47159218	4.58E-10	GO:0015803,GO:0005839,GO:0004298		ATLG79233.2		N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	NA
Sapur.01BG090600.1	3.37316188	2.66852143	0.33956466	7.96787	6.25E-15	1.60E-14	ppm	0.30664467	9.51E-05	GO:0055114		ATLG15731.1		F-box/RNI-like superfamily protein	F-box/FBD/LRR protein
Sapur.00LG168200.1	12.10104387	1.38809961	0.18149314	7.650427	2.00E-14	5.07E-14	ppm	0.37278066	1.52E-06			ATLG17620.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.01BG143400.1	231.6807663	1.12229847	0.14747258	7.609979	2.74E-14	6.90E-14	ppm	0.46320191	8.25E-10	GO:0006468,GO:0005524,GO:0004672		ATLG07192.1	MAPKKK13	mitogen-activated protein kinase kinase kinase 13	Serine/Threonine kinase domain protein
Sapur.01BG088000.1	454.8918867	1.12748182	0.15159027	7.437251	1.05E-13	2.54E-13	ppm	0.36773454	2.16E-06	GO:0005085,GO:0016020		ATLG17681.1	CAX7	calcium exchanger 7	cation/calcium exchanger
Sapur.01TC031900.1	312.895579	0.74339565	0.10145996	7.330884	2.29E-13	5.59E-13	ppm	0.39917084	2.24E-07			ATLG05910.1		cell division cycle protein 48-related / CDC48-related	NA
Sapur.00BG125500.1	24.53679956	1.08609283	0.14950367	7.263934	5.59E-13	9.12E-13	ppm	0.31398215	5.16E-05	GO:0055114		ATLG02600.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	2S albumin/trypsin-inhibitor family protein
Sapur.01BG127300.1	205.5841375	0.97861291	0.13495698	7.254349	4.04E-13	9.77E-13	ppm	0.34191018	1.20E-05			ATLG92830.2		VQ motif-containing protein	DNA-binding WRKY; VQ protein, putative
Sapur.01BG092600.1	1.96956609	2.19197324	0.30360059	7.21655	5.24E-13	1.27E-12	ppm	0.39621925	7.80E-07			ATLG17240.1			NA
Sapur.00BG082800.1	102.6549601	0.62689865	0.08697768	7.207583	5.70E-13	1.37E-12	ppm	0.44076832	7.60E-09	GO:0055114,GO:0020037,GO:0016705,GO:0005506		ATLG46550.1	CYP76C4	cytochrome P450, family 76, subfamily C, polypeptide 4	cytochrome P450 family protein
Sapur.00GB082200.1	1.96808049	1.92208432	0.31233348	7.06998	1.55E-12	3.88E-12	ppm	0.42862324	2.18E-07						transmembrane protein, putative
Sapur.00SG157600.1	9.110436245	1.82021847	0.25829747	7.047241	1.83E-12	4.33E-12	ppm	0.37146587	1.67E-06	GO:0055114,GO:0016491,GO:0055037		ATLG09360.1	LAC14	laccase 14	NA
Sapur.00LG171100.1	16.38750264	1.27402192	0.19298959	6.965515	3.27E-12	7.68E-12	ppm	0.37456812	5.52E-07			ATLG17463.1			hypothetical protein
Sapur.00TG104900.1	5711.132644	0.91653215	0.13179487	6.958603	3.44E-12	8.07E-12	ppm	0.47475901	1.34E-10	GO:0016829,GO:0010333,GO:0008152,GO:0000287		ATLG16745.1	ATTPS03,TPS03	terpene synthase 03	(E)-beta-ocimene synthase
Sapur.00TG031600.1	1.932426819	1.96501503	0.28377991	6.95625	7.08E-12	1.66E-11	ppm	0.46751455	6.67E-10			ATLG16460.1		Protein of unknown function (DUF1640)	coiled-coil protein 9G8
Sapur.00BG092300.1	131.9150562	1.07164291	0.15811297	6.828517	1.59E-11	3.57E-11	ppm	0.39384137	2.36E-07			ATLG08420.1		Lactoylglutathione lyase (GLYoxalase I)/PF10129	hypothetical protein
Sapur.00LG191100.1	2079.039697	0.52005511	0.07617528	6.664608	2.65E-11	6.03E-11	ppm	0.4093719	1.02E-07	GO:0003993		ATLG15510.1		HAD superfamily, subfamily IIIB acid phosphatase	acid phosphatase
Sapur.00LG182400.1	602.0182413	1.05207102	0.09073862	6.501122	8.00E-11	1.82E-10	ppm	0.38230704	1.72E-07			ATLG15120.1	AGP12,ATAGP12	Arabinogalactan protein 12	transmembrane protein, putative
Sapur.00TG017300.1	733.0921928	0.87190411	0.10738493	6.279236	3.40E-10	7.40E-10	ppm	0.43761383	9.94E-09	GO:0055114,GO:0020037,GO:0016705,GO:0005506		ATLG36230.1	CYP84A1,FAH1	ferulic acid 5-hydroxylase 1	coniferyl aldehyde 5-hydroxylase
Sapur.00TG020800.1	83.13845249	0.37572381	0.06052214	5.911147	3.46E-09	7.08E-09	ppm	0.44816026	1.27E-08	GO:0005802,GO:0005768		ATLG14561.1	ATEXO70G1,EXO70G1	exocyst subunit exo70 family protein G1	exocyst complex component
Sapur.01BG055300.1	4.9693625	1.03284228	0.18442458	5.629436	1.81E-08	3.66E-08	ppm	0.3810109	8.53E-07	GO:0007275,GO:0006511,GO:0005634		ATLG58040.1	SINAT2	seven in absentia of Arabidopsis 2	E3 ubiquitin-protein ligase SINA2
Sapur.00TG028100.1	2203.572335	0.67752219	0.13715612	5.16038	2.60E-08	5.42E-08	ppm	-0.64202578	3.30E-10	GO:0016787,GO:0005789		ATLG66680.1	DGL1	dolichyl diphosphooligosaccharide-protein glycosyltransferase 48kDa subunit family protein	dolichyl-diphosphooligosaccharide-protein glycosyltransferase, putative
Sapur.00GG253900.1	77.93437069	0.75275046	0.14213761	5.266555	1.18E-07	2.31E-07	ppm	0.28980896	0.00231771	GO:0006355,GO:0005634		ATLG09560.2	BDL,IAA12	AUX/IAA transcriptional regulator family protein	IAA5, putative
Sapur.01WG137200.1	3640.854754	0.80522334	0.15495321	5.243607	1.58E-07	3.03E-07	ppm	0.32973012	2.48E-05	GO:0004857		ATLG15120.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	NA
Sapur.01BG080900.1	645.0428586	0.60205926	0.11475219	5.11668	2.83E-07	5.45E-07	ppm	0.34185904	9.14E-06			ATLG48900.1			hypothetical protein
Sapur.00BG125200.2	2.395409298	1.01176786	0.19897091	5.061429	4.18E-07	7.94E-07	ppm	0.35203155	6.85E-06			ATLG22600.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	lipid transfer/seed storage/trypsin-alpha amylase inhibitor, putative
Sapur.01WG116800.1	1.04923671	1.29000000	0.25488221	5.031407	4.87E-07	9.26E-07	ppm	0.24386011	0.01691159	GO:0005975,GO:0004553		ATLG07010.1	ATGHB1,CEL1,GHRB1	glycosyl hydrolase 9B1	endo-1,3(2),4-beta-glucanase
Sapur.00GG093000.1	810.1428844	0.23424624	0.04603158	4.960589	6.02E-07	1.14E-06	ppm	0.38947658	4.62E-07	GO:0006468,GO:0006672		ATLG51850.1	CPK13	calcium-dependent protein kinase 13	calcium-dependent kinase
Sapur.01BG064700.1	227.6438073	0.66860163	0.10406788	4.76085	1.67E-06	3.08E-06	ppm	0.32623274	2.71E-05			ATLG79020.1		PLATZ transcription factor	PLATZ transcription factor
Sapur.00BG135400.1	25.50353649	0.62342967	0.14223227	4.383438	1.17E-05	2.07E-05	ppm	0.28794916	0.00025526			ATLG41380.1			
Sapur.00BG100400.1	24.77376133	0.46079742	0.11223016	4.107884	1.22E-05	2.16E-05	ppm	0.31606506	7.52E-05			ATLG02750.1	BR11	BR11 kinase inhibitor 1	hypothetical protein
Sapur.01TG010000.1	190.8289951	0.57785934	0.13485571	4.283749	1.84E-05	3.22E-05	ppm	0.27028184	0.00048863	GO:0045454,GO:0015035,GO:0009055		ATLG28480.1	GRX480,rxe1y9	Thioredoxin superfamily protein	glutaredoxin family protein
Sapur.01BG201200.1	435.2813369	0.56466145	0.14400625	4.126665	3.48E-05	6.01E-05	ppm	0.27763438	0.00244687	GO:0016747		ATLG45040.1		HXXXD-type acyl-transferase family protein	hydroxycinnamoyl Coa shikimate/quinate hydroxycinnamoyl transferase
Sapur.01BG141700.1	383.2178198	0.76325164	0.18449543	4.138809	3.52E-05	6.08E-05	ppm	0.20638836	0.00950435			ATLG10985.1	ATWI-12,SAG20,WI12	senescence associated gene 20	wound-induced protein
Sapur.00BG082800.1	653.2605622	0.22538856	0.05902237	3.818701	0.00014156	0.00022846	ppm	0.26273589	0.00988208			ATLG17030.1		sequence-specific DNA binding transcription factors	transcription factor bHLH148, putative
Sapur.00SG146300.1	40.05569909	0.67763219	0.17751612	3.76038	0.00019656	0.00028126	ppm	0.26889874	0.00707684			ATLG17910.1	ATMYB52,BWS2,MYB52	myb domain protein 52	R2R3-MYB transcription factor, putative
Sapur.01BG147800.1	326.3010749	0.46008519	0.12748959	3.678866	0.00023423	0.00038448	ppm	0.25146249	0.01490024	GO:0006468,GO:0005524,GO:0004672		ATCRK1,CCR3	CRK9,LYK4 related 3		Serine/Threonine kinase-like protein
Sapur.00BG138500.1	69.62257806	0.29144169	0.08527627	3.417202	0.00063461	0.00091758	ppm	0.26129221	0.02848157					Cyclophosphate-dependent phosphodiesterase	cyclophosphate-fatty acyl phosphodiester
Sapur.01GG094600.1	52.56541224	0.42958111	0.13685921	3.139909	0.00169005	0.00261645	ppm	0.22760845	0.0418094			ATLG22810.1		Predicted AT-hook DNA-binding family protein	AT-hook motif nuclear localized protein
Sapur.01BG165100.1	16.78805019	0.47878279	0.15164791	3.11893	0.00172026	0.00266872	ppm	0.19188416	0.03402031						NA
Sapur.00SG193100.1	802.6769954	0.17742182	0.06448968	2.75322	0.00590124	0.00874694	ppm	0.20468781	0.03124882	GO:0016567,GO:0006842		ATPIB8,PIB9	plant U-box 9		spotted leaf protein, putative
Sapur.01BG161500.1	336.4053883	0.15437886	0.07841081	1.96891	0.04884973	0.06430275	ppm	0.15365429	0.05432415			ATMAL5,MLO5	Domain of unknown function (DUF623)	Seven transmembrane MLO family protein	glycosylphosphatidylinositol-anchored lipid protein
Sapur.01BG075300.1	574.6387238	0.11265956	0.07818239	1.568853	0.11682225	0.15255572	ppm	0.11854782	0.13928386			ATWRTL,WTF1	Ubiquitin carboxyl-terminal hydrolase family protein		plant organelle RNA recognition domain protein
Sapur.01BG125700.1	65.02127575	0.09275289	0.15438035	1.236245	0.21618478	0.26837947	ppm	0.07865349	0.32689616			ATLG19180.1			hypothetical protein
Sapur.00GG097000.6	0.06427246	0.12866139	2.90483276	0.044302	0.96457126	NA	ppm	0.42450365	3.14E-08	GO:0043169,GO:0005975,GO:0003824		ATLG76130.1	AMY2,ATAMY2	alpha-amylase like 2	alpha-amylase
Sapur.01GG003300.1	10773.68226	0.95985264	2.34585051	38.62126	0	0	ppm	0.76993334	4.77E-32	GO:0055114,GO:0016491,GO:0005507		ATLG55570.1	sks12	SKS: similar 12	L-ascorbate oxidase-like protein
Sapur.00GG082000.1	5853.287878	0.69149609	2.2574154	37.68883	0	0	ppm	0.73431320	7.22E-28			ATLG21660.1	FLA34	FASCILIN-like arabinogalactan protein 14 precursor	fasciclin-like arabinogalactan protein
Sapur.01BG042100.1	474.9743915	0.38738433	0.15132367	52.81603	0	0	ppm	0.81579301	1.08E-28	GO:0005515,GO:0006468,GO:0004672		ATLG24715.1			tyrosine kinase family protein
Sapur.00GG059400.1	874.0388524	1.69035784	0.11771868	44.6172	0	0	ppm	0.78909057	1.81E-33			ATLG34920.1	EDA18	RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.01GG073800.1	3206.717814	5.18816364	0.12916405	40.16726	0	0	ppm	0.72381452	9.21E-27	GO:0005515,GO:0016773		ATLG46500.1	ATPK6 GAMMA 4,PHK GAMMA	phosphoinositide-4-kinase gamma 4	phosphatidylinositol 3- and 4-kinase family protein
Sapur.01GG166600.1	277.70869	3.50791286	0.18273689	39.99643	0	0	ppm	0.75631997	2.30E-30	GO:0008270,GO:0005515		ATLG79320.1		RING/U-box superfamily protein	RING-H2 finger protein ATL28
Sapur.01GG093900.1	422.2778444	8.5172619	0.17115146	49.19998	0	0	ppm	0.78273697	9.69E-34			ATLG33690.1		Late embryogenesis abundant protein, group 6	late embryogenesis abundant protein
Sapur.00BG094900.1	410.1227825	7.51465209	0.16882553	44.50919	0	0	ppm	0.77023407	2.48E-33	GO:0016021,GO:0006952		ATMLO5,MLO5	Seven transmembrane MLO family protein		MLO-like protein
Sapur.00GG083900.1	2413.073924	7.86507545	0.19580928	40.17134	0	0	ppm	0.75427638	2.32E-30			ATLG58120.1			NA
Sapur.00GG088800.1	4717.87601	5.51302618	0.12897476	44.46919	0	0	ppm	0.73020446	2.09E-27			ATLG08890.1		Rhamnogalacturonate lyase family protein	rhamnogalacturonate lyase
Sapur.01BG165500.1	276.3116162	6.61658187	0.23062764	41.67684	0	0	ppm	0.82897941	5.87E-41			ATLG02180.1			transmembrane protein, putative
Sapur.00GG081800.1	356.6754781	7.11600221	0.16291796	43.69689	0	0	ppm	0.77316198	1.72E-32	GO:0006468,GO:0005524,GO:0004672		ATLG08600.1		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.00GG084800.1	373.7470224	6.70123949	0.15155674	40.75367	0	0	ppm	0.77630466	6.96E-33	GO:0003824,GO:0005515		ATLG56790.2	ATPUDDELTA,PUDELTA	phosphodiesterase delta	NA
Sapur.00GG231100.1	202.0772315	8.81007125	0.25158049	39.055	0	0	ppm	0.84688389	3.28E-64			ATLG31850.1	LBD22	LOB domain-containing protein 22	hypothetical protein
Sapur.00GG060700.6	0.06427246	0.12866139	2.90483276	0.044302	0.96457126	NA	ppm	0.42450365	3.14E-08	GO:0043169,GO:0005975,GO:0003824		ATLG76130.1	AMY2,ATAMY2	alpha-amylase like 2	flog-gamine nucleotide exchange factor
Sapur.01GG003300.1	10773.68226	6.95985264	2.34585051	38.62126	0	0	ppm	0.76993334	4.77E-32	GO:0055114,GO:0016491,GO:0005507		ATLG55570.1	sks12	SKS: similar 12	L-ascorbate oxidase-like protein
Sapur.00GG082000.1	5853.287878	6.69149609	2.2574154	37.68883	0	0	ppm	0.73431320	7.22E-28			ATLG21660.1	FLA34	FASCILIN-like arabinogalactan protein 14 precursor	fasciclin-like arabinogalactan protein
Sapur.01BG042100.1	474.9743915	0.38738433	0.15132367	52.81603	0	0	ppm	0.81579301	1.08E-28	GO:0005515,GO:0006468,GO:0004672		ATLG24715.1			tyrosine kinase family protein
Sapur.00GG059400.1	874.0388524	1.69035784	0.11771868	44.6172	0	0	ppm	0.78909057	1.81E-33			ATLG34920.1	EDA18	RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.01GG073800.1	3206.717814	5.18816364	0.12916405	40.16726	0	0	ppm	0.72381452	9.21E-27	GO:0005515,GO:0016773		ATLG46500.1	ATPK6 GAMMA 4,PHK GAMMA	phosphoinositide-4-kinase gamma 4	phosphatidylinositol 3- and 4-kinase family protein
Sapur.01GG166600.1	277.70869	3.50791286	0.18273689	39.99643	0	0	ppm	0.75631997	2.30E-30	GO:0008270,GO:0005515		ATLG79320.1		RING/U-box superfamily protein	RING-H2 finger protein ATL28
Sapur.01BG093900.1	422.2778444	8.5172619	0.17115146	49.19998	0	0	ppm	0.78273697	9.69E-34			ATLG33690.1		Late embryogenesis abundant protein, group 6	late embryogenesis abundant protein
Sapur.00BG094900.1	410.1227825	7.51465209	0.16882553	44.50919	0	0	ppm	0.77023407	2.48E-33	GO:0016021,GO:0006952		ATMLO5,MLO5	Seven transmembrane MLO family protein		MLO-like protein
Sapur.00GG083900.1	2413.073924	7.86507545	0.19580928	40.17134	0	0	ppm	0.75427638	2.32E-30			ATLG58120.1			NA
Sapur.00GG088800.1	4717.87601	5.51302618	0.12897476	44.46919	0	0	ppm	0.73020446	2.09E-27			ATLG08890.1		Rhamnogalacturonate lyase family protein	rhamnogalacturonate lyase
Sapur.01BG165500.1	276.3116162	6.61658187	0.23062764	41.67684	0	0	ppm	0.82897941	5.87E-41			ATLG02180.1			transmembrane protein, putative
Sapur.00GG081800.1	356.6754781	7.11600221	0.16291796	43.69689	0	0	ppm	0.77316198	1.72E-32	GO:0006468,GO:0005524,GO:0004672		ATLG08600.1		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.00GG084800.1	373.7470224	6.70123949	0.15155674	40.75367	0	0	ppm	0.77630466	6.96E-33	GO:0003824,GO:0005515		ATLG56790.2	ATPUDDELTA,PUDELTA	phosphodiesterase delta	NA
Sapur.00GG231100.1	202.0772315	8.81007125	0.25158049	39.055	0	0	ppm	0.84688389	3.28E-64			ATLG31850.1	LBD22	LOB domain-containing protein 22	hypothetical protein
Sapur.00GG060700.6	815.6427299	5.17980989	0.10962593	43.11129	0	0	ppm	0.81222284	4.11E-38	GO:0005089		ATLG79860.1	ATROPGEF12,MEE64,ROPG	RHO guanyl-nucleotide exchange factor 12	flog-gamine nucleotide exchange factor
Sapur.00GG045800.1	280.292572	7.48624980	0.15374858	48.69151	0	0	ppm	0.81470479	1.62E-28	GO:0016021,GO:0016020,GO:0022857		ATLG47470.1		Nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4
Sapur.00GG087400.1	175.1210007	5.27133977	0.12752315	38.86518	0	0	ppm	0.72600837	5.99E-28			ATLG44890.1		NHL domain-containing protein	potassium transporter, putative
Sapur.00GG089300.1	1647.433612	9.68392278	0.23422729	41.34413	0	0	ppm	0.74240873	9.32E-29	GO:0008270		ATLG61230.1		GATA type zinc finger transcription factor family protein	LIM2-SF3 domain protein
Sapur.00GG092000.1	738.5019237	7.40575388	0.14288788	51.82921	0	0	ppm	0.79374198	2.77E-35	GO:0005524,GO:0003779,GO:0030042,GO:0015629		ATLG06880.1	ADF8	actin depolymerizing factor 8	actin-depolymerizing factor
Sapur.00GG100400.1	534.7874859	7.15280417	0.18259527	39.17291	0	0	ppm	0.68684025	3.06E-23	GO:0006468,GO:0004672		ATLG64300.1		Protein kinase family protein	NA
Sapur.00GG135500.1	567.9685651	5.30942106	0.14488207	37.5254	0	0	ppm	0.71951753	1.79E-25			ATLG34920.1	EDA18	RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.00GG139000.1	2299.661594	5.75932897	0.18508906	32.75075	0	0	ppm	0.81459411	1.68E-38			ATLG20060.1			hypothetical protein
Sapur.00GG141700.1	431.7608863	6.23619487	0.12833890	48.59158	0	0	ppm	0.79290675	3.63E-35			ATLG79640.1		Protein kinase superfamily protein	NA
Sapur.00GG170000.1	17324.47223	8.96164112	0.26682347	37.85912	0	0	ppm	0.79539848	9.36E-31	GO:0055114,GO:0016491,GO:0005507		ATLG55570.1	sks12	SKS: similar 12	L-ascorbate oxidase-like protein
Sapur.00GG029800.1	2134.145807	8.96901578	0.23612973	37.55761	0	0	ppm	0.80970194	7.44E-37			ATLG28270.1	RALFL4	ralf-like 4	rapid alkalinization factor
Sapur.00GG084900.1	1861.491882	7.96337984	0.18234659	37.61845	0	0	ppm	0.78841708	1.58E-34			ATLG28270.1	RALFL4	ralf-like 4	rapid alkalinization factor
Sapur.00GG082300.1	1186.968286	5.96484706	0.13008086	44.82164	0	0	ppm	0.76024447	7.71E-31	GO:0006468,GO:0004672		ATLG18640.1	MRH1	Leucine-rich repeat protein kinase family protein	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.00GG139400.1	952.3278674	7.22499136	0.19006993	38.03089	0	0	ppm	0.64284856	4.12E-23	GO:0006468,GO:0004672		ATLG39110.1		Protein kinase superfamily protein	receptor-like kinase, putative
Sapur.00LG131000.1	1387.478882	6.76007853	0.13853123	48.80189	0	0	ppm	0.74045394	1.54E-28	GO:0016246,GO:0005975,GO:0004553		ATLG16730.1	BGAL13	glycosyl hydrolase family 35 protein	beta-galactosidase
Sapur.00GG142700.1	1388.727587	7.45786669	0.19557591	40.73316	0	0	ppm	0.74153276	1.36E-32			ATLG27180.1			hypothetical protein
Sapur.00GG175000.1	290.111545	4.10584163	0.10589688	39.21085	0	0	ppm	0.69683665	1.68E-27	GO:0016787		ATLG08465.1	TOPP4	type-one serine/threonine protein phosphatase 4	serine/threonine-protein phosphatase
Sapur.00GG094000.1	526.0449069	3.32948051	0.11548782	54.79806	0	0	ppm	0.80650032	3.14E-37			ATLG05725.1		Protein of unknown function (DUF3511)	DUF3511 domain protein
Sapur.00GG080800.1	376.6202939	7.03807386	0.18277889	38.61328	0	0	ppm	0.71918249	1.05E-26	GO:0005515,GO:0006468,GO:0004672		ATLG37521.1		Transducin/WD40 repeat-like superfamily protein	receptor-like kinase 8kgt, putative
Sapur.00GG047000.1	4695.45922	8.92314804	0.19195539	44.7959	0	0	ppm	0.72653746	4.77E-27	GO:0016020,GO:0006075,GO:0003843,GO:0000148		ATLG13680.1	ATGLG2,CALS5,GLS2	callose synthase 5	1%2C3-beta-glucan synthase
Sapur.00GG066100.1	324.0315344	4.46645853	0.10585016	41.9326	0	0	ppm	0.76375261	1.51E-27			ATLG21990.1		Protein of unknown function, DUF617	plant-specific domain TIGR01570 family protein
Sapur.00GG096200.1	1929.275805	8.61420053	0.17255889	49.86412	0	0	ppm	0.82723905	1.20E-40			ATLG46490.1	ATSHK12,SPH12	SCL14-like 12	SCL14-like cytosolic factor, putative
Sapur.00GG089400.1	1960.235457	6.13881086	0.12712358	49.86358	0	0	ppm	0.78042	7.00E-32	GO:0006468,GO:0004672		ATLG18670.1	PERK4	receptor-like protein kinase 4	proline-rich receptor-like kinase
Sapur.00GG132200.1	216.6911264	7.98795425	0.17788485	44.90318	0	0	ppm	0.80728555	2.49E-37			ATLG22110.1		structural constituent of ribosome	RUP32449 family protein
Sapur.00GG181000.1	596.7014633	7.23499152	0.15168514	46.46291	0	0	ppm	0.77382926	1.50E-32	GO:0016301,GO:0006468,GO:0005524,GO:0004674,GO:0004672		ATLG04570.1		AGC (cAMP-dependent, cGMP-dependent and protein kinase C)-kinase family protein	serine/threonine kinase family protein
Sapur.00GG181700.1	296.6142808	5.42083809	0.10867079	49.88164	0	0	ppm	0.85438092	6.40E-46			ATLG28556.1	RICT	PAS kos/PTA-RNA binding protein family	PT1-RNa binding domain protein
Sapur.00GG194400.1	318.8299921	8.25235509	0.20969191	39.35409	0	0	ppm	0.75835781	1.31E-30			ATLG65070.1		SBP (S-ribonuclease binding protein) family protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.00GG201300.1	574.9071504	8.04202227	0.20600429	39.6615	0	0	ppm	0.79462474	2.04E-35	GO:0008270		ATLG65070.1		DHHC-type zinc finger family protein	zinc finger protein, putative
Sapur.00GG063900.1	2315.436721	7.01978572	0.12157523	57.7582	0	0	ppm	0.79195803	5.06E-35	GO:0005515,GO:0006468,GO:0005524,GO:0004672		ATLG35260.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.00GG088000.1	290.6576744	9.50032484	0.21418812	44.69008	0	0	ppm	0.75064079	1.07E-29	GO:0016787		ATLG37670.1		Transducin/WD40 repeat-like superfamily protein	WD domain, G-beta repeat protein
Sapur.00GG078000.1	1454.671485	3.69212835	0.08230758	45.21734	0	0	ppm	0.81231198	3.95E-38	GO:0016302,GO:0007017,GO:0005874		ATLG21860.1	TUB8	tubulin beta 8	beta-tubulin
Sapur.00GG085900.1	586.9083843	4.23827394	0.09188224	46.07329	0	0	ppm	0.80501627	1.61E-37	GO:0003824,GO:0006470,GO:0004722		ATLG01720.2		protein phosphatase 2C family protein	inorganic phosphatase 2C
Sapur.00GG091500.1	517.7738868	7.04604456	0.13875385	50.80248	0	0	ppm	0.84088803	3.59E-43			ATLG03970.1			hypothetical protein
Sapur.00TG027000.1	650.2356677	4.66090764	0.22604928	38.82071	0	0	ppm	0.73933267	2.04E-28	GO:0005543		ATLG00501.1		ENTH/ANTH/VHS superfamily protein	NA
Sapur.00GG103700.1	580.4600683	7.95365589	0.17968987	44.26548	0	0	ppm	0.71697096	4.56E-26	GO:0016887,GO:0005524		ATLG37010.1	ATMAP12,NAP12	non-intrinsic ABC protein 12	white-brown complex ABC transporter family protein, putative
Sapur.00GG054500.1	1663.392568	8.85247352	0.19296461	41.65101	0	0	ppm	0.78327412	2.61E-35			ATLG29470.1			hypothetical protein
Sapur.00GG133300.1	548.8511842	6.95468756	0.20741768	43.17353	0	0	ppm	0.76887042	6.48E-32	GO:0016021,GO:0015116,GO:0008272,GO:0055085,GO:0016020,GO:0008271,GO:1902235		ATLG19680.1	SULTR3;5	sulfate transporter 3;5	sulfate/bicarbonate/oxalate-exchanger and transporter sat-1
Sapur.00GG158200.1	389.1951466	8.17247119	0.20564291	39.74122	0	0	ppm	0.75429368	2.25E-30	GO:0006468,GO:0004672		ATLG41970.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.00GG167000.1	272.1801004	5.85027293	0.11867589	49.29622	0	0	ppm	0.81294856	4.38E-38	GO:0008872,GO:0000146		ATLG24461.1	ATEXO70A2,EXO70A2	exocyst subunit exo70 family protein A2	EXO70 exocyst complex subunit
Sapur.00GG175700.1	176.6271334	8.94299483	0.19217658	43.55233	0	0	ppm	0.81033394	8.23E-38			ATLG09550.1		Ankyrin repeat family protein	ankyrin repeat plant protein
Sapur.00GG185000.1	358.4319344	6.60218531	0.16466488	40.104	0	0	ppm	0.73862855	2.52E-28	GO:0006950,GO:0006468,GO:0005524,GO:0004672		ATLG10200.1		Protein kinase superfamily with adenine nucleotide alpha hydrolases-like domain	kinase domain protein
Sapur.00GG227200.1	6767.123906	6.71507404	0.12401459	54.15471	0	0	ppm	0.77852237	3.02E-32			ATLG24950.1	FLA3	FASCILIN-like arabinogalactan protein 3 precursor	NA
Sapur.00TG089000.1	1160.326313	9.34294882	0.11117418	53.26458	0	0	ppm	0.76758204	9.

Sapur.006G113000.1	184.6815677	7.758746027	0.230170002	33.70876	4.30E-249	1.75E-247	cyan	0.737371335	3.36E-28	GO:0042545,GO:0030599,GO:0005618	AT1G69940.1	ATPPME1,PPME1	Pectin lyase-like superfamily protein	pectinesterase
Sapur.006G211300.1	243.6390726	4.877671443	0.145371506	33.55315	8.10E-247	3.25E-245	cyan	0.712913539	1.15E-25		AT4G32270.1		Ubiquitin-like superfamily protein	hypothetical protein
Sapur.014G062300.1	2154.760095	2.849958857	0.085163433	33.46458	1.58E-245	6.32E-244	cyan	0.800361938	2.89E-36	GO:0008270	AT1G01780.1		GATA type zinc finger transcription factor family protein	LIM domain protein PLIM-2
Sapur.011G029000.1	131.5994386	8.521461611	0.254691749	33.45794	1.97E-245	7.88E-244	cyan	0.766958796	1.14E-31	GO:0005515,GO:0016020	AT1G61290.1	ATSYP124,SYP124	syntaxin of plants 124	syntaxin-124 protein
Sapur.007G001500.1	504.0296889	8.28231949	0.248157854	33.37521	3.14E-244	1.24E-242	cyan	0.706523892	4.78E-25	GO:0005515,GO:0006468,GO:0004672	AT3G20190.1		Leucine-rich repeat protein kinase family protein	receptor-like kinase
Sapur.009G095300.1	515.1930294	3.462151734	0.103800358	33.35395	6.39E-244	2.52E-242	cyan	0.774432941	1.25E-32		AT3G03170.1			hypothetical protein
Sapur.009G052600.1	274.4852587	5.457978245	0.163849188	33.31099	2.68E-243	1.06E-241	cyan	0.697561589	3.31E-24		AT5G19473.1		RPM1-interacting protein 4 (RIN4) family protein	pathogenic type III effector avirulence factor Avr AvrRpt-cleavage: cleavage site protein
Sapur.006G003000.1	180.9529334	6.17975535	0.185942162	33.23483	3.38E-242	1.33E-240	cyan	0.6802088	1.16E-22		AT1G12150.1		Plant protein of unknown function (DUF827)	weak movement under blue light protein
Sapur.007G001400.1	566.1772712	7.718936657	0.232714394	33.16914	3.00E-241	1.17E-239	cyan	0.64023561	1.75E-19	GO:0006950,GO:0006468,GO:0005524,GO:0004672	AT1G16760.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	adenine nucleotide alpha hydrolase-like domain kinase
Sapur.017G050500.1	956.0985059	8.368732476	0.252673374	33.12075	1.49E-240	5.78E-239	cyan	0.684221086	5.20E-23					NA
Sapur.002G160800.1	601.6133075	7.562869477	0.228689342	33.07049	7.90E-240	3.05E-238	cyan	0.680259856	1.14E-22		AT5G61710.1			DUF761 domain protein
Sapur.019G067500.1	3011.193171	10.20221252	0.308983677	33.01861	4.39E-239	1.69E-237	cyan	0.680233439	1.15E-22	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	NA
Sapur.004G022200.1	217.8243935	8.856965464	0.269351254	32.88258	3.90E-237	1.48E-235	cyan	0.71910594	2.78E-26	GO:0005515,GO:0016020	AT1G61290.1	ATSYP124,SYP124	syntaxin of plants 124	syntaxin-124 protein
Sapur.013G143100.1	118.8189234	5.299270121	0.1622657	32.65798	6.17E-234	2.30E-232	cyan	0.781819982	1.29E-33		AT2G46170.1		Reticulon family protein	NA
Sapur.010G105800.1	4232.271596	9.194551364	0.282224906	32.57881	8.19E-233	3.03E-231	cyan	0.692577039	9.43E-24	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	NA
Sapur.008G089000.1	48.325345	5.717730677	0.17593287	32.4995	1.08E-231	3.98E-230	cyan	0.766913142	1.15E-31		AT3G25600.1		Calcium-binding EF-hand family protein	NA
Sapur.010G003800.1	1265.178099	8.480584581	0.261665809	32.40998	1.99E-230	7.21E-229	cyan	0.750274464	1.18E-29	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT3G17630.1	ATCHX19,CHX19	cation/H+ exchanger 19	cation proton exchanger
Sapur.006G043600.1	544.9175788	7.635315015	0.235753611	32.38684	4.21E-230	1.52E-228	cyan	0.670301886	7.89E-22		AT2G41905.1			transmembrane protein, putative
Sapur.002G020400.1	978.5595028	7.123762838	0.220128165	32.36189	9.44E-230	3.41E-228	cyan	0.633381166	5.51E-19	GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT3G51150.2		ATP binding microtubule motor family protein	kinesin motor domain protein
Sapur.009G046600.1	597.5176507	11.66772542	0.360552324	32.3607	9.81E-230	3.54E-228	cyan	0.549864256	8.74E-14	GO:0005975,GO:0004650	AT3G07970.1	QRT2	Pectin lyase-like superfamily protein	polygalacturonase
Sapur.008G122000.1	7067.613639	8.519931976	0.263493384	32.33452	2.29E-229	8.26E-228	cyan	0.719634474	2.46E-26	GO:0055085,GO:0016021	AT5G26250.1		Major facilitator superfamily protein	sugar transporter, putative
Sapur.019G067100.1	2343.264848	9.637325019	0.298081096	32.33122	2.55E-229	9.18E-228	cyan	0.584932095	8.69E-16	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	NA
Sapur.005G052700.1	174.7256781	6.123388618	0.1899109	32.24348	4.34E-228	1.55E-226	cyan	0.681984376	8.13E-23		AT1G07710.1		Ankyrin repeat family protein	ankyrin-like protein
Sapur.012G000900.1	2297.963216	8.115089995	0.252150326	32.18354	3.00E-227	1.07E-225	cyan	0.772688629	2.11E-32					hypothetical protein
Sapur.012G044800.1	583.3884434	4.119667491	0.128007083	32.18312	3.04E-227	1.08E-225	cyan	0.712490107	1.27E-25		AT1G74220.1			hypothetical protein
Sapur.001G171800.1	1214.249263	6.309818989	0.19658751	32.09674	4.90E-226	1.72E-224	cyan	0.687774936	2.53E-23					hypothetical protein
Sapur.018G073100.1	87.09112622	7.715616796	0.240924543	32.02503	4.89E-225	1.71E-223	cyan	0.748669503	1.81E-29		AT1G70420.1		Protein of unknown function (DUF1645)	hypothetical protein
Sapur.007G050900.1	1293.608594	2.836431373	0.08858276	32.02013	5.72E-225	1.99E-223	cyan	0.784785005	5.07E-34	GO:0008270,GO:0006355,GO:0005634,GO:0004402,GO:0003712,GO:0005515	AT5G67480.2	ATBT4,BT4	BTB and TAZ domain protein 4	speckle-type POZ protein-like protein B
Sapur.002G157800.1	2072.512937	3.760317392	0.117522605	31.99655	1.22E-224	4.22E-223	cyan	0.726135845	5.31E-27	GO:0006950	AT4G02380.1	AtLEA5,SAG21	senescence-associated gene 21	late embryogenesis abundant protein
Sapur.001G106100.1	116.2754705	8.563202407	0.267852222	31.96988	2.86E-224	9.89E-223	cyan	0.731970596	1.29E-27	GO:0016021	AT2G23810.1	TET8	tetraspanin8	NA
Sapur.15WG092700.1	921.3570305	8.41442025	0.265106289	31.7398	4.39E-221	1.48E-219	cyan	0.696388008	4.25E-24		AT5G62850.1	AtVEX1	Nodulin MtN3 family protein	bidirectional sugar transporter SWEET6b
Sapur.013G070100.1	274.7593007	2.898909612	0.091421884	31.70914	1.16E-220	3.93E-219	cyan	0.789981266	9.50E-35		AT3G45400.1		exostosin family protein	secondary cell wall-related glycosyltransferase family 47 protein
Sapur.006G196800.1	107.0274544	4.536392415	0.143428541	31.62824	1.51E-219	5.04E-218	cyan	0.761468127	5.46E-31	GO:0008270,GO:0005515	AT5G11620.1		SWIM zinc finger family protein / mitogen-activated protein kinase kinase kinase (MAPKKK)-related	SWIM zinc finger protein
Sapur.008G113400.1	363.3004779	8.191034983	0.258997995	31.62586	1.63E-219	5.43E-218	cyan	0.733001002	1.00E-27	GO:0005543	AT1G25240.1		ENTH/VHS/GAT family protein	clathrin assembly protein
Sapur.002G147300.1	238.7402308	4.186573216	0.132463972	31.60537	3.11E-219	1.04E-217	cyan	0.747694531	2.35E-29		AT2G46300.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.010G179700.1	250.0179803	9.538023054	0.302067496	31.5758	7.94E-219	2.62E-217	cyan	0.713275489	1.06E-25		AT5G36805.1		Plant thionin family protein	NA
Sapur.001G049400.1	317.7088645	7.399239311	0.234963695	31.49099	1.15E-217	3.79E-216	cyan	0.725843153	5.69E-27	GO:0006887,GO:0000145	AT5G13150.1	ATEXO70C1,EXO70C1	exocyst subunit exo70 family protein C1	Exo70 exocyst complex subunit
Sapur.004G070200.1	2488.372711	9.40326911	0.300787968	31.26212	1.53E-214	4.93E-213	cyan	0.669584088	9.04E-22	GO:0042545,GO:0030599,GO:0005618	AT1G69940.1	ATPPME1,PPME1	Pectin lyase-like superfamily protein	pectinesterase
Sapur.006G075100.1	447.8342182	5.9425096	0.190363451	31.21665	6.33E-214	2.04E-212	cyan	0.734425061	7.03E-28	GO:0016020,GO:0006810,GO:0005215	AT5G28470.1		Major facilitator superfamily protein	peptide/nitrate transporter, putative
Sapur.006G174000.1	2821.195883	8.200454943	0.262835451	31.19996	1.07E-213	3.43E-212	cyan	0.722542926	1.25E-26		AT3G52720.1	ACA1,ATACA1,CAH1	alpha carbonic anhydrase 1	carbonate dehydratase
Sapur.019G072800.1	3085.416525	8.701761401	0.279699251	31.11114	1.70E-212	5.41E-211	cyan	0.658952059	6.52E-21	GO:0005975,GO:0004650	AT3G07840.1		Pectin lyase-like superfamily protein	NA
Sapur.019G054500.1	2707.52804	9.397809959	0.304715504	30.84126	7.34E-209	2.30E-207	cyan	0.668715337	1.07E-21	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	polygalacturonase
Sapur.011G034900.1	1658.542582	2.363548954	0.076637645	30.84057	7.49E-209	2.34E-207	cyan	0.79833804	5.80E-36	GO:0006629	AT4G04930.1	DES-1-LIKE	fatty acid desaturase family protein	sphingolipid Delta4-desaturase
Sapur.006G153000.1	756.5258166	7.806088554	0.254333604	30.69232	7.21E-207	2.23E-205	cyan	0.634109016	4.89E-19	GO:0008081,GO:0006629,GO:0008889	AT5G58050.1	SVL4	SHV3-like 4	glycerophosphoryl diester phosphodiesterase family protein
Sapur.003G100100.1	1283.579434	4.007353367	0.13057382	30.69033	7.66E-207	2.37E-205	cyan	0.713006473	1.13E-25		AT3G61640.1	AGP20,AtAGP20	arabinogalactan protein 20	transmembrane protein, putative
Sapur.019G085900.1	115.0095728	8.585047205	0.279863735	30.67581	1.20E-206	3.69E-205	cyan	0.694630387	6.15E-24		AT2G42560.1		late embryogenesis abundant domain-containing protein / LEA domain-containing protein	late embryogenesis abundant protein
Sapur.005G167900.1	1566.145237	8.715237929	0.28424034	30.66151	1.86E-206	5.72E-205	cyan	0.723044324	1.11E-26					NA
Sapur.012G099900.1	183.82936	4.26218494	0.139013456	30.66023	1.93E-206	5.94E-205	cyan	0.753813484	4.55E-30	GO:0060236,GO:0032147,GO:0005874,GO:0005819	AT4G22860.1		Cell cycle regulated microtubule associated protein	cell cycle regulated microtubule-associated protein
Sapur.002G006400.1	79.25397718	8.252943108	0.26919142	30.65827	2.05E-206	6.30E-205	cyan	0.746860585	2.92E-29	GO:0016567,GO:0004842,GO:0005515	AT5G42340.1	PUB15	Plant U-Box 15	spotted leaf protein, putative
Sapur.019G066900.1	475.0086605	9.564468964	0.312243597	30.63143	4.67E-206	1.43E-204	cyan	0.63396189	5.01E-19		AT3G07830.1		Pectin lyase-like superfamily protein	NA
Sapur.016G310700.1	1148.949501	8.409724583	0.274559725	30.62986	4.90E-206	1.50E-204	cyan	0.659005472	6.45E-21		AT1G58110.2		Basic-leucine zipper (bZIP) transcription factor family protein	BZIP transcription factor, putative
Sapur.005G060000.1	93.95243174	7.330121245	0.239373011	30.62217	6.20E-206	1.90E-204	cyan	0.721032907	1.78E-26		AT2G22180.1		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative
Sapur.018G026200.1	280.126673	5.243033076	0.17123925	30.61817	7.01E-206	2.15E-204	cyan	0.656341819	1.05E-20		AT4G30380.1		Barwin-related endoglucanase	rare lipoprotein A-like double-psi beta-barrel protein
Sapur.15ZG048000.1	207.4650839	8.473845665	0.277459272	30.54086	7.48E-205	2.27E-203	cyan	0.695090755	5.58E-24		AT1G68490.1			hypothetical protein
Sapur.017G063000.1	131.1495988	5.068183982	0.166265822	30.48242	4.46E-204	1.35E-202	cyan	0.713364797	1.04E-25		AT1G27100.1		Actin cross-linking protein	actin cross-linking protein, putative
Sapur.014G028700.1	779.4725255	6.81356173	0.223621458	30.46918	6.68E-204	2.01E-202	cyan	0.641604887	1.38E-19	GO:0005515	AT2G26490.1		Transducin/WD40 repeat-like superfamily protein	F-box and WD40 domain protein, putative
Sapur.010G165400.1	436.6265589	8.300838939	0.272471359	30.465	7.58E-204	2.29E-202	cyan	0.63145601	7.57E-19	GO:0004857	AT5G64620.1	ATC/VIF2,C/VIF2	cell wall / vacuolar inhibitor of fructosidase 2	pectinesterase inhibitor
Sapur.002G069400.1	956.374816	9.34442024	0.30785105	30.35371	2.24E-202	6.73E-201	cyan	0.643212076	1.05E-19	GO:0055114,GO:0016491	AT5G08640.1	ATFLS1,FLS,FLS1	flavonol synthase 1	flavonol synthase/flavanone 3-hydroxylase
Sapur.016G065400.1	67.91748231	8.449893215	0.279065161	30.27928	2.15E-201	6.41E-200	cyan	0.750246228	1.19E-29		AT3G52460.1		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative
Sapur.011G041200.1	69.62998232	5.664421181	0.187109682	30.27327	2.58E-201	7.67E-200	cyan	0.669952113	8.43E-22		AT5G46060.1		Protein of unknown function, DUF599	NBS-LRR type disease resistance protein
Sapur.016G159800.1	452.612517	7.992158765	0.264008347	30.27237	2.65E-201	7.87E-200	cyan	0.693745485	7.40E-24	GO:0006468,GO:0004672	AT5G12180.1	CPK17	calcium-dependent protein kinase 17	calcium-dependent kinase
Sapur.011G071800.1	89.10127851	9.559215991	0.315978405	30.25275	4.80E-201	1.43E-199	cyan	0.699193792	2.34E-24		AT5G55980.1		serine-rich protein-related	hypothetical protein
Sapur.001G146400.1	540.7314243	3.676035202	0.121643314	30.21979	1.30E-200	3.85E-199	cyan	0.70209076	1.26E-24		AT1G80160.1		Lactoylglutathione lyase / glyoxalase I family protein	lactoylglutathione lyase, putative
Sapur.006G139200.1	54.18785578	8.202351137	0.271653648	30.19415	2.83E-200	8.35E-199	cyan	0.776055857	7.64E-33		AT5G12060.1		Plant self-incompatibility protein S1 family	self-incompatibility protein, putative
Sapur.001G008800.1	296.4778286	4.64647445	0.154565994	30.06143	1.55E-198	4.53E-197	cyan	0.68907645	1.94E-23		AT5G06700.1	TBR	Plant protein of unknown function (DUF828)	NA
Sapur.018G018100.1	515.0211101	2.919247318	0.097139591	30.05209	2.05E-198	5.99E-197	cyan	0.771421113	3.07E-32		AT5G25170.1		PPPDE putative thiol peptidase family protein	PPPDE peptidase domain protein, putative
Sapur.012G041400.1	1466.814928	1.973076971	0.065688499	30.03687	3.24E-198	9.44E-197	cyan	0.82510068	2.85E-40	GO:0006468,GO:0005524,GO:0004672	AT5G08160.1	ATPK3,PK3	serine/threonine protein kinase 3	Serine/Threonine kinase
Sapur.001G175200.1	46.71608081	8.06555575	0.26866374	30.02101	5.22E-198	1.52E-196	cyan	0.788618151	1.48E-34		AT1G11040.1		HSP40/DnaJ peptide-binding protein	NA
Sapur.002G127100.1	880.3358539	2.157768583	0.072095785	29.92919	8.21E-197	2.38E-195	cyan	0.823913561	4.58E-40	GO:0005515	AT1G63220.1		Calcium-dependent lipid-binding (CaLB domain) family protein	elicitor-responsive protein
Sapur.006G176600.1	810.6673124	7.797933878	0.261039068	29.87267	4.46E-196	1.29E-194	cyan	0.694989618	5.70E-24		AT1G01310.1		CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein	cysteine-rich secretory family protein
Sapur.002G012700.1	74.68344541	5.035929642	0.169044791	29.7905	5.19E-195	1.48E-193	cyan	0.626856157	1.60E-18		AT1G20180.1		Protein of unknown function (DUF677)	NA
Sapur.017G050400.1	813.2407777	8.654329691	0.290859688	29.75431	1.53E-194	4.36E-193	cyan	0.60123032	8.38E-17					NA
Sapur.018G000200.1	3067.086882	2.449338497	0.082782317	29.5877	2.15E-192	6.05E-191	cyan	0.786033503	3.41E-34		AT4G31130.1		Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.016G006700.1	115.703306	8.804371998	0.298977909	29.44824	1.33E-190	3.70E-189	cyan	0.671759053	5.98E-22		AT5G55630.2	ATKCO1,ATTPK1,KCO1,TPK1	Outward rectifying potassium channel protein	outward rectifying potassium channel protein
Sapur.012G056100.1	1409.485484	8.01672929	0.272259661	29.44516	1.45E-190	4.04E-189	cyan	0.692421651	9.74E-24	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT4G17690.1		Peroxidase superfamily protein	peroxidase
Sapur.010G006400.1	4819.242069	8.363475493	0.28450862	29.39621	6.14E-190	1.70E-188	cyan	0.683395133	6.14E-23	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT5G27870.1		Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.003G036500.1	149.2291472	2.713010039	0.092426101	29.35329	2.17E-189	6.00E-188	cyan	0.787372644	2.21E-34		AT1G72600.2		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative
Sapur.018G062100.1	2995.865015	5.115107067	0.1743686	29.33502	3.71E-189	1.02E-187	cyan	0.713499809	1.01E-25	GO:0055085,GO:0016021	AT1G77210.2	AtSTP14,STP14	sugar transporter 14	sugar transporter, putative
Sapur.008G120100.1	3690.127178	8.17133114	0.279131349	29.27414	2.21E-188	6.07E-187	cyan	0.698831322	2.53E-24	GO:0030570	AT5G15110.1		Pectate lyase family protein	pectate lyase
Sapur.006G049100.1	835.2460373	9.931930861	0.339473275	29.25689	3.67E-188	1.00E-186	cyan	0.561559548	1.99E-14		AT3G48675.1		Protein of unknown function (DUF1278)	NA
Sapur.006G111400.1	2855.703811	8.39549154	0.287008178	29.25175	4.27E-188	1.17E-186	cyan	0.698776098	2.56E-24	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT2G26450.1		Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.019G067400.1	2783.907274	9.33370633	0.319656343	29.19919	1.99E-187	5.38E-186	cyan	0.641917933	1.31E-19	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	NA
Sapur.017G002800.1	738.562902	4.612147494	0.15838848	29.11921	2.05E-186	5.51E-185	cyan	0.708496853	3.09E-25		AT2G43900.1		Endonuclease/exonuclease/phosphatase family protein	type I inositol 1%2C4%2C5-trisphosphate 5-phosphatase
Sapur.010G163400.1	32.26356448	7.749470418	0.266443258	29.08488	5.58E-186	1.50E-184	cyan	0.77154775	2.96E-32	GO:0005515	AT4G12560.1	CPR30	F-box and associated interaction domains-containing protein	F-box protein interaction domain protein
Sapur.006G126200.1	713.6604267	7.332278608	0.252253551	29.0671	9.36E-186	2.50E-184	cyan	0.610522932	2.08E-17	GO:0055114,GO:0050660,GO:0016491,GO:0019139,GO:0009690	AT5G56970.1	ATCKX3,CKX3	cytokinin oxidase 3	cytokinin oxidase/dehydrogenase
Sapur.007G107000.1	203.9673709	3.681709776	0.126674679	29.06429	1.02E-185	2.71E-184	cyan	0.716187746	5.46E-26		AT5G54650.2	ATFH5,FH5	formin homology5	NA
Sapur.019G072900.1	628.3346356	9.827974031	0.338340997	29.04754	1.65E-185	4.40E-184	cyan	0.589645826	4.48E-16	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	NA
Sapur.016G048300.1	259.8419555	3.833633576	0.132259973	28.98559	1.00E-184	2.63E-183	cyan	0.676997309	2.17E-22		AT3G21550.1	AtDMP2,DMP2	DUF679 domain membrane protein 2	plant/MIL23-11 protein
Sapur.009G094500.1	230.6643233	7.387025324	0.254946455	28.97481	1.37E-184	3.59E-183	cyan	0.626713479	1.64E-18		AT2G21540.2	ATSFH3,SFH3	SEC14-like 3	SEC14 cytosolic factor, putative
Sapur.019G051700.1	243.2394941	3.341608774	0.115470771	28.939	3.86E-184	1.01E-182	cyan	0.726809188	4.52E-27		AT5G16490.1	RIC4	ROP-interactive CRIB motif-containing protein 4	wiscott-aldrich syndrome, carboxy-terminal protein%2C putative
Sapur.009G084900.1	3622.386664	8.123328625	0.281248825	28.88307	1.95E-183	5.05E-182	cyan	0.637632503	2.71E-19	GO:0005515	AT3G19020.1		Leucine-rich repeat (LRR) family protein	NA
Sapur.018G005000.1	47.91395837	4.044170022	0.140145522	28.85693	4.15E-183	1.07E-181	cyan	0.701201152	1.52E-24	GO:0008270,GO:0005515	AT5G24870.2		RING/U-box superfamily protein	zinc finger protein, putative
Sapur.008G147500.1	1532.442979	8.162582985	0.283221109	28.82053	1.19E-182	3.06E-181	cyan	0.714151626	8.69E-26		AT1G24520.1	BCP1	homolog of Brassica campestris pollen protein 1	transmembrane protein, putative
Sapur.010G056700.1	115.2079775	7.444123206	0.258366863	28.81222	1.51E-182	3.89E-181	cyan	0.661650842	3.98E-21		AT1G67670.1			hypothetical protein
Sapur.018G038700.1	2074.883045	8.285495203	0.287718038	28.79727	2.32E-182	5.97E-181	cyan	0.706669536	4.63E-25	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT2G26450.1		Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.019G029400.1	579.5832435	8.171790846	0.28391579	28.78245	3.56E-182	9.13E-181	cyan	0.677001303	2.17E-22	GO:0005515	AT2G33320.1		Calcium-dependent lipid-binding (CaLB domain) family protein	calcium-dependent lipid-binding (CaLB domain) family protein, putative
Sapur.008G140200.1	97.15763064	6.840074697	0.23800333	28.73941	1.23E-181	3.13E-180	cyan	0.675587286	2.86E-22	GO:0005515	AT2G33320.1		Calcium-dependent lipid-binding (CaLB domain) family protein	calcium-dependent lipid-binding domain protein, putative
Sapur.005G015200.1	527.1164838	4.336110612	0.150922216	28.73076	1.58E-181	4.01E-180	cyan	0.727515932	3.81E-27	GO:0005515,GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT5G27000.1	ATK4,KATD	kinesin 4	kinesin heavy chain, putative
Sapur.019G067200.1	1505.453195	9.138544225	0.318326997	28.70804	3.03E-181	7.70E-180	cyan	0.633685146	5.24E-19	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	NA
Sapur.009G065200.1	934.1340363	8.553726141	0.298348519	28.67025	8.97E-181	2.26E-179	cyan	0.64274029	1.14E-19		AT2G14610.1	ATPR1,PR 1,PR1	pathogenesis-related gene 1	pathogenesis-related protein
Sapur.010G014500.1	277.025777	5.479282727	0.191204674	28.65664	1.33E-180	3.34E-179	cyan	0.66832059	1.15E-21	GO:0006468,GO:0004672	AT5G18910.1		Protein kinase superfamily protein	receptor tyrosine kinase
Sapur.002G187000.1	77.4566565	8.301252744	0.289984057	28.62658	3.14E-180	7.90E-179	cyan	0.728557119	2.96E-27	GO:0006468,GO:0005524,GO:0004672	AT3G07070.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.012G069000.1	535.8429042	5.266099542	0.184480387	28.54558	3.19E-179	7.97E-178	cyan	0.717885318	3.69E-26		AT2G04410.1		RPM1-interacting protein 4 (RIN4) family protein	pathogenic type III effector avirulence factor Avr AvrRpt-cleavage: cleavage site protein
Sapur.016G104700.1	545.9679116	2.402951207	0.084198771	28.53903	3.84E-179	9.59E-178	cyan	0.777424642	5.03E-33		AT3G08970.1	ATERDJ3A,TMS1	DNAJ heat shock N-terminal domain-containing protein	heat shock protein-binding protein, putative
Sapur.008G121700.1	4321.5577	8.208932907	0.288262559	28.47728	2.24E-178	5.57E-177	cyan	0.665654645	1.89E-21	GO:0055085,GO:0016021	AT5G26250.1		Major facilitator superfamily protein	NA
Sapur.003G159100.1	257.040191	8.450373452	0.297227252	28.43068	8.45E-178	2.09E-176	cyan	0.649051445	3.82E-20		AT5G12930.1			hypothetical protein
Sapur.001G115500.1	1184.905333	3.446470638	0.121376993	28.39476	2.35E-177	5.76E-176	cyan	0.692848203	8.92E-24	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT4G25960.1	PGP2	P-glycoprotein 2	multidrug/pheromone exporter, MDR family, ABC transporter family protein
Sapur.011G055000.1	116.6222291	8.503522241	0.300914429	28.25894	1.11E-175	2.66E-174	cyan	0.658910149	6.57E-21					transmembrane protein, putative
Sapur.006G167100.1	597.4887112	6.278945167	0.222308805	28.24425	1.67E-175	4.03E-174	cyan	0.723446935	1.01E-26		AT3G52460.1		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative
Sapur.008G112900.1	117.7148319	7.633663904	0.270867904	28.18224	9.65E-175	2.31E-173	cyan	0.680074025	1.19E-22	GO:0005544,GO:0005509	AT1G68090.1	ANN5,ANNAT5	annexin 5	annexin
Sapur.006G204200.1	181.4557019	3.528291372	0.125507448	28.11221	6.95E-174	1.66E-172	cyan	0.766278422	1.38E-31		AT5G25530.1		DNAJ heat shock family protein	DnaJ family B protein
Sapur.010G053900.1	1876.861654	7.420495471	0.264252676	28.08106	1.67E-173	3.96E-172	cyan	0.60220891	7.25E-17		AT5G40780.1	LHT1	lysine histidine transporter 1	NA
Sapur.017G054100.1	1505.064411	10.23109591	0.365143025	28.01942	9.42E-173	2.23E-171	cyan	0.494420669	4.67E-11	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	NA
Sapur.001G173000.1	6857.834356	8.260178872	0.295553053	27.94821	6.93E-172	1.63E-170	cyan	0.701560149	1.41E-24	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT5G49180.1		Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.006G040300.1	180.5976937	9.509928062	0.340424594	27.93549	9.89E-172	2.32E-170	cyan	0.603897171	5.65E-17	GO:0005975,GO:0004650	AT3G07970.1	QRT2	Pectin lyase-like superfamily protein	polygalacturonase
Sapur.014G095400.1	434.3703594	8.035269602	0.287915743	27.90841	2.11E-171	4.93E-170	cyan	0.659769382	5.61E-21	GO:0004857	AT1G02550.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	NA
Sapur.016G235600.1	4634.277526	8.415625644	0.302337201	27.83523	1.63E-170	3.77E-169	cyan	0.668508121	1.11E-21	GO:0055085	AT4G26590.1	ATOPT5,OPT5	oligopeptide transporter 5	oligopeptide transporter OPT family protein
Sapur.019G067000.1	1784.414155	8.64143519	0.310648876	27.81737	2.67E-170	6.19E-169	cyan	0.582697334	1.18E-15	GO:0005975,GO:0004650	AT3G07820.1		Pectin lyase-like superfamily protein	NA
Sapur.019G087500.1	1803.52979	7.043375319	0.253222048	27.81502	2.86E-170	6.60E-169	cyan	0.663931385	2.61E-21		AT1G23145.1	RALFL2	RALF-like 2	rapid aLkalinization factor
Sapur.010G083700.1	643.5916477	4.078840148	0.146668903	27.80985	3.30E-170	7.62E-169	cyan	0.681226047	9.45E-23	GO:0005515	AT1G70790.1		Calcium-dependent lipid-binding (CaLB domain) family protein	Arf GTPase activator, putative
Sapur.008G096200.1	233.4938814	3.706743984	0.133332876	27.80068	4.26E-170	9.83E-169	cyan	0.720774354	1.89E-26	GO:0051861,GO:0046836,GO:0017089,GO:0005737	AT4G39670.1		Glycolipid transfer protein (GLTP) family protein	glycolipid transfer protein
Sapur.15WG087100.1	97.16194501	5.790100627	0.208342278	27.79129	5.53E-170	1.27E-168	cyan	0.707928257	3.51E-25		AT1G74830.1		Protein of unknown function, DUF593	zein-binding protein
Sapur.005G198800.1	515.563319	1.801647787	0.06507878	27.68411	1.08E-168	2.47E-167	cyan	0.822183664	9.09E-40		AT1G20460.1			NA
Sapur.016G189800.1	106.1127928	9.101251646	0.328813004	27.67911	1.25E-168	2.83E-167	cyan	0.660321301	5.08E-21		AT5G09430.1		alpha/beta-Hydrolases superfamily protein	alpha/beta-hydrolase domain protein
Sapur.005G017000.1	4125.528164	8.141843089	0.294867972	27.61183	8.02E-168	1.81E-166	cyan	0.663981332	2.59E-21	GO:0004857	AT5G46930.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	plant invertase/pectin methylesterase inhibitor protein
Sapur.001G040300.1	544.6020214	3.894964312	0.141309159	27.56342	3.06E-167	6.83E-166	cyan	0.800865859	2.42E-36		AT2G33100.1	ATCSLD1,CSLD1	cellulose synthase-like D1	cellulose synthase-like protein D
Sapur.008G121800.1	5120.691213	8.164925116	0.29682654	27.5074	1.43E-166	3.18E-165	cyan	0.658943342	6.53E-21	GO:0055085,GO:0016021	AT5G26250.1		Major facilitator superfamily protein	NA
Sapur.009G091100.1	228.6258668	7.482853318	0.272251154	27.48511	2.65E-166	5.87E-165	cyan	0.622436868	3.25E-18	GO:0006468,GO:0004672	AT1G49270.1		Protein kinase superfamily protein	proline-rich receptor-like kinase
Sapur.016G305400.1	70.73450479	3.769452238	0.137392108	27.43573	1.03E-165	2.28E-164	cyan	0.77523276	9.80E-33		AT2G04220.1		Plant protein of unknown function (DUF868)	kinesin-4 protein, putative
Sapur.016G094300.1	146.7465623	3.452939466	0.125915511	27.42267	1.47E-165	3.25E-164	cyan	0.694020606	6.98E-24		AT3G54040.1		PAR1 protein	PAR1 protein
Sapur.007G008900.1	2253.781013	2.942790124	0.107354166	27.41198	1.97E-165	4.35E-164	cyan	0.726264637	5.15E-27	GO:0006094,GO:0005524,GO:0004612	AT4G37870.1	PCK1,PEPCK	phosphoenolpyruvate carboxykinase 1	phosphoenolpyruvate carboxykinase (ATP)
Sapur.003G093900.1	1025.997503	7.322361892	0.267245447	27.39939	2.79E-165	6.15E-164	cyan	0.579225305	1.91E-15	GO:0006468,GO:0005524,GO:0004672	AT5G55090.1	MAPKKK15	mitogen-activated protein kinase kinase kinase 15	Serine/Threonine kinase family protein
Sapur.002G204100.1	43.80283826	8.382204306	0.306076714	27.38596	4.03E-165	8.86E-164	cyan	0.736678876	4.00E-28		AT1G75160.1		Protein of unknown function (DUF620)	NA
Sapur.011G071200.1	57.42527414	6.298149173	0.230082916	27.37339	5.69E-165	1.25E-163	cyan	0.713561509	9.94E-26	GO:0055114,GO:0016491	AT1G78440.1	ATGA2OX1,GA2OX1	Arabidopsis thaliana gibberellin 2-oxidase 1	gibberellin 2-oxidase
Sapur.002G065200.1	89.50207971	6.425392506	0.234853296	27.35918	8.40E-165	1.84E-163	cyan	0.621239299	3.94E-18	GO:0055114,GO:0016491,GO:0008152	AT1G44170.2	ALDH3H1,ALDH4	aldehyde dehydrogenase 3H1	aldehyde dehydrogenase (NAD) family protein
Sapur.002G032900.1	91.71176603	8.348461593	0.305448514	27.33181	1.78E-164	3.89E-163	cyan	0.724010991	8.81E-27	GO:0016301,GO:0005524	AT2G30630.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.009G090200.1	29.13309338	7.598318434	0.278322287	27.30043	4.19E-164	9.15E-163	cyan	0.726776927	4.55E-27		AT1G49330.1		hydroxyproline-rich glycoprotein family protein	hypothetical protein
Sapur.019G045600.1	46.03896724	7.864176435	0.288096953	27.29698	4.61E-164	1.01E-162	cyan	0.749977802	1.28E-29		AT5G17590.1		Putative membrane lipoprotein	transmembrane protein, putative
Sapur.004G016800.1	923.9984975	4.555683424	0.167270955	27.23535	2.48E-163	5.39E-162	cyan	0.675066774	3.16E-22		AT5G54490.1	PBP1	pinoid-binding protein 1	centrin protein
Sapur.016G054300.1	634.6119453	5.007249211	0.184939145	27.07512	1.93E-161	4.13E-160	cyan	0.555723684	4.20E-14	GO:0016758,GO:0008152	AT2G15490.1	UGT73B4	UDP-glycosyltransferase 73B4	trans-zeatin O-beta-D-glucosyltransferase
Sapur.017G054000.1	1525.862432	8.7984813	0.325152625	27.05954	2.95E-161	6.27E-160	cyan	0.497036115	3.56E-11	GO:0005975,GO:0004650	AT3G07840.1		Pectin lyase-like superfamily protein	NA
Sapur.15ZG040000.1	51.29677132	8.08918631	0.299926221	26.97059	3.27E-160	6.92E-159	cyan	0.660185479	5.20E-21	GO:0016021	AT1G18520.1	TET11	tetraspanin11	tetraspanin family protein
Sapur.004G087600.1	3407.41115	8.096696503	0.300215073	26.96965	3.36E-160	7.09E-159	cyan	0.641034057	1.53E-19	GO:0030570	AT5G15110.1		Pectate lyase family protein	pectate lyase, putative
Sapur.002G168500.1	258.5142015	4.41408422	0.16369524	26.96526	3.78E-160	7.98E-159	cyan	0.627466481	1.45E-18	GO:0016887,GO:0005524,GO:0016020	AT3G53480.1	ABCG37,ATPDR9,PDR9,PIS1	pleiotropic drug resistance 9	ABC transporter G family protein
Sapur.017G029500.1	125.1428486	3.866224217	0.143833543	26.87985	3.78E-159	7.90E-158	cyan	0.675911134	2.68E-22	GO:0016757,GO:0016020	AT1G05280.1		Protein of unknown function (DUF604)	fringe-like protein
Sapur.003G012700.1	8086.634811	8.0711859	0.301116877	26.80416	2.89E-158	6.00E-157	cyan	0.676520542	2.38E-22	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT5G27870.1		Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.019G098100.1	2141.226607	7.994691739	0.298773117	26.7584	9.86E-158	2.04E-156	cyan	0.68989051	1.64E-23		AT1G60815.1	RALFL7	RALF-like 7	rapid aLkalinization factor
Sapur.006G180400.1	102.2352334	2.768772536	0.103530328	26.74359	1.47E-157	3.03E-156	cyan	0.7878759	1.88E-34		AT4G33180.1		alpha/beta-Hydrolases superfamily protein	NA
Sapur.008G083000.1	1283.98063	8.394132038	0.318084355	26.38964	1.80E-153	3.64E-152	cyan	0.615286525	1.00E-17	GO:0042545,GO:0030599,GO:0005618	AT3G17060.1		Pectin lyase-like superfamily protein	pectinesterase
Sapur.018G061100.1	3339.287371	7.873111876	0.299590105	26.27961	3.28E-152	6.54E-151	cyan	0.635513752	3.87E-19		AT5G19580.1		glyoxal oxidase-related protein	glyoxal oxidase
Sapur.012G072000.1	563.1251815	7.936246625	0.302002914	26.27871	3.36E-152	6.69E-151	cyan	0.651187642	2.62E-20		AT1G24520.1	BCP1	homolog of Brassica campestris pollen protein 1	transmembrane protein, putative
Sapur.018G038600.1	791.5357048	1.563967291	0.059596792	26.24247	8.71E-152	1.73E-150	cyan	0.839405648	6.88E-43		AT5G35460.1			plant/MOK9-4 protein
Sapur.010G183800.1	407.773024	5.372701405	0.204756185	26.23951	9.42E-152	1.87E-150	cyan	0.58781375	5.80E-16		AT5G04390.1		C2H2-type zinc finger family protein	C2H2-type zinc-finger protein, putative
Sapur.15WG010800.1	570.3853669	1.876220477	0.072038734	26.04461	1.55E-149	3.01E-148	cyan	0.814456399	1.78E-38	GO:0007275,GO:0006511,GO:0005634	AT4G27880.1		Protein with RING/U-box and TRAF-like domains	E3 ubiquitin-protein ligase SINAT4
Sapur.005G016800.1	4655.409526	7.98792425	0.307188446	26.00334	4.54E-149	8.79E-148	cyan	0.626691419	1.65E-18	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT3G05610.1		Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.15WG153000.1	902.3738498	8.095388457	0.312344356	25.91815	4.16E-148	7.99E-147	cyan	0.616694306	8.04E-18		AT1G58110.2		Basic-leucine zipper (bZIP) transcription factor family protein	NA
Sapur.001G117700.1	1542.26778	1.141244205	0.044099984	25.87856	1.16E-147	2.22E-146	cyan	0.843284948	1.21E-43	GO:0005096	AT4G17890.1	AGD8	ARF-GAP domain 8	ADP-ribosylation factor GTPase-activating protein AGD10
Sapur.019G098200.1	1263.999342	7.831737917	0.302708523	25.87221	1.37E-147	2.62E-146	cyan	0.699874677	2.03E-24		AT1G60815.1	RALFL7	RALF-like 7	rapid aLkalinization factor
Sapur.006G114600.1	2368.38303	6.723268261	0.260133396	25.84546	2.74E-147	5.22E-146	cyan	0.528532726	1.12E-12	GO:0030246,GO:0005975,GO:0004553	AT5G20710.1	BGAL7	beta-galactosidase 7	beta-galactosidase
Sapur.011G090900.1	1858.213479	1.607703125	0.06221874	25.83953	3.19E-147	6.09E-146	cyan	0.807382245	2.41E-37	GO:0005096	AT5G54310.1	AGD5,NEV	ARF-GAP domain 5	ADP-ribosylation factor GTPase-activating protein AGD5, putative
Sapur.018G028400.1	302.4165041	2.706969802	0.105113408	25.75285	3.00E-146	5.67E-145	cyan	0.744475444	5.46E-29		AT5G25530.1		DNAJ heat shock family protein	DnaJ family B protein
Sapur.003G137500.1	1173.929261	1.138899784	0.044354578	25.67716	2.10E-145	3.96E-144	cyan	0.846246825	3.12E-44	GO:0005634	AT1G80780.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	CCR4-associated factor, putative
Sapur.006G039700.1	1262.476772	2.526137638	0.098550169	25.63301	6.54E-145	1.23E-143	cyan	0.750171223	1.22E-29		AT2G41830.1		Uncharacterized protein	cyclin-like protein
Sapur.005G049400.1	1452.197725	2.863383956	0.11183386	25.60391	1.38E-144	2.58E-143	cyan	0.750001102	1.27E-29	GO:0008168	AT5G64030.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase PMT26, putative
Sapur.011G030500.1	918.0710207	1.229192513	0.048022204	25.59634	1.68E-144	3.13E-143	cyan	0.847389195	1.83E-44		AT1G61240.4		Protein of unknown function (DUF707)	lysine ketoglutarate reductase trans-splicing-like protein
Sapur.017G128500.1	94.42272675	5.49958499	0.215040985	25.57459	2.93E-144	5.46E-143	cyan	0.635485492	3.89E-19	GO:0006468,GO:0005524,GO:0004672	AT1G48480.1	RKL1	receptor-like kinase 1	receptor kinase
Sapur.005G042700.1	714.7186346	8.039251095	0.314509849	25.56121	4.12E-144	7.67E-143	cyan	0.647786318	4.77E-20		AT1G08790.1		Protein of unknown function (DUF1685)	DUF1685 family protein
Sapur.008G170100.1	863.5104136	3.059561305	0.120104122	25.47424	3.80E-143	7.02E-142	cyan	0.74605508	3.61E-29		AT5G18980.1		ARM repeat superfamily protein	armadillo/beta-catenin-like repeat protein
Sapur.011G053800.1	801.450362	7.866655719	0.3092864	25.43486	1.04E-142	1.91E-141	cyan	0.62973711	1.00E-18	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	AT4G30270.1	MERI-5,MERI5B,SEN4,XTH2	xyloglucan endotransglucosylase/hydrolase 24	xyloglucan endotransglycosylase/hydrolase
Sapur.001G106200.1	34.51851141	5.252906384	0.207110652	25.3628	6.49E-142	1.19E-140	cyan	0.716615715	4.95E-26		AT4G12560.2	CPR30	F-box and associated interaction domains-containing protein	cytochrome P450 family protein
Sapur.004G109900.1	1825.613692	7.806365482	0.308129945	25.33465	1.33E-141	2.42E-140	cyan	0.628662665	1.20E-18	GO:0005515	AT2G15880.1		Leucine-rich repeat (LRR) family protein	NA
Sapur.018G064500.1	1025.851089	1.690365438	0.066894392	25.26917	6.97E-141	1.26E-139	cyan	0.804774897	6.14E-37	GO:0016757	AT2G19880.2		Nucleotide-diphospho-sugar transferases superfamily protein	ceramide glucosyltransferase
Sapur.017G114200.1	261.5530789	4.486277064	0.177540552	25.26903	7.00E-141	1.27E-139	cyan	0.574191181	3.78E-15	GO:0005515	AT5G17220.1	ATGSTF12,GST26,GSTF12,T1	glutathione S-transferase phi 12	glutathione S-transferase
Sapur.003G141400.1	929.8320751	1.640201996	0.065063081	25.20941	3.16E-140	5.68E-139	cyan	0.834252233	6.44E-42		AT1G79660.1			plant/F20B17-9 protein
Sapur.003G151800.1	431.0698967	3.2676668	0.129723625	25.18945	5.23E-140	9.40E-139	cyan	0.73694282	3.75E-28	GO:0046488,GO:0016307	AT3G07960.1		Phosphatidylinositol-4-phosphate 5-kinase family protein	phosphatidylinositol-4-phosphate 5-kinase
Sapur.007G082700.1	255.9876955	7.700201817	0.305852066	25.17623	7.30E-140	1.31E-138	cyan	0.65618806	1.07E-20		AT2G22180.1		hydroxyproline-rich glycoprotein family protein	late embryogenesis abundant protein
Sapur.017G117800.1	52.04063176	4.001842853	0.159702417	25.05812	1.42E-138	2.51E-137	cyan	0.693924356	7.13E-24	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT3G47570.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.15WG017700.1	709.2612899	7.77204859	0.311314019	24.9653	1.46E-137	2.54E-136	cyan	0.636389714	3.34E-19		AT3G61640.1	AGP20,AtAGP20	arabinogalactan protein 20	arabinogalactan peptide protein
Sapur.005G016100.1	1166.784014	7.549079774	0.302745612	24.93539	3.08E-137	5.36E-136	cyan	0.636821732	3.11E-19	GO:0004857				plant invertase/pectin methylesterase inhibitor protein
Sapur.019G017800.1	49.99934901	5.82906449	0.234744996	24.83147	4.10E-136	7.08E-135	cyan	0.601380412	8.20E-17	GO:0006468,GO:0004672	AT1G07650.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.014G049800.1	910.629664	2.570874254	0.10354453	24.82868	4.39E-136	7.58E-135	cyan	0.72207318	1.39E-26	GO:0055114,GO:0016616,GO:0006694,GO:0003854	AT4G00110.1	GAE3	UDP-D-glucuronate 4-epimerase 3	UDP-D-glucuronate 4-epimerase
Sapur.016G266700.1	332.5575877	7.087156331	0.28780982	24.62444	6.91E-134	1.17E-132	cyan	0.535005336	5.27E-13		AT5G08240.1			transmembrane protein, putative
Sapur.004G040400.1	555.8515295	2.155617837	0.087780094	24.55702	3.64E-133	6.11E-132	cyan	0.780268685	2.10E-33	GO:0007165	AT4G18700.1	ATWL4,CIPK12,SnRK3.9,WL	CBL-interacting protein kinase 12	CBL-interacting Serine/Threonine-kinase
Sapur.007G101400.1	2092.307967	3.176281544	0.129754277	24.47921	2.46E-132	4.10E-131	cyan	0.661308899	4.24E-21		AT1G58120.1			transmembrane protein, putative
Sapur.007G100000.1	142.9404941	5.97786206	0.244296366	24.46971	3.10E-132	5.17E-131	cyan	0.560829791	2.19E-14	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT1G05580.1	ATCHX23,CHX23	cation/H+ exchanger 23	cation proton exchanger
Sapur.010G042600.1	67.90582342	3.812605759	0.155881535	24.45835	4.10E-132	6.82E-131	cyan	0.694958656	5.74E-24		AT2G33460.1	RIC1	ROP-interactive CRIB motif-containing protein 1	P21-Rho-binding domain protein
Sapur.004G160700.1	86.25195978	7.992545751	0.328366329	24.34033	7.34E-131	1.21E-129	cyan	0.671685194	6.06E-22					NA
Sapur.013G011800.1	1290.883714	7.671639923	0.315846819	24.28912	2.55E-130	4.18E-129	cyan	0.638556019	2.32E-19	GO:0004857	AT5G50030.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	plant invertase/pectin methylesterase inhibitor protein
Sapur.016G133500.1	186.6760495	3.90951569	0.161129106	24.26325	4.79E-130	7.83E-129	cyan	0.636158408	3.47E-19	GO:0016021,GO:0004252,GO:0006508	AT2G29050.1	ATRBL1,RBL1	RHOMBOID-like 1	rhomboid family protein
Sapur.013G012500.1	3038.831047	7.380453553	0.304233392	24.25918	5.29E-130	8.64E-129	cyan	0.592584837	2.95E-16	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT3G05610.1		Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.010G129700.1	63.02226794	6.098741152	0.251437641	24.25548	5.79E-130	9.44E-129	cyan	0.631131752	7.99E-19		AT1G09157.1		Protein of unknown function (DUF679)	transmembrane protein, putative
Sapur.001G108000.1	71.37967944	4.407404032	0.182073566	24.20672	1.89E-129	3.07E-128	cyan	0.660698345	4.74E-21					hypothetical protein
Sapur.005G179200.1	613.3082695	5.749654209	0.238497716	24.1078	2.07E-128	3.32E-127	cyan	0.624076655	2.50E-18		AT1G30690.1		Sec14p-like phosphatidylinositol transfer family protein	NA
Sapur.016G041600.1	49.6429003	6.041275298	0.250706736	24.09698	2.69E-128	4.30E-127	cyan	0.665740435	1.86E-21		AT2G42140.1		VQ motif-containing protein	VQ motif protein
Sapur.15WG111200.1	355.1677819	7.737703421	0.321109077	24.09681	2.70E-128	4.31E-127	cyan	0.582508527	1.22E-15		AT1G24520.1	BCP1	homolog of Brassica campestris pollen protein 1	transmembrane protein, putative
Sapur.007G020400.1	17.17284025	4.521906263	0.188213578	24.0254	1.51E-127	2.39E-126	cyan	0.761095937	6.07E-31	GO:0016020	AT2G18260.1	ATSYP112,SYP112	syntaxin of plants 112	syntaxin, putative
Sapur.010G071900.1	802.0237578	8.265001073	0.344730192	23.97527	5.04E-127	7.92E-126	cyan	0.613553793	1.31E-17	GO:0016787	AT3G17790.1	ATACP5,ATPAP17,PAP17	purple acid phosphatase 17	NA
Sapur.001G104800.1	229.8501247	7.544506598	0.31548358	23.9141	2.18E-126	3.42E-125	cyan	0.563441792	1.56E-14	GO:0004857	AT4G02250.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	plant invertase/pectin methylesterase inhibitor protein
Sapur.003G057700.1	249.1404426	9.820471348	0.410689694	23.91214	2.29E-126	3.58E-125	cyan	0.551054554	7.54E-14	GO:0015743	AT4G17970.1	ALMT12,ATALMT12	aluminum-activated, malate transporter 12	aluminum activated malate transporter
Sapur.018G043500.1	57.67068139	4.424676321	0.1854975	23.85302	9.42E-126	1.46E-124	cyan	0.673285408	4.46E-22	GO:0006950,GO:0006468,GO:0005524,GO:0004672	AT5G12000.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	Serine/Threonine kinase domain protein
Sapur.15ZG040100.1	134.3453008	8.558699574	0.359690655	23.79461	3.80E-125	5.86E-124	cyan	0.608840697	2.69E-17	GO:0016021	AT1G18520.1	TET11	tetraspanin11	tetraspanin family protein
Sapur.019G087600.1	294.4770092	6.823073403	0.286974479	23.77589	5.93E-125	9.13E-124	cyan	0.617729605	6.84E-18		AT1G23145.1	RALFL2	RALF-like 2	NA
Sapur.017G093300.1	440.845077	2.639048122	0.111282083	23.71494	2.53E-124	3.86E-123	cyan	0.750102446	1.24E-29	GO:0008152,GO:0003824	AT4G05160.1		AMP-dependent synthetase and ligase family protein	4-coumarate-CoA ligase
Sapur.T055800.1	53.59460318	7.451950753	0.314370426	23.70436	3.25E-124	4.96E-123	cyan	0.589956353	4.28E-16	GO:0004857	AT1G02550.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	NA
Sapur.003G111300.1	1868.040474	1.027507271	0.04335003	23.70257	3.39E-124	5.17E-123	cyan	0.846898857	2.30E-44	GO:0005525	AT1G02130.1	ARA-5,ARA5,ATRAB1B,ATRA	RAS 5	small GTPase family Rab protein
Sapur.T043000.1	53.71312767	7.575690749	0.320328466	23.64976	1.19E-123	1.80E-122	cyan	0.590838485	3.78E-16	GO:0004857	AT1G02550.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	NA
Sapur.007G094700.1	264.6068242	2.69103477	0.11395997	23.61386	2.78E-123	4.19E-122	cyan	0.726997257	4.32E-27		AT4G33440.1		Pectin lyase-like superfamily protein	glycoside hydrolase family 28 protein/polygalacturonase (pectinase) family protein
Sapur.008G078100.1	487.8675685	3.091079294	0.130942369	23.60641	3.31E-123	4.98E-122	cyan	0.587104967	6.41E-16	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G64940.1	CYP89A6	cytochrome P450, family 87, subfamily A, polypeptide 6	cytochrome P450 family protein
Sapur.006G177400.1	888.6459968	1.365701426	0.057887754	23.59223	4.63E-123	6.96E-122	cyan	0.797975342	6.56E-36	GO:0009264,GO:0008253	AT4G33140.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	5' nucleotidase, deoxy (pyrimidine)%2C cytosolic type C protein (NT5C)
Sapur.012G013000.1	340.7111858	1.359909529	0.057729092	23.55675	1.07E-122	1.60E-121	cyan	0.806935488	2.84E-37	GO:0007275,GO:0006511,GO:0005634	AT4G27880.1		Protein with RING/U-box and TRAF-like domains	ubiquitin ligase SINAT3, putative
Sapur.012G074900.1	2485.825453	1.817765469	0.077514039	23.45079	1.30E-121	1.93E-120	cyan	0.748126188	2.09E-29		AT5G14120.1		Major facilitator superfamily protein	nodulin-like protein
Sapur.002G175300.1	284.9417025	2.4106334	0.103034625	23.39634	4.66E-121	6.88E-120	cyan	0.755032178	3.27E-30		AT3G21610.1		Acid phosphatase/vanadium-dependent haloperoxidase-related protein	acid phosphatase/vanadium-dependent haloperoxidase-like protein
Sapur.012G084800.1	109.6849097	3.840614046	0.164589772	23.33446	1.98E-120	2.91E-119	cyan	0.661622871	4.00E-21		AT2G28710.3		Nucleotide-diphospho-sugar transferase family protein	NA
Sapur.019G018000.1	81.25726353	2.508727548	0.107572092	23.32136	2.69E-120	3.95E-119	cyan	0.769933207	4.77E-32	GO:0006468,GO:0004672	AT1G07650.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.006G092000.1	1432.19669	4.781577335	0.205131276	23.30984	3.52E-120	5.16E-119	cyan	0.669701538	8.84E-22	GO:0005509	AT4G20780.1	CML42	calmodulin like 42	calcium-binding protein CML27, putative
Sapur.016G228100.1	17.37523604	7.565969119	0.32504403	23.27675	7.63E-120	1.11E-118	cyan	0.624324672	2.41E-18		AT1G50720.1		Stigma-specific Stig1 family protein	NA
Sapur.001G161900.1	390.9507079	1.657380378	0.071226991	23.26899	9.14E-120	1.33E-118	cyan	0.802479454	1.38E-36		AT3G16350.1		Homeodomain-like superfamily protein	MYB transcription factor-like protein, putative
Sapur.017G066400.1	1803.399062	5.740921575	0.246937485	23.24848	1.47E-119	2.15E-118	cyan	0.586962396	6.54E-16	GO:0016853,GO:0005975	AT5G15140.1		Galactose mutarotase-like superfamily protein	aldose 1-epimerase
Sapur.013G139700.1	2228.291572	1.936726849	0.083456406	23.20645	3.92E-119	5.69E-118	cyan	0.759497622	9.50E-31	GO:0007165	AT2G30360.1	CIPK11,PKS5,SIP4,SNRK3.22	SOS3-interacting protein 4	CBL-interacting Serine/Threonine-kinase, putative
Sapur.006G040500.1	544.873238	2.75162897	0.118690439	23.18324	6.72E-119	9.73E-118	cyan	0.689543609	1.76E-23	GO:0006468,GO:0004672	AT3G57530.1	ATCPK32,CDPK32,CPK32	calcium-dependent protein kinase 32	calcium-dependent kinase
Sapur.006G142200.1	445.4294389	8.208858253	0.354738929	23.14056	1.81E-118	2.60E-117	cyan	0.627600497	1.42E-18	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT3G44900.1	ATCHX4,CHX4	cation/H+ exchanger 4	NA
Sapur.017G073600.1	514.9548508	7.618820686	0.329366923	23.13171	2.22E-118	3.18E-117	cyan	0.59834346	1.28E-16	GO:0008138,GO:0006470	AT5G39400.1	ATPTEN1,PTEN1	Calcium/lipid-binding (CaLB) phosphatase	phosphatidylinositol-3%2C4%2C5-trisphosphate 3-phosphatase
Sapur.016G273200.1	588.9764807	2.544282833	0.110051057	23.11911	2.97E-118	4.26E-117	cyan	0.627185042	1.52E-18	GO:0005975,GO:0004553	AT5G54570.1	BGLU41	beta glucosidase 41	glycoside hydrolase family 1 protein
Sapur.012G083600.1	105.3600163	4.601109333	0.199029449	23.11773	3.07E-118	4.40E-117	cyan	0.596866645	1.59E-16	GO:0035194,GO:0003712	AT5G07350.2	AtTudor1,TSN1,Tudor1	TUDOR-SN protein 1	tudor protein
Sapur.013G045100.1	30.36030589	6.902235487	0.298622779	23.11356	3.38E-118	4.83E-117	cyan	0.618387285	6.17E-18	GO:0005515	AT2G33320.1		Calcium-dependent lipid-binding (CaLB domain) family protein	NA
Sapur.010G103400.1	184.387587	2.881087974	0.124779213	23.08949	5.91E-118	8.40E-117	cyan	0.741223881	1.26E-28		AT3G25600.1		Calcium-binding EF-hand family protein	calcium-binding protein CML16, putative
Sapur.003G152900.1	49.20020044	3.085709864	0.133882745	23.04785	1.55E-117	2.18E-116	cyan	0.698067303	2.98E-24	GO:0055085,GO:0016021,GO:0016020,GO:0006810,GO:0005215	AT3G54450.1		Major facilitator superfamily protein	peptide transporter, putative
Sapur.004G152000.1	95.08336675	3.334298665	0.144845015	23.01977	2.96E-117	4.15E-116	cyan	0.661980883	3.74E-21	GO:0005509	AT2G27480.1		Calcium-binding EF-hand family protein	EF-hand calcium-binding protein, putative
Sapur.012G018000.1	32.06628934	3.457118678	0.150302234	23.00111	4.54E-117	6.37E-116	cyan	0.722959993	1.13E-26	GO:0005992,GO:0003824	AT1G78090.1	ATTPPB,TPPB	trehalose-6-phosphate phosphatase	trehalose-phosphate phosphatase
Sapur.T018100.1	50.94082644	2.474119643	0.107582226	22.99748	4.94E-117	6.92E-116	cyan	0.782026393	1.21E-33	GO:0006468,GO:0004672	AT1G07650.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.003G027300.1	866.0456228	1.633199048	0.071028728	22.9935	5.41E-117	7.58E-116	cyan	0.781408264	1.47E-33		AT3G16350.1		Homeodomain-like superfamily protein	MYB transcription factor
Sapur.003G165900.1	483.0355599	3.009068438	0.131529774	22.87747	7.79E-116	1.08E-114	cyan	0.697970332	3.04E-24		AT3G13600.1		calmodulin-binding family protein	calmodulin-binding family protein, putative
Sapur.15WG008200.1	196.3307261	4.908969426	0.214682999	22.86613	1.01E-115	1.40E-114	cyan	0.597212165	1.51E-16	GO:0005509	AT4G27790.1		Calcium-binding EF hand family protein	calcium-binding EF hand protein, putative
Sapur.003G012400.1	2510.838586	7.7682145	0.340540462	22.81143	3.53E-115	4.84E-114	cyan	0.60373963	5.78E-17	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT2G47030.1	VGDH1	Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.009G053700.1	399.4953791	6.979511061	0.306214296	22.7929	5.39E-115	7.38E-114	cyan	0.594847725	2.13E-16	GO:0006468,GO:0005524,GO:0004672	AT5G12180.1	CPK17	calcium-dependent protein kinase 17	calcium-dependent kinase
Sapur.003G104300.1	75.50647455	3.405589553	0.149573245	22.76871	9.37E-115	1.28E-113	cyan	0.684162112	5.26E-23	GO:0005509	AT5G24270.2	ATSOS3,CBL4,SOS3	Calcium-binding EF-hand family protein	calcineurin B-like protein
Sapur.010G196100.1	270.1774321	7.136959713	0.314591051	22.68647	6.09E-114	8.24E-113	cyan	0.546628669	1.30E-13	GO:0016757	AT3G06260.1	GATL4	galacturonosyltransferase-like 4	CAZy family GT8 glycosyltransferase

Sapur.016G227900.1	989.2866305	1.268197588	0.055919207	22.67911	7.20E-114	9.73E-113	cyan	0.802791697	1.24E-36		AT3G20290.1	ATEHD1,EHD1	EPS15 homology domain 1	calcium-binding EF hand protein
Sapur.009G079600.1	1152.055893	1.156478207	0.051295518	22.5454	1.49E-112	1.98E-111	cyan	0.805751786	4.34E-37	GO:0016021,GO:0005783	AT3G19260.1	LAG1 HOMOLOG 2,LOH2	LAG1 homologue 2	longevity assurance-like protein
Sapur.018G074500.1	137.0325842	7.127710091	0.318698861	22.36503	8.62E-111	1.12E-109	cyan	0.601381343	8.20E-17	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT5G22900.1	ATCHX3,CHX3	cation/H+ exchanger 3	cation/H(+) antiporter
Sapur.002G050700.1	19.02382929	7.440798143	0.333375545	22.31957	2.39E-110	3.08E-109	cyan	0.650742924	2.84E-20	GO:0009733	AT1G20470.1		SAUR-like auxin-responsive protein family	NA
Sapur.018G115100.1	553.4461817	2.899686359	0.129987352	22.30745	3.13E-110	4.04E-109	cyan	0.680089448	1.18E-22	GO:0055085,GO:0008324,GO:0006812	AT4G10310.1	ATHKT1,HKT1	high-affinity K+ transporter 1	sodium transporter HKT1
Sapur.016G181900.1	102.8906582	3.869401599	0.173925596	22.24745	1.19E-109	1.53E-108	cyan	0.653629208	1.70E-20		AT4G06744.1		Leucine-rich repeat (LRR) family protein	Serine/Threonine kinase, plant-type protein%2C putative
Sapur.001G152500.1	194.015342	3.542040199	0.159667672	22.18383	4.92E-109	6.26E-108	cyan	0.650465266	2.98E-20		AT1G79910.1		Regulator of Vps4 activity in the MVB pathway protein	regulator of Vps4 activity in the MVB pathway protein
Sapur.008G050000.1	511.8106314	2.600904997	0.117435321	22.14755	1.10E-108	1.39E-107	cyan	0.649689953	3.42E-20		AT2G39890.1	ATPROT1,PROT1	proline transporter 1	betaine/proline transporter
Sapur.019G029900.1	275.8980185	7.653871511	0.346465982	22.09126	3.84E-108	4.83E-107	cyan	0.586389097	7.09E-16	GO:0008408,GO:0006139,GO:0003676	AT5G06450.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	3'-5' exonuclease
Sapur.003G064800.1	264.9654501	1.3417373	0.060861664	22.04569	1.05E-107	1.32E-106	cyan	0.808078023	1.88E-37		AT5G45610.1	SUV2	protein dimerizations	ATR interacting protein, putative
Sapur.008G008200.1	2028.667702	7.215641573	0.329197922	21.91886	1.72E-106	2.12E-105	cyan	0.552670633	6.16E-14	GO:0005975,GO:0004553	AT5G20950.2		Glycosyl hydrolase family protein	B-1%2C4-glucanase
Sapur.001G180400.1	183.3211908	1.333971006	0.060937343	21.89086	3.17E-106	3.91E-105	cyan	0.801747228	1.78E-36	GO:0051536,GO:0016226,GO:0005506	AT5G49940.1	ATCNFU2,NFU2	NIFU-like protein 2	NA
Sapur.014G001000.1	215.4308314	7.419616781	0.339308917	21.86685	5.37E-106	6.61E-105	cyan	0.555359746	4.40E-14	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT3G20190.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.004G161700.1	634.4731391	3.39579789	0.155514084	21.83595	1.06E-105	1.30E-104	cyan	0.630840137	8.38E-19	GO:0016758,GO:0008152	AT2G28080.1		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase, putative
Sapur.010G028800.1	166.0677164	2.527656404	0.115762064	21.83493	1.08E-105	1.32E-104	cyan	0.72342382	1.01E-26		AT1G23710.1		Protein of unknown function (DUF1645)	DUF1645 family protein
Sapur.009G114600.1	779.9568733	2.113496109	0.096838301	21.825	1.34E-105	1.64E-104	cyan	0.720826902	1.86E-26	GO:0008270,GO:0003677	AT2G36320.1		A20/AN1-like zinc finger family protein	zinc finger A20 and AN1 domain stress-associated protein
Sapur.010G176900.1	526.6233654	1.322193886	0.060846725	21.72991	1.07E-104	1.30E-103	cyan	0.817295287	6.07E-39	GO:0016833,GO:0009058	AT2G28880.1	ADCS,emb1997	para-aminobenzoate (PABA) synthase family protein	aminodeoxychorismate synthase
Sapur.006G113100.2	43.64779394	2.280378711	0.105023707	21.71299	1.55E-104	1.87E-103	cyan	0.569913313	6.69E-15	GO:0009733	AT5G20810.1		SAUR-like auxin-responsive protein family	SAUR-like auxin-responsive protein
Sapur.016G249900.1	847.1070705	1.144063628	0.052711878	21.7041	1.88E-104	2.27E-103	cyan	0.800264994	2.99E-36	GO:0005515	AT1G53320.1	AtTLP7,TLP7	tubby like protein 7	Tub transcription factor
Sapur.T053700.1	44.43976922	2.336219748	0.107747024	21.68245	3.00E-104	3.62E-103	cyan	0.77046361	4.08E-32	GO:0006468,GO:0004672	AT1G07650.1		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.002G163800.1	574.6730735	1.317848464	0.060783965	21.68086	3.11E-104	3.74E-103	cyan	0.811113633	6.19E-38	GO:0031011	AT2G47350.1		HIT zinc finger ;PAPA-1-like conserved region	INO80 complex subunit B
Sapur.007G051500.1	67.17275786	8.148256607	0.375877386	21.67796	3.31E-104	3.98E-103	cyan	0.598047521	1.34E-16	GO:0006468,GO:0005524,GO:0004672	AT4G28670.1		Protein kinase family protein with domain of unknown function (DUF26)	NA
Sapur.017G064700.1	2094.166271	7.289612263	0.336643052	21.65383	5.59E-104	6.70E-103	cyan	0.548741193	1.00E-13	GO:0030570	AT5G15110.1		Pectate lyase family protein	pectate lyase, putative
Sapur.008G028300.1	672.502491	1.883266839	0.087009335	21.64442	6.86E-104	8.19E-103	cyan	0.731914871	1.31E-27		AT2G38970.1		Zinc finger (C3HC4-type RING finger) family protein	NA
Sapur.005G202100.1	78.31972575	1.810086678	0.08363291	21.64323	7.04E-104	8.40E-103	cyan	0.783050917	8.78E-34		AT4G37420.1		Domain of unknown function (DUF23)	glycosyltransferase family 92 protein
Sapur.016G189400.1	41.59343491	7.934753964	0.367754176	21.57624	3.00E-103	3.56E-102	cyan	0.599124338	1.14E-16		AT5G09430.1		alpha/beta-Hydrolases superfamily protein	alpha/beta-hydrolase domain protein
Sapur.003G126600.1	17.11050954	5.244583304	0.243218808	21.56323	3.98E-103	4.72E-102	cyan	0.681823429	8.40E-23	GO:0006355,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AT1G26310.1	AGL10,CAL,CAL1	K-box region and MADS-box transcription factor family protein	NA
Sapur.005G182100.1	340.048709	7.594230455	0.35259024	21.5384	6.80E-103	8.03E-102	cyan	0.535935308	4.72E-13					NA
Sapur.019G059000.1	63.45111673	2.405378543	0.111883883	21.49888	1.59E-102	1.88E-101	cyan	0.747006133	2.81E-29	GO:0005515,GO:0006468,GO:0004672	AT3G14840.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.003G137200.1	241.6428895	1.009956478	0.04706227	21.46	3.68E-102	4.31E-101	cyan	0.810951372	6.57E-38	GO:0016021,GO:0006888,GO:0005801,GO:0000139	AT1G15880.1	atgos11,GOS11	golgi snare 11	SNAP receptor complex protein
Sapur.003G082100.1	744.4745643	1.258296681	0.058763245	21.41299	1.01E-101	1.18E-100	cyan	0.777238402	5.33E-33		AT1G12450.1		SNARE associated Golgi protein family	SNARE associated family protein
Sapur.007G101300.1	373.4728795	3.441488787	0.160917509	21.38666	1.78E-101	2.06E-100	cyan	0.599331543	1.11E-16		AT1G58122.1	CPuORF45	conserved peptide upstream open reading frame 45	peptide upstream ORF protein
Sapur.014G000800.1	64.39913855	6.184522877	0.290063207	21.32129	7.20E-101	8.30E-100	cyan	0.610015405	2.25E-17	GO:0005515,GO:0006468,GO:0004672	AT1G78980.1	SRF5	STRUBBELIG-receptor family 5	NA
Sapur.002G148800.1	4214.338852	2.276736733	0.106795361	21.31869	7.62E-101	8.77E-100	cyan	0.70079251	1.66E-24	GO:0006629	AT2G46210.1		Fatty acid/sphingolipid desaturase	fatty acid/sphingolipid desaturase
Sapur.019G098300.1	146.9618897	7.723865551	0.362758452	21.29203	1.35E-100	1.54E-99	cyan	0.533021675	6.65E-13		AT1G65690.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.006G120500.1	95.09255408	2.921107056	0.137339116	21.2693	2.19E-100	2.50E-99	cyan	0.684226277	5.19E-23		AT5G35460.1			plant/MOK9-4 protein
Sapur.006G013600.1	266.784578	5.20672977	0.246727979	21.10312	7.45E-99	8.36E-98	cyan	0.564595911	1.35E-14		AT5G41761.1			NA
Sapur.016G273400.1	215.922701	2.744479495	0.130216089	21.07635	1.31E-98	1.47E-97	cyan	0.645814032	6.72E-20		AT5G54585.1			hypothetical protein
Sapur.003G003300.1	374.0775061	3.780384444	0.180222968	20.97615	1.08E-97	1.20E-96	cyan	0.652893753	1.94E-20	GO:0005515	AT5G49920.1		Octicosapeptide/Phox/Bem1p family protein	PB1 domain protein
Sapur.013G039400.1	148.2209441	6.581604872	0.31423899	20.94458	2.10E-97	2.32E-96	cyan	0.538515013	3.47E-13		AT1G08790.1		Protein of unknown function (DUF1685)	NA
Sapur.004G115400.1	224.2668748	5.964440731	0.28649347	20.81877	2.93E-96	3.18E-95	cyan	0.508508556	1.05E-11	GO:0006468,GO:0004672	AT4G34440.1		Protein kinase superfamily protein	NA
Sapur.001G114300.1	963.7195304	0.903019957	0.043569621	20.72591	2.02E-95	2.17E-94	cyan	0.806591149	3.21E-37	GO:0005515	AT5G46860.1	ATSYP22.ATVAM3.SGR3.SYF	Syntaxin/t-SNARE family protein	syntaxin
Sapur.014G051800.1	103.2715764	2.590073851	0.125413811	20.65222	9.32E-95	9.95E-94	cyan	0.65173852	2.38E-20		AT4G00220.1	JLO,LBD30	Lateral organ boundaries (LOB) domain family protein	LOB domain protein
Sapur.006G099900.1	67.21016804	3.34850287	0.162174687	20.64751	1.03E-94	1.10E-93	cyan	0.665674221	1.89E-21		AT2G28200.1		C2H2-type zinc finger family protein	C2H2-type zinc-finger protein, putative
Sapur.15WG003200.1	38.97343227	4.361060375	0.211365522	20.63279	1.39E-94	1.49E-93	cyan	0.507120815	1.22E-11		AT5G19650.1	ATOFP8,OFP8	ovate family protein 8	ovate transcriptional repressor
Sapur.011G099800.1	651.8480521	2.212047561	0.10748231	20.58057	4.10E-94	4.34E-93	cyan	0.666335528	1.67E-21		AT4G27100.2		Ypt/Rab-GAP domain of gyp1p superfamily protein	GTPase-activating protein
Sapur.007G110700.1	1014.46333	0.953329728	0.046438109	20.52904	1.18E-93	1.25E-92	cyan	0.811991049	4.48E-38	GO:0006468,GO:0004672	AT2G43230.2		Protein kinase superfamily protein	PTI1-like tyrosine-kinase
Sapur.016G243700.1	1107.222471	2.374216685	0.115918784	20.48173	3.13E-93	3.28E-92	cyan	0.679461925	1.34E-22		AT3G62730.1			plant/F26K9-160 protein
Sapur.010G146500.1	28.52575236	5.60334316	0.274122092	20.44105	7.22E-93	7.53E-92	cyan	0.621799596	3.60E-18	GO:0003824,GO:0006470,GO:0004722	AT2G40180.1	ATHPP2C5,PP2C5	phosphatase 2C5	protein phosphatase 2C
Sapur.013G011300.1	415.778334	2.435456366	0.11926615	20.42035	1.10E-92	1.15E-91	cyan	0.678758571	1.54E-22	GO:0003824	AT3G05630.1	PDLZ2,PLDP2,PLDZETA2	phospholipase D P2	phospholipase D
Sapur.008G083500.1	31.90842178	3.790000432	0.186044861	20.37143	3.00E-92	3.10E-91	cyan	0.661668825	3.96E-21	GO:0006468,GO:0004672	AT3G04690.1	ANX1	Malectin/receptor-like protein kinase family protein	feronia receptor-like kinase
Sapur.005G071900.1	18.40676006	6.788733554	0.333454696	20.35879	3.88E-92	4.01E-91	cyan	0.634925374	4.27E-19					NA
Sapur.006G180700.1	1169.558239	7.134595163	0.350525379	20.354	4.28E-92	4.41E-91	cyan	0.505188567	1.50E-11	GO:0005975,GO:0004553	AT3G43860.1	AtGH9A4,GH9A4	glycosyl hydrolase 9A4	endoglucanase
Sapur.017G078100.1	15.32669743	5.309081016	0.261414747	20.30903	1.07E-91	1.10E-90	cyan	0.689460938	1.79E-23		AT5G39200.1			NA
Sapur.017G103000.1	2321.373952	1.81871106	0.089644525	20.28803	1.64E-91	1.68E-90	cyan	0.717692187	3.86E-26		AT1G23170.2		Protein of unknown function DUF2359, transmembrane	DUF2359 family protein
Sapur.T001000.1	28.24927387	5.278734979	0.260805849	20.24009	4.34E-91	4.43E-90	cyan	0.589745277	4.41E-16	GO:0006468,GO:0004672	AT1G07650.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.007G017200.1	1238.633332	2.149842555	0.106615671	20.16441	2.01E-90	2.03E-89	cyan	0.715015955	7.14E-26	GO:0006468,GO:0005524,GO:0004672	AT2G18170.1	ATMPK7,MPK7	MAP kinase 7	MAP kinase
Sapur.012G079500.1	1807.936497	0.947479929	0.047043784	20.14039	3.27E-90	3.28E-89	cyan	0.783290297	8.14E-34	GO:0016829,GO:0006520	AT5G23670.2	LCB2	long chain base2	long chain base biosynthesis protein 2a
Sapur.010G005600.1	627.7069461	6.952550611	0.345378908	20.13021	4.01E-90	4.02E-89	cyan	0.566811176	1.01E-14		AT1G02790.1	PGA4	polygalacturonase 4	polygalacturonase
Sapur.010G051900.1	424.9368817	4.721932549	0.234665512	20.12197	4.74E-90	4.74E-89	cyan	0.514382819	5.54E-12					hypothetical protein
Sapur.011G060700.1	171.1958292	1.582884115	0.078671192	20.12025	4.91E-90	4.91E-89	cyan	0.785145891	4.52E-34	GO:0030983,GO:0006298,GO:0005524	AT3G20475.1	ATMSH5,MSH5	MUTS-homologue 5	NA
Sapur.016G278500.1	197.6739698	7.391623806	0.367753005	20.09942	7.47E-90	7.45E-89	cyan	0.540865928	2.62E-13	GO:0006468,GO:0005524,GO:0004672	AT3G20530.1		Protein kinase superfamily protein	receptor Serine/Threonine kinase, putative
Sapur.010G068000.1	629.3482304	1.547675177	0.077037074	20.09	9.03E-90	8.99E-89	cyan	0.740543515	1.50E-28	GO:0007165	AT4G14580.1	CIPK4,SnRK3.3	CBL-interacting protein kinase 4	CBL-interacting kinase
Sapur.019G019700.1	194.3571715	3.00275965	0.149555144	20.07794	1.15E-89	1.14E-88	cyan	0.646348034	6.12E-20					hypothetical protein
Sapur.001G081500.1	378.6935257	2.678907021	0.133572176	20.05588	1.79E-89	1.78E-88	cyan	0.667380364	1.37E-21		AT1G63930.1	ROH1	from the Czech \'roh\' meaning \'corner\'	plant/F6A14-15 protein, putative
Sapur.003G084600.1	4604.830099	1.358898984	0.06784763	20.02869	3.10E-89	3.07E-88	cyan	0.747095171	2.75E-29		AT1G63000.1	NRS/ER,UER1	nucleotide-rhamnose synthase/epimerase-reductase	3%2C5-epimerase/4-reductase
Sapur.009G106400.1	80.60135856	3.432045736	0.171830433	19.97345	9.38E-89	9.20E-88	cyan	0.604356379	5.27E-17		AT5G09220.1	AAP2	amino acid permease 2	amino acid transporter
Sapur.001G075900.1	2159.154032	2.42345905	0.121741659	19.90657	3.57E-88	3.48E-87	cyan	0.728594249	2.94E-27		AT5G41860.1			hypothetical protein
Sapur.005G017700.1	608.1427502	0.983553701	0.049431755	19.8972	4.30E-88	4.19E-87	cyan	0.801273546	2.10E-36	GO:0016787	AT5G27840.1	TOPP8	Calcineurin-like metallo-phosphoesterase superfamily protein	serine/threonine-protein phosphatase PP1
Sapur.003G128000.1	1091.744937	1.144193496	0.057526628	19.88981	4.99E-88	4.85E-87	cyan	0.784243405	6.02E-34	GO:0005783	AT1G27350.1		Ribosome associated membrane protein RAMP4	ribosome associated membrane protein RAMP4
Sapur.005G000600.1	874.9591146	2.606979078	0.131594361	19.81072	2.41E-87	2.32E-86	cyan	0.664012001	2.57E-21		AT3G62020.1	GLP10	germin-like protein 10	germin-like protein
Sapur.012G064400.1	76.32360717	2.305651424	0.116724179	19.75299	7.56E-87	7.25E-86	cyan	0.777421624	5.04E-33	GO:0006468,GO:0005524,GO:0004672	AT5G40380.1	CRK42	cysteine-rich RLK (RECEPTOR-like protein kinase) 42	cysteine-rich receptor-like kinase
Sapur.016G061500.1	152.0404799	4.16801268	0.211446861	19.71187	1.71E-86	1.63E-85	cyan	0.627096198	1.54E-18		AT3G52360.1			transmembrane protein, putative
Sapur.018G006500.1	48.5116205	5.599442334	0.286677031	19.53223	5.84E-85	5.46E-84	cyan	0.627064707	1.55E-18		AT1G61566.1	RALFL9	ralf-like 9	rapid aLkalinization factor
Sapur.002G008300.2	10.07672767	4.401501904	0.225366305	19.53043	6.05E-85	5.65E-84	cyan	0.507873522	1.13E-11		AT4G35190.1		Putative lysine decarboxylase family protein	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG5, putative
Sapur.008G011500.1	219.3939466	6.32990917	0.324879406	19.48387	1.50E-84	1.40E-83	cyan	0.46404659	9.29E-10	GO:0016757	AT3G06260.1	GATL4	galacturonosyltransferase-like 4	CAZy family GT8 glycosyltransferase
Sapur.002G158900.1	1047.592427	7.199621449	0.369683731	19.47508	1.79E-84	1.66E-83	cyan	0.535922536	4.73E-13	GO:0005975,GO:0004650	AT1G02790.1	PGA4	polygalacturonase 4	polygalacturonase
Sapur.002G058700.1	25.72297618	3.318135627	0.170846169	19.42177	5.05E-84	4.66E-83	cyan	0.605533377	4.42E-17					NA
Sapur.016G089600.1	454.3676471	7.74996074	0.399284732	19.40961	6.40E-84	5.90E-83	cyan	0.49130261	6.43E-11		AT2G39700.1	ATEXP4.ATEXPA4.ATHEXP A	expansin A4	alpha expansin
Sapur.018G114700.1	142.8818122	2.634665928	0.135768021	19.40564	6.91E-84	6.37E-83	cyan	0.660837242	4.62E-21	GO:0055085,GO:0008324,GO:0006812	AT4G10310.1	ATHKT1,HKT1	high-affinity K+ transporter 1	NA
Sapur.013G006200.1	419.7227123	0.963266845	0.049675449	19.39121	9.16E-84	8.42E-83	cyan	0.803987847	8.12E-37	GO:0033926	AT1G56560.1		Plant neutral invertase family protein	neutral/alkaline invertase
Sapur.013G066300.1	410.9238977	2.052020674	0.10594786	19.36821	1.43E-83	1.31E-82	cyan	0.70667065	4.63E-25	GO:0043565,GO:0006355,GO:0003700	AT2G40620.1		Basic-leucine zipper (bZIP) transcription factor family protein	BZIP transcription factor
Sapur.010G172600.1	25.15910534	3.832351428	0.198620135	19.29488	5.93E-83	5.39E-82	cyan	0.591763457	3.31E-16					NA
Sapur.016G147300.1	44.89362404	1.798582715	0.09335154	19.26677	1.02E-82	9.24E-82	cyan	0.727174526	4.14E-27	GO:0046872	AT5G12850.1		CCCH-type zinc finger protein with ARM repeat domain	zinc finger CCCH domain protein
Sapur.002G148400.1	40.90752802	2.278720814	0.11848072	19.23284	1.97E-82	1.77E-81	cyan	0.69628408	4.34E-24	GO:0051087	AT2G46240.1	ATBAG6,BAG6	BCL-2-associated athanogene 6	BAG domain protein
Sapur.016G307600.1	559.3219466	1.877360154	0.097748548	19.20602	3.30E-82	2.96E-81	cyan	0.71775132	3.81E-26		AT5G23810.1	AAP7	amino acid permease 7	amino acid permease
Sapur.008G158400.1	8.616994546	6.184219461	0.322077083	19.20105	3.63E-82	3.26E-81	cyan	0.654062102	1.57E-20	GO:0046872,GO:0030001	AT3G21490.1		Heavy metal transport/detoxification superfamily protein	NA
Sapur.010G007000.1	371.0867595	6.862644009	0.358376437	19.14926	9.82E-82	8.76E-81	cyan	0.534455313	5.62E-13		AT1G02790.1	PGA4	polygalacturonase 4	polygalacturonase
Sapur.001G094100.1	664.3245897	1.607830538	0.083981919	19.14496	1.07E-81	9.52E-81	cyan	0.722597634	1.23E-26	GO:0008270,GO:0003677	AT4G12040.2		A20/AN1-like zinc finger family protein	zinc finger A20 and AN1 domain stress-associated protein
Sapur.008G061000.1	20.66237491	4.3578685	0.227637372	19.14391	1.09E-81	9.70E-81	cyan	0.591432204	3.47E-16	GO:0006511	AT2G29070.2		Ubiquitin fusion degradation UFD1 family protein	ubiquitin fusion degradation protein
Sapur.019G072500.1	635.2574375	2.62709257	0.138110588	19.02166	1.13E-80	9.92E-80	cyan	0.719660736	2.45E-26	GO:0080019	AT4G33790.1	CER4,FAR3,G7	Jojoba acyl CoA reductase-related male sterility protein	fatty acyl-CoA reductase
Sapur.016G107300.1	1153.50698	1.671700474	0.087985763	18.99967	1.72E-80	1.50E-79	cyan	0.706818602	4.48E-25	GO:0005515	AT3G51770.2	ATEOL1,ETO1	tetratricopeptide repeat (TPR)-containing protein	ethylene-overproduction protein
Sapur.018G102100.1	62.08634879	2.770847838	0.146118538	18.96301	3.45E-80	3.01E-79	cyan	0.607591988	3.24E-17		AT1G80133.1			epidermal patterning factor-like protein, putative
Sapur.011G031800.1	45.71266415	5.305510172	0.280492124	18.91501	8.58E-80	7.46E-79	cyan	0.47463549	3.38E-10		AT4G04980.1			CHUP1, putative
Sapur.008G033500.1	15.50918005	2.368350224	0.125231267	18.91181	9.12E-80	7.93E-79	cyan	0.750132462	1.23E-29		AT3G53320.1			hypothetical protein
Sapur.018G085100.1	205.5292802	1.826381017	0.096596038	18.90741	9.91E-80	8.61E-79	cyan	0.745273509	4.43E-29		AT4G31020.2		alpha/beta-Hydrolases superfamily protein	alpha/beta hydrolase family protein
Sapur.004G058700.1	17.96951739	3.157911065	0.167303329	18.87536	1.82E-79	1.57E-78	cyan	0.677362818	2.02E-22	GO:0055085,GO:0016020,GO:0006811,GO:0005216	AT3G02850.1	SKOR	STELAR K+ outward rectifier	outward rectifying potassium channel protein
Sapur.009G003300.1	645.6301569	3.872549801	0.205283883	18.86436	2.24E-79	1.93E-78	cyan	0.524792785	1.72E-12	GO:0055085,GO:0016021	AT2G28120.1		Major facilitator superfamily protein	nitrate and chloride transporter
Sapur.003G061100.1	113.0130815	3.319047134	0.176037397	18.85422	2.71E-79	2.34E-78	cyan	0.615000048	1.05E-17		AT5G46840.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif protein
Sapur.011G112400.1	1555.632823	1.282001007	0.068059938	18.83635	3.80E-79	3.27E-78	cyan	0.76804729	8.28E-32		AT5G42110.1			hypothetical protein
Sapur.017G053900.1	89.26248864	5.674599552	0.302983798	18.72905	2.87E-78	2.43E-77	cyan	0.526618959	1.40E-12	GO:0016788	AT1G71691.2		GDSL-like Lipase/Acylhydrolase superfamily protein	NA
Sapur.001G112100.1	922.9782519	1.867861433	0.09976531	18.72255	3.24E-78	2.75E-77	cyan	0.681479529	8.99E-23	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	AT1G32170.1	XTH30,XTR4	xyloglucan endotransglucosylase/hydrolase 30	xyloglucan endotransglycosylase/hydrolase
Sapur.012G027100.1	101.310173	2.390285633	0.128101597	18.6593	1.06E-77	8.94E-77	cyan	0.670982772	6.93E-22	GO:0005544,GO:0005509	AT1G68090.1	ANN5,ANNAT5	annexin 5	annexin
Sapur.014G060000.1	185.3849154	2.354655608	0.126725494	18.58076	4.60E-77	3.84E-76	cyan	0.659269143	6.15E-21	GO:0006468,GO:0004672	AT4G00720.1	ASKTHETA,ATSK32,SK32	shaggy-like protein kinase 32	shaggy-related kinase
Sapur.003G089400.3	11.95156055	4.24976624	0.228747843	18.57839	4.81E-77	4.01E-76	cyan	0.671422844	6.37E-22		AT5G23750.2		Remorin family protein	remorin, carboxy-terminal region protein
Sapur.016G238800.1	1486.865002	1.008179617	0.054280358	18.57356	5.26E-77	4.39E-76	cyan	0.782435062	1.07E-33	GO:0008270,GO:0005515	AT1G53190.2		RING/U-box superfamily protein	RING finger protein
Sapur.15WG009700.1	373.7513223	1.569367062	0.084745228	18.51865	1.46E-76	1.21E-75	cyan	0.702091251	1.26E-24		AT5G52990.1		SNARE-like superfamily protein	VAMP-like protein, putative
Sapur.004G053500.1	4215.979654	1.251564933	0.067611363	18.51116	1.68E-76	1.39E-75	cyan	0.775208088	9.88E-33		AT1G65840.1	ATPAO4,PAO4	polyamine oxidase 4	polyamine oxidase, putative
Sapur.013G094700.1	255.8714179	2.717905482	0.147003021	18.48877	2.54E-76	2.10E-75	cyan	0.644628135	8.24E-20		AT4G32480.1		Protein of unknown function (DUF506)	plant/F8B4-180 protein, putative
Sapur.008G147100.1	2865.976211	1.785514043	0.096671915	18.46983	3.61E-76	2.98E-75	cyan	0.722251665	1.33E-26		AT1G67730.1	ATKCR1,KCR1,YBR159	beta-ketoacyl reductase 1	3-ketoacyl-CoA reductase
Sapur.007G042900.1	4.962723236	5.016335645	0.272120275	18.43426	6.98E-76	5.73E-75	cyan	0.711169182	1.70E-25	GO:0008270,GO:0005515	AT4G34040.1		RING/U-box superfamily protein	NA
Sapur.018G118000.1	1270.276616	4.18876838	0.227369476	18.42274	8.63E-76	7.08E-75	cyan	0.504632586	1.60E-11	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT5G36110.1	CYP716A1	cytochrome P450, family 716, subfamily A, polypeptide 1	cytochrome P450 family 716 monooxygenase
Sapur.012G075500.1	769.6677752	1.080358953	0.058767763	18.38353	1.78E-75	1.45E-74	cyan	0.745438704	4.25E-29	GO:0005515	AT5G50530.1		CBS / octicosapeptide/Phox/Bemp1 (PB1) domains-containing protein	meiotically up-regulated protein
Sapur.002G130200.1	1311.263707	1.864198816	0.101434021	18.37844	1.96E-75	1.59E-74	cyan	0.659861233	5.52E-21		AT2G45900.1		Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-related	DUF4378 domain protein
Sapur.016G001000.1	874.4376184	0.715136323	0.03898807	18.34244	3.79E-75	3.07E-74	cyan	0.797324059	8.20E-36	GO:0005525	AT4G17170.1	AT-RAB2.ATRAB-B1B.ATRAE	RAB GTPase homolog B1C	small GTPase family Rab protein
Sapur.011G118700.1	40.41143569	6.150478153	0.335333945	18.34135	3.87E-75	3.13E-74	cyan	0.428247749	2.21E-08	GO:0055114,GO:0050660,GO:0016491	AT2G34790.1	EDA28,MEE23	FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.011G119400.1	1633.334163	1.057918415	0.057683502	18.34005	3.96E-75	3.21E-74	cyan	0.789740668	1.03E-34	GO:0055114,GO:0016491,GO:0006633,GO:0005506	AT2G34770.1	ATFAH1,FAH1	fatty acid hydroxylase 1	fatty acid hydroxylase
Sapur.002G158800.1	811.4676937	6.624622777	0.362290784	18.28537	1.08E-74	8.70E-74	cyan	0.503676242	1.77E-11	GO:0005975,GO:0004650	AT1G02790.1	PGA4	polygalacturonase 4	polygalacturonase
Sapur.T001100.1	50.33192774	2.391703922	0.131230387	18.22523	3.26E-74	2.60E-73	cyan	0.709765708	2.33E-25	GO:0006468,GO:0004672	AT1G07650.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.019G035900.1	1434.240938	1.052929803	0.058042113	18.14079	1.52E-73	1.20E-72	cyan	0.759215481	1.03E-30	GO:0005515,GO:0016020	AT3G03800.1	ATSYP131,SYP131	syntaxin of plants 131	syntaxin-132 protein
Sapur.008G098000.1	43.44281724	1.574716291	0.086991919	18.10187	3.08E-73	2.43E-72	cyan	0.736104169	4.62E-28					NA
Sapur.016G176000.1	1102.991863	1.740206668	0.096260371	18.07812	4.74E-73	3.73E-72	cyan	0.718609082	3.12E-26		AT1G27730.1	STZ,ZAT10	salt tolerance zinc finger	C2H2-type zinc-finger protein
Sapur.006G153500.1	84.38229818	2.552338993	0.141599712	18.02503	1.24E-72	9.70E-72	cyan	0.658769786	6.74E-21		AT4G31020.1		alpha/beta-Hydrolases superfamily protein	alpha/beta hydrolase family protein
Sapur.008G138900.1	76.75810816	1.633374172	0.090625167	18.02341	1.28E-72	9.98E-72	cyan	0.723632639	9.63E-27		AT2G33390.1			hypothetical protein
Sapur.016G181700.1	1892.062423	1.323985138	0.073736139	17.95572	4.33E-72	3.36E-71	cyan	0.67261174	5.08E-22	GO:0008234,GO:0006508	AT1G47128.1	RD21,RD21A	Granulin repeat cysteine protease family protein	cysteine protease
Sapur.016G114400.1	19.20561756	5.872201781	0.327277503	17.94258	5.49E-72	4.25E-71	cyan	0.536953499	4.18E-13	GO:0016567,GO:0004842	AT3G11840.1	PUB24	plant U-box 24	spotted leaf protein, putative
Sapur.018G096400.1	176.307103	2.289914932	0.127943346	17.89788	1.22E-71	9.45E-71	cyan	0.631021938	8.13E-19	GO:0016758,GO:0009247	AT5G20410.1	ATMGD2,MGD2	monogalactosyldiacylglycerol synthase 2	monogalactosyldiacylglycerol synthase
Sapur.T017100.1	79.49422117	2.29502321	0.128359841	17.8796	1.70E-71	1.31E-70	cyan	0.706235639	5.10E-25	GO:0006468,GO:0004672	AT3G14840.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.014G056500.1	465.8349801	2.507589576	0.140347982	17.86694	2.13E-71	1.64E-70	cyan	0.683326569	6.22E-23	GO:0003824,GO:0005515	AT2G42010.1	PLDBETA,PLDBETA1	phospholipase D beta 1	phospholipase D
Sapur.014G113200.1	101.9229527	1.44170577	0.081057545	17.7862	9.04E-71	6.89E-70	cyan	0.724097502	8.63E-27		AT3G26680.3	ATSNM1,SNM1	DNA repair metallo-beta-lactamase family protein	DNA cross-link repair protein SNM1
Sapur.002G160200.1	855.7649374	1.030763224	0.058017225	17.7665	1.28E-70	9.77E-70	cyan	0.751560027	8.38E-30	GO:0016757	AT3G62660.1	GATL7	galacturonosyltransferase-like 7	glycosyltransferase family 8 protein
Sapur.018G058100.1	1336.365055	1.08217905	0.060937422	17.75886	1.47E-70	1.12E-69	cyan	0.743415879	7.19E-29	GO:0005524	AT3G24530.1		AAA-type ATPase family protein / ankyrin repeat family protein	AAA-type ATPase family protein/ankyrin repeat protein
Sapur.011G069800.1	1231.442052	1.06539751	0.060135224	17.7167	3.12E-70	2.35E-69	cyan	0.750681274	1.06E-29	GO:0008270,GO:0005515	AT1G53190.2		RING/U-box superfamily protein	zinc finger protein, putative
Sapur.001G139700.1	276.8521138	2.605776049	0.147269983	17.69387	4.68E-70	3.52E-69	cyan	0.641039216	1.52E-19	GO:0016021,GO:0016020,GO:0022857	AT5G47470.1		Nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4
Sapur.014G004800.1	27.11026424	2.271745459	0.12912325	17.59362	2.76E-69	2.05E-68	cyan	0.64377601	9.55E-20					NA
Sapur.002G174100.1	154.9275161	1.710366657	0.097619945	17.52067	9.96E-69	7.34E-68	cyan	0.66440253	2.39E-21		AT2G32970.2			NA
Sapur.019G020200.1	42.55491965	3.017466202	0.172358032	17.50697	1.27E-68	9.33E-68	cyan	0.630627991	8.67E-19					NA
Sapur.001G077700.1	1011.897871	1.400336362	0.08012185	17.47758	2.12E-68	1.56E-67	cyan	0.732910429	1.02E-27		AT3G61640.1	AGP20,AtAGP20	arabinogalactan protein 20	transmembrane protein, putative
Sapur.007G105100.1	610.1812593	2.612368237	0.149600257	17.46232	2.77E-68	2.03E-67	cyan	0.615934157	9.04E-18	GO:0016829,GO:0010333,GO:0008152,GO:0000287	AT4G16740.1	ATTPS03,TPS03	terpene synthase 03	(E)-beta-ocimene synthase
Sapur.008G056400.1	38.1569631	2.906167517	0.16655908	17.44827	3.55E-68	2.59E-67	cyan	0.654839129	1.37E-20	GO:0016747	AT2G40230.1		HXXXD-type acyl-transferase family protein	taxadien-5-alpha-ol O-acetyltransferase, putative
Sapur.016G102900.1	66.0872699	3.16394439	0.181728917	17.41024	6.90E-68	5.02E-67	cyan	0.554350292	4.99E-14	GO:0016192,GO:0016021	AT5G05570.1		transducin family protein / WD-40 repeat family protein	synaptobrevin protein
Sapur.002G013600.1	25.80658841	2.310538974	0.132752763	17.40483	7.58E-68	5.51E-67	cyan	0.673961705	3.92E-22	GO:0006468,GO:0005524,GO:0004672	AT1G77280.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	tyrosine kinase domain protein
Sapur.010G185400.1	497.2961825	1.33622495	0.076789688	17.4011	8.09E-68	5.88E-67	cyan	0.720439766	2.04E-26		AT3G20898.1			cyclin-dependent kinase inhibitor siamese protein, putative
Sapur.019G056700.1	736.114178	0.732572818	0.042139209	17.38459	1.08E-67	7.83E-67	cyan	0.776482606	6.71E-33	GO:0016021,GO:0006810,GO:0005524,GO:0005471	AT5G05310.2		TLC ATP/ADP transporter	TLC ATP/ADP transporter
Sapur.018G020000.1	88.67674179	2.439148814	0.140532153	17.35652	1.76E-67	1.27E-66	cyan	0.621101291	4.02E-18	GO:0005515	AT2G25290.1		Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protei	heat shock protein 70 (HSP70)-interacting protein, putative
Sapur.009G076700.1	2476.336951	1.684876204	0.097415849	17.29571	5.07E-67	3.64E-66	cyan	0.683882022	5.56E-23	GO:0008234,GO:0006508	AT1G47128.1	RD21,RD21A	Granulin repeat cysteine protease family protein	cysteine protease
Sapur.006G063800.1	208.5807876	2.025059608	0.117189358	17.28023	6.63E-67	4.75E-66	cyan	0.608886942	2.67E-17	GO:0006950,GO:0006468,GO:0005524,GO:0004672	AT2G24370.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	tyrosine kinase domain protein
Sapur.006G096700.1	373.1562933	0.897452161	0.052080633	17.23197	1.53E-66	1.09E-65	cyan	0.734003792	7.80E-28		AT3G53000.1	AtPP2-A15,PP2-A15	phloem protein 2-A15	F-box protein PP2-A15
Sapur.001G148600.1	1392.601517	1.036809454	0.060174276	17.23011	1.58E-66	1.12E-65	cyan	0.698101426	2.96E-24	GO:0015969	AT1G54130.1	AT-RSH3,ATRSH3,RSH3	RELA/SPOT homolog 3	RelA/SpoT-like protein, putative
Sapur.T009900.1	6.439279168	4.288066408	0.249351996	17.19684	2.80E-66	1.99E-65	cyan	0.69014793	1.56E-23					NA
Sapur.003G086600.1	20.90172855	2.85087534	0.16610108	17.1635	4.98E-66	3.53E-65	cyan	0.6956166	5.00E-24	GO:0016020,GO:0009055,GO:0008137	AT4G26965.1		NADH:ubiquinone oxidoreductase, 17.2kDa subunit	NA
Sapur.009G019600.1	10.71561712	6.644434281	0.387859153	17.13105	8.71E-66	6.14E-65	cyan	0.538620521	3.43E-13	GO:0006412,GO:0005840,GO:0003735	AT3G55280.1	RPL23AB	ribosomal protein L23AB	60S ribosomal protein L23a
Sapur.016G154400.1	697.9300657	1.156070285	0.067567737	17.1098	1.25E-65	8.82E-65	cyan	0.739118358	2.16E-28	GO:0008270,GO:0005515,GO:0046872	AT3G08505.2		zinc finger (CCCH-type/C3HC4-type RING finger) family protein	NA
Sapur.001G079700.3	21.06996042	2.699247138	0.158074434	17.0758	2.25E-65	1.57E-64	cyan	0.700429894	1.80E-24	GO:0009378,GO:0006310,GO:0006281	AT1G64110.2		P-loop containing nucleoside triphosphate hydrolases superfamily protein	P-loop nucleoside triphosphate hydrolase-like protein
Sapur.15WG147700.1	994.4814567	1.146555788	0.067362559	17.02067	5.77E-65	4.03E-64	cyan	0.730483441	1.86E-27		AT5G07270.1	XBAT33	XB3 ortholog 3 in Arabidopsis thaliana	E3 ubiquitin-protein ligase
Sapur.005G149800.1	14.29999087	3.104223739	0.182682542	16.99245	9.34E-65	6.49E-64	cyan	0.57904529	1.96E-15	GO:0030170,GO:0019752,GO:0016831	AT1G43710.1	emb1075	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	serine decarboxylase
Sapur.001G082300.1	415.9950099	1.556999569	0.091718628	16.97583	1.24E-64	8.60E-64	cyan	0.663059182	3.07E-21	GO:0006355,GO:0003677	AT5G41410.1	BEL1	POX (plant homeobox) family protein	BEL1-related homeotic protein, putative
Sapur.011G081100.1	760.7983898	1.403216818	0.082732174	16.96096	1.60E-64	1.11E-63	cyan	0.680525529	1.09E-22		AT1G64980.1		Nucleotide-diphospho-sugar transferases superfamily protein	hypothetical protein
Sapur.013G059700.1	175.6675257	1.20542641	0.071113723	16.95069	1.90E-64	1.32E-63	cyan	0.758698625	1.19E-30	GO:0016020,GO:0015171,GO:0003333	AT1G58030.1	CAT2	cationic amino acid transporter 2	NA
Sapur.009G067000.1	259.9741728	3.782385445	0.223474297	16.92537	2.92E-64	2.02E-63	cyan	0.568852116	7.70E-15	GO:0008283,GO:0008083,GO:0005576	AT3G49780.1	ATPSK3 (FORMER SYMBOL)	phytosulfokine 4 precursor	phytosulfokine peptide protein, putative
Sapur.006G039800.1	287.6603457	0.782349728	0.046264678	16.9103	3.78E-64	2.60E-63	cyan	0.75564129	2.76E-30	GO:0008270	AT3G57480.1		zinc finger (C2H2 type, AN1-like) family protein	NA
Sapur.002G108000.1	297.4679732	1.030119162	0.061109383	16.85697	9.32E-64	6.38E-63	cyan	0.746622031	3.11E-29	GO:0008270	AT1G19270.1	DA1	DA1	zinc ion-binding protein, putative
Sapur.003G060400.1	415.2835803	6.232033746	0.370533767	16.81907	1.77E-63	1.20E-62	cyan	0.46319194	1.01E-09	GO:0055114,GO:0050113,GO:0019310,GO:0005737,GO:0005506	AT2G19800.1	MIOX2	myo-inositol oxygenase 2	Myo-inositol oxygenase
Sapur.005G018400.1	1372.543357	0.845779497	0.050338652	16.80179	2.37E-63	1.61E-62	cyan	0.76995142	4.74E-32		AT3G16640.1	TCTP	translationally controlled tumor protein	translationally-controlled tumor-like protein
Sapur.008G111700.1	24.23232058	3.506320815	0.20920177	16.76047	4.75E-63	3.21E-62	cyan	0.607610268	3.24E-17	GO:0016567,GO:0004842	AT5G37490.1		ARM repeat superfamily protein	Avr9/Cf-9 rapidly elicited protein
Sapur.018G078300.1	739.0942466	0.711019272	0.04248022	16.73765	6.97E-63	4.70E-62	cyan	0.760419253	7.34E-31		AT2G24100.1			hypothetical protein
Sapur.009G053000.1	245.7638847	2.903395112	0.174126315	16.67407	2.02E-62	1.36E-61	cyan	0.567560685	9.13E-15	GO:0005515	AT2G32560.1		F-box family protein	F-box plant protein
Sapur.016G253700.1	1717.163097	1.907111968	0.114607527	16.64037	3.55E-62	2.37E-61	cyan	0.559852102	2.48E-14		AT3G14440.1	ATNCED3.NCED3.SIS7.STO1	nine-cis-epoxycarotenoid dioxygenase 3	9-cis-epoxycarotenoid dioxygenase, putative
Sapur.005G018600.1	123.5952514	4.059111361	0.244203906	16.62181	4.84E-62	3.23E-61	cyan	0.499737456	2.68E-11	GO:0016788	AT1G28650.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-like lipase/acylhydrolase
Sapur.003G040200.1	14.26983746	7.136167183	0.4293913	16.61926	5.05E-62	3.37E-61	cyan	0.498404441	3.08E-11		AT1G54070.1		Dormancy/auxin associated family protein	NA
Sapur.002G138800.1	175.9654041	1.777280242	0.106959035	16.61646	5.30E-62	3.53E-61	cyan	0.696048143	4.56E-24	GO:0003676	AT2G46780.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in RNA-binding protein musashi-like musashi protein
Sapur.018G043700.1	396.6019586	0.760535843	0.045782641	16.61188	5.72E-62	3.80E-61	cyan	0.74208528	1.01E-28	GO:0016021,GO:0015693,GO:0015095	AT5G11960.1		Protein of unknown function (DUF803)	magnesium transporter NIPA protein
Sapur.014G005700.1	471.7359478	0.917638701	0.055248501	16.6093	5.97E-62	3.97E-61	cyan	0.737449957	3.30E-28		AT1G10720.1		BSD domain-containing protein	NA
Sapur.014G077500.1	1193.409455	1.339659241	0.08073331	16.59364	7.75E-62	5.15E-61	cyan	0.684751739	4.67E-23	GO:0005515,GO:0016773	AT2G46500.2	ATPI4K GAMMA 4.PI4K GAN	phosphoinositide 4-kinase gamma 4	phosphatidylinositol 3- and 4-kinase family protein
Sapur.019G041000.1	314.3444192	0.94944137	0.05722219	16.59219	7.94E-62	5.27E-61	cyan	0.732449183	1.15E-27		AT3G02910.1		AIG2-like (avirulence induced gene) family protein	AIG2 family protein
Sapur.014G076700.1	14.86455849	2.946199304	0.179194714	16.44133	9.68E-61	6.32E-60	cyan	0.623099318	2.93E-18	GO:0008270,GO:0005515	AT5G53110.1		RING/U-box superfamily protein	RING-H2 finger protein ATL22
Sapur.003G167300.1	5144.067819	1.345045217	0.081887759	16.42547	1.26E-60	8.20E-60	cyan	0.699854216	2.03E-24		AT5G56540.1	AGP14,ATAGP14	arabinogalactan protein 14	NA
Sapur.005G061500.1	87.96908584	1.730311604	0.105528397	16.39664	2.02E-60	1.31E-59	cyan	0.64652752	5.93E-20					NA
Sapur.15WG026400.1	50.82357004	1.644537776	0.100339843	16.38968	2.27E-60	1.47E-59	cyan	0.691713606	1.13E-23		AT1G17950.1	ATMYB52,BW52,MYB52	myb domain protein 52	R2R3-Myb transcription factor MYB3
Sapur.005G019100.1	2266.494538	1.447120601	0.088402652	16.36965	3.15E-60	2.04E-59	cyan	0.668021891	1.21E-21		AT3G05500.1		Rubber elongation factor protein (REF)	rubber elongation factor
Sapur.016G014500.1	1404.210606	0.613924042	0.037561922	16.34432	4.77E-60	3.09E-59	cyan	0.77124496	3.23E-32	GO:0009058,GO:0003824	AT2G32260.1	ATCCT1,CCT1	phosphorylcholine cytidylyltransferase	choline-phosphate cytidylyltransferase
Sapur.006G030000.1	20.69201219	2.161433365	0.132248901	16.34368	4.83E-60	3.12E-59	cyan	0.698093626	2.96E-24		AT2G41290.1	SSL2	strictosidine synthase-like 2	NA
Sapur.011G053300.1	305.86572	1.947425371	0.119468267	16.30078	9.74E-60	6.27E-59	cyan	0.63025301	9.22E-19		AT1G29640.1		Protein of unknown function, DUF584	senescence regulator
Sapur.004G172300.1	114.9246784	1.258517734	0.077441271	16.25125	2.19E-59	1.40E-58	cyan	0.727176302	4.13E-27	GO:0045454,GO:0015035,GO:0006662	AT3G08710.2	ATH9,TH9,TRX H9	thioredoxin H-type 9	thioredoxin H-type 9 protein
Sapur.012G072100.1	4.208277509	5.412834649	0.334263551	16.19331	5.62E-59	3.57E-58	cyan	0.657422656	8.60E-21					NA
Sapur.006G085300.1	579.3108127	1.353915867	0.083673158	16.18101	6.87E-59	4.35E-58	cyan	0.673046311	4.67E-22		AT2G38360.1	PRA1.B4	prenylated RAB acceptor 1.B4	prenylated rab acceptor family protein
Sapur.011G091500.1	873.5353305	1.906547767	0.117887523	16.1726	7.87E-59	4.98E-58	cyan	0.622258702	3.35E-18		AT5G54240.1		Protein of unknown function (DUF1223)	membrane lipoprotein lipid attachment site-like protein, putative
Sapur.016G199400.1	474.1700317	0.999664831	0.061975271	16.13006	1.57E-58	9.89E-58	cyan	0.70961872	2.41E-25		AT2G33490.1		hydroxyproline-rich glycoprotein family protein	hydroxyproline-rich glycoprotein family protein, putative
Sapur.019G053400.1	784.682364	1.381941899	0.086006777	16.06783	4.29E-58	2.68E-57	cyan	0.653643759	1.70E-20	GO:0006508,GO:0004190	AT3G02740.1		Eukaryotic aspartyl protease family protein	aspartyl protease-like protein
Sapur.005G051500.1	6.135140959	4.069078016	0.253860453	16.0288	8.04E-58	5.01E-57	cyan	0.581301299	1.44E-15		AT1G16260.2		Wall-associated kinase family protein	NA
Sapur.T008100.1	3.787667818	4.841246745	0.302266652	16.01648	9.81E-58	6.10E-57	cyan	0.60747219	3.30E-17					NA
Sapur.006G186500.1	684.9556745	1.000855193	0.062556504	15.99922	1.29E-57	8.04E-57	cyan	0.705028387	6.64E-25		AT1G14560.1		Mitochondrial substrate carrier family protein	graves disease carrier protein
Sapur.006G180400.2	8.088068705	2.588955812	0.162365383	15.94525	3.07E-57	1.90E-56	cyan	0.723646304	9.60E-27		AT4G33180.1		alpha/beta-Hydrolases superfamily protein	NA
Sapur.013G040100.1	230.9651069	3.191983308	0.200246565	15.94027	3.33E-57	2.06E-56	cyan	0.470399015	5.09E-10		AT1G08800.1		Protein of unknown function, DUF593	zein-binding protein
Sapur.002G060800.1	303.2279308	0.906017814	0.056857392	15.93492	3.63E-57	2.24E-56	cyan	0.703634405	9.00E-25	GO:0005515	AT4G08455.1		BTB/POZ domain-containing protein	C2-BTB1+-+bric-A-brac+tramtrack+broad+complex+BTB+domain+with+C2+subfamil protein Y
Sapur.005G151800.1	467.0344843	1.509508257	0.094758806	15.93	3.92E-57	2.42E-56	cyan	0.690278474	1.52E-23		AT1G18740.1		Protein of unknown function (DUF793)	plant/F6A14-15 protein
Sapur.016G088600.1	87.57988041	6.414435087	0.403963414	15.87875	8.89E-57	5.44E-56	cyan	0.434154091	1.34E-08		AT2G39700.1	ATEXP4.ATEXPA4.ATHEXP A	expansin A4	NA
Sapur.019G059300.1	34.4784615	2.702280484	0.170896657	15.81237	2.56E-56	1.56E-55	cyan	0.624615477	2.30E-18					NA
Sapur.001G125200.1	24.11202274	4.177874786	0.265400608	15.74177	7.82E-56	4.72E-55	cyan	0.514634163	5.39E-12	GO:0016020,GO:0015171,GO:0003333	AT5G04770.1	ATCAT6,CAT6	cationic amino acid transporter 6	cationic amino acid transporter, putative
Sapur.008G028100.1	5.592436469	4.377883452	0.27833464	15.72885	9.59E-56	5.78E-55	cyan	0.685259887	4.22E-23	GO:0005515	AT5G04220.2	ATSYTC.NTMC2T1.3.NTMC	Calcium-dependent lipid-binding (CaLB domain) family protein	calcium lipid-binding protein, putative
Sapur.002G074300.1	6.599676274	5.88226326	0.374850492	15.69229	1.71E-55	1.03E-54	cyan	0.547784021	1.13E-13	GO:0006412,GO:0005840,GO:0003735,GO:0019843	ATCG00790.1		ribosomal protein L16	50S ribosomal protein L16
Sapur.013G011900.1	26.48865382	7.807826563	0.501465697	15.57001	1.16E-54	6.90E-54	cyan	0.438597912	9.16E-09	GO:0004857	AT4G24640.1	APPB1	Plant invertase/pectin methylesterase inhibitor superfamily protein	plant invertase/pectin methylesterase inhibitor protein
Sapur.004G130600.1	1216.891993	1.433265711	0.092065919	15.56782	1.20E-54	7.14E-54	cyan	0.687227222	2.83E-23		AT4G38620.1	ATMYB4,MYB4	myb domain protein 4	MYB transcription factor
Sapur.008G149400.1	145.2816015	2.010310898	0.129174673	15.56273	1.30E-54	7.72E-54	cyan	0.606734055	3.69E-17	GO:0016788	AT3G26430.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.002G123900.1	138.5570873	0.879955641	0.05683468	15.48272	4.54E-54	2.67E-53	cyan	0.735508533	5.37E-28	GO:0016746,GO:0008152	AT2G45670.1		calcineurin B subunit-related	1-acylglycerophosphocholine O-acyltransferase
Sapur.001G044100.1	7.45536224	6.191175659	0.402827341	15.3693	2.63E-53	1.53E-52	cyan	0.445070882	5.21E-09					NA
Sapur.007G107900.1	264.9742914	2.634989356	0.171910173	15.32771	4.99E-53	2.89E-52	cyan	0.69574773	4.86E-24	GO:0008270,GO:0005622	AT4G15248.1		B-box type zinc finger family protein	B-box type zinc finger protein
Sapur.007G105000.1	23.998931	2.756166513	0.179834746	15.32611	5.12E-53	2.96E-52	cyan	0.592510523	2.98E-16	GO:0016829,GO:0010333,GO:0008152,GO:0000287	AT4G16740.1	ATTPS03,TPS03	terpene synthase 03	(E)-beta-ocimene synthase
Sapur.013G028400.1	466.9932572	1.552835247	0.10153381	15.29378	8.41E-53	4.84E-52	cyan	0.667982933	1.22E-21	GO:0006468,GO:0004672	AT3G05140.1	RBK2	ROP binding protein kinases 2	cysteine-rich receptor-like kinase
Sapur.019G016300.1	162.0066838	1.315198705	0.08613391	15.26923	1.23E-52	7.04E-52	cyan	0.688843842	2.04E-23		AT1G34320.1		Protein of unknown function (DUF668)	DUF668 family protein
Sapur.016G310800.1	59.27249051	2.233422739	0.146282772	15.26785	1.25E-52	7.19E-52	cyan	0.605187953	4.66E-17		AT5G37010.1			NA
Sapur.017G057800.1	11.82929359	2.64964996	0.173820268	15.24362	1.82E-52	1.04E-51	cyan	0.591789964	3.30E-16		AT3G28150.1	TBL22	TRICHOME BIREFRINGENCE-LIKE 22	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.016G151700.1	27.14381748	6.231684855	0.408891599	15.24043	1.91E-52	1.09E-51	cyan	0.46902959	5.80E-10		AT3G57450.1			hypothetical protein
Sapur.012G074800.1	196.5610127	1.225818125	0.08063566	15.20194	3.43E-52	1.95E-51	cyan	0.620559332	4.38E-18		AT2G25560.1		DNAJ heat shock N-terminal domain-containing protein	NA
Sapur.15ZG040500.1	149.2998366	0.93041976	0.061459171	15.13883	8.98E-52	5.06E-51	cyan	0.745586527	4.09E-29	GO:0007067,GO:0007049,GO:0005634,GO:0000775	AT5G35520.1	ATMIS12,MIS12	minichromosome instability 12 (mis12)-like	kinetochore protein
Sapur.T008200.1	2.994894565	3.991323051	0.264625441	15.08292	2.10E-51	1.18E-50	cyan	0.668167101	1.18E-21					NA
Sapur.003G155300.1	34.24022919	2.260098371	0.150951834	14.97231	1.11E-50	6.18E-50	cyan	0.597298959	1.49E-16		AT1G29050.1	TBL38	TRICHOME BIREFRINGENCE-LIKE 38	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.002G102600.1	193.4735437	1.105028123	0.073840282	14.96511	1.24E-50	6.89E-50	cyan	0.719861073	2.34E-26		AT4G17650.1		Polyketide cyclase / dehydrase and lipid transport protein	polyketide cyclase/dehydrase
Sapur.014G105400.2	11.06005431	2.419920403	0.161706818	14.96486	1.25E-50	6.91E-50	cyan	0.683528808	5.97E-23		AT4G15802.1	AtHSBP,HSBP	heat shock factor binding protein	NA
Sapur.008G172400.1	943.8710789	1.422783463	0.095101614	14.96067	1.33E-50	7.35E-50	cyan	0.646665863	5.79E-20		AT4G02040.1			proline-rich nuclear receptor coactivator protein
Sapur.006G128500.1	403.203561	1.439014232	0.096406427	14.92654	2.21E-50	1.22E-49	cyan	0.691872739	1.09E-23		AT1G18740.1		Protein of unknown function (DUF793)	NA
Sapur.010G116100.1	22.85817374	2.559608329	0.171802118	14.89858	3.37E-50	1.85E-49	cyan	0.52841096	1.14E-12	GO:0055114,GO:0016491	AT1G47990.1	ATGA2OX4,GA2OX4	gibberellin 2-oxidase 4	gibberellin 2-oxidase
Sapur.006G055400.1	2305.523826	1.817156565	0.122129607	14.87892	4.52E-50	2.48E-49	cyan	0.638481962	2.35E-19	GO:0005515	AT2G25490.1	EBF1,FBL6	EIN3-binding F box protein 1	Ein3-binding F-box protein
Sapur.016G169200.1	450.8366471	0.844322918	0.056808469	14.86262	5.76E-50	3.16E-49	cyan	0.699314211	2.28E-24	GO:0055114,GO:0050661,GO:0033014,GO:0008883	AT1G58290.1	HEMA1	Glutamyl-tRNA reductase family protein	glutamyl-tRNA reductase
Sapur.010G026200.1	378.9995993	1.068698523	0.071969131	14.8494	7.02E-50	3.84E-49	cyan	0.664699202	2.26E-21		AT1G10740.4		alpha/beta-Hydrolases superfamily protein	NA
Sapur.011G066000.1	600.00147	0.770444108	0.051923935	14.83794	8.33E-50	4.55E-49	cyan	0.731896563	1.31E-27	GO:0016773,GO:0016020,GO:0005524	AT3G14720.1	ATMPK19,MPK19	MAP kinase 19	MAP kinase
Sapur.006G206800.1	18.15786605	3.671225226	0.248524462	14.77209	2.22E-49	1.20E-48	cyan	0.625895575	1.87E-18	GO:0016021,GO:0006820,GO:0016020,GO:0005452	AT1G15460.1	ATBOR4,BOR4	HCO3- transporter family	anion exchanger family protein
Sapur.010G148100.1	8.985798074	3.632431506	0.246917625	14.71111	5.47E-49	2.95E-48	cyan	0.613993315	1.22E-17	GO:0035556	AT2G40116.1		Phosphoinositide-specific phospholipase C family protein	NA
Sapur.001G003000.1	2094.876182	1.214594824	0.082645634	14.69642	6.80E-49	3.66E-48	cyan	0.655616825	1.19E-20					transmembrane protein, putative
Sapur.016G235000.1	29.57453799	2.44647732	0.166498642	14.69368	7.08E-49	3.81E-48	cyan	0.672142518	5.55E-22	GO:0055085	AT4G26590.1	ATOPT5,OPT5	oligopeptide transporter 5	oligopeptide transporter OPT family protein
Sapur.019G087300.1	886.2933676	0.848496543	0.057952905	14.64114	1.53E-48	8.22E-48	cyan	0.738168741	2.75E-28	GO:0043565,GO:0006355,GO:0003700	AT3G58120.1	ATBZIP61,BZIP61	Basic-leucine zipper (bZIP) transcription factor family protein	bZIP transcription factor
Sapur.008G118500.1	13.86352611	4.469583503	0.305297919	14.64007	1.56E-48	8.35E-48	cyan	0.538428226	3.51E-13					NA
Sapur.008G166100.1	41.8850906	5.613778876	0.383720315	14.62987	1.81E-48	9.69E-48	cyan	0.492275536	5.82E-11					NA
Sapur.006G094100.1	8749.289929	0.75458785	0.051610652	14.62078	2.07E-48	1.11E-47	cyan	0.704812573	6.96E-25	GO:0055114,GO:0016491	AT3G52880.1	ATMDAR1,MDAR1	monodehydroascorbate reductase 1	monodehydroascorbate reductase
Sapur.006G041000.1	1055.963905	0.77940417	0.053392638	14.5976	2.91E-48	1.55E-47	cyan	0.725419925	6.30E-27		AT3G57550.2	AGK2,GK-2	guanylate kinase	guanylate kinase
Sapur.014G083000.1	446.1622675	1.528284559	0.104762811	14.58804	3.35E-48	1.78E-47	cyan	0.619008499	5.59E-18	GO:0003676	AT2G46780.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in RNA-binding protein musashi-like musashi protein
Sapur.019G020300.1	264.4105954	1.035672667	0.071083149	14.56988	4.37E-48	2.32E-47	cyan	0.660993061	4.49E-21		AT2G18465.1		Chaperone DnaJ-domain superfamily protein	hypothetical protein

Sapur.01T0881700.1	449.67135	1.47669783	0.10173161	14.55835	5.17E-48	2.74E-47	open	0.64309735	1.07E-19	ATG02030.1	Regulator of chromosome condensation (RCC1) family protein
Sapur.002G0285900.1	156.7237021	1.47258534	0.10149604	14.51128	1.03E-47	5.42E-47	open	0.6084169	2.31E-17	GO:0006355;GO:0003677	NAC domain containing protein 74
Sapur.010G0895400.1	6.16683751	1.32636473	0.12000349	14.4618	2.11E-47	1.11E-46	open	0.61797886	5.68E-18		LOB domain-containing protein 42
Sapur.T183500.1	216.9204024	0.93337027	0.06456369	14.44936	2.53E-47	1.32E-46	open	0.74785461	2.25E-20	GO:0005085;GO:0016020;GO:0006810;GO:0015171;GO:0003333	CAT2
Sapur.002G0412300.1	7.10314823	1.92422432	0.13268871	14.43758	3.02E-47	1.57E-46	open	0.62663613	3.33E-19		Homeodomain-like superfamily protein
Sapur.010G0213500.1	24.44063263	2.24617495	0.43281763	14.43145	3.28E-47	1.71E-46	open	0.44843157	1.87E-09	GO:0016021	TSPO(outer membrane tryptophan-rich sensory protein)-related
Sapur.012G0275200.1	381.0262009	0.92585189	0.06413523	14.43004	3.35E-47	1.75E-46	open	0.70481698	6.96E-25		hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein
Sapur.010G0260001.1	137.7219979	0.98238241	0.06818241	14.40983	4.49E-47	2.34E-46	open	0.61853607	4.18E-20		alpha/beta-Hydrolases superfamily protein
Sapur.013G0264400.1	225.3684368	1.60282235	0.11172384	14.3419	1.20E-46	6.20E-46	open	0.63224503	5.66E-19	GO:0046872	zinc finger protein 1
Sapur.005G0221700.1	765.6502279	0.7983502	0.05571169	14.29147	2.27E-46	1.17E-45	open	0.69227416	1.09E-17		myb-domain protein 73
Sapur.016G1714000.1	24.65862956	1.51634485	0.10748548	14.2591	3.93E-46	2.02E-45	open	0.40148868	1.87E-07		pathogenesis-related gene 1
Sapur.010G0260001.1	184.2262863	0.98252277	0.10813569	14.2167	6.88E-46	3.54E-45	open	0.68007818	1.98E-22	GO:0016020;GO:0008810;GO:0005215	nitrate transporter 1.1
Sapur.005G0795600.1	194.9701955	1.68341119	0.11892459	14.15302	1.79E-45	9.08E-45	open	0.56793615	8.69E-15		Transmembrane amino acid transporter family protein
Sapur.016G2777700.1	3.48756066	1.92240188	0.29723796	14.15009	1.84E-45	9.34E-45	open	0.69227416	1.09E-17		F-box plant protein, putative
Sapur.001G1910900.3	56.63836398	1.45648399	0.10170584	14.1157	3.04E-45	1.54E-44	open	0.63053663	8.80E-19	GO:0016787	Pectinacetylesterase family protein
Sapur.010G0260001.1	2.98043812	1.45648399	0.10640533	14.10534	3.52E-45	1.78E-44	open	0.61546583	4.05E-20		hypothetical protein
Sapur.006G0782800.1	1.79948601	0.07840214	0.29169181	13.98153	2.02E-44	1.01E-43	open	0.65208805	1.07E-20		O-fucosyltransferase family protein
Sapur.012G0255600.1	289.8202235	0.95086826	0.05436231	13.97682	2.16E-44	1.07E-43	open	0.67934867	1.27E-20		RING/U-box superfamily protein
Sapur.001G1910900.1	28.78074677	1.02478591	0.07329453	13.96829	2.64E-44	1.31E-43	open	0.64477753	8.06E-20	ATGRAS2;GRAS2;SCL14	SCARECROW-like 14
Sapur.005G1885500.1	218.3763038	2.76300407	0.19846072	13.92619	4.39E-44	2.18E-43	open	0.46272108	1.91E-09		glycosyl oxidase-related protein
Sapur.T053900.1	21.1154222	0.78385012	0.05662529	13.52986	6.04E-42	2.88E-41	open	0.64892456	1.22E-20	GO:0006468;GO:0004672	Leucine-rich repeat transmembrane-4 kinase
Sapur.010G0732300.1	19.79468878	1.49188244	0.10754754	13.87101	9.49E-44	4.67E-43	open	0.67326847	2.06E-22	GO:0016020;GO:0008378;GO:0006486	Galactosyltransferase family protein
Sapur.010G0217900.1	72.60003689	1.55483626	0.11979738	13.85495	1.19E-43	5.88E-43	open	0.64470179	2.96E-21	GO:0005515;GO:0006468;GO:0004672	Leucine-rich repeat transmembrane protein kinase
Sapur.017G1184000.1	5632.515929	0.83469422	0.06038196	13.82774	1.73E-43	8.49E-43	open	0.64497584	8.46E-20	GO:0016758;GO:0008152	UDP-glycosyltransferase BBA1
Sapur.006G0367600.1	3061.75665	0.92240188	0.06708709	13.74974	5.12E-43	2.48E-42	open	0.65407504	4.08E-20	GO:0005515	Calcium-dependent lipid-binding (CaLB domain) family protein
Sapur.018G1127700.1	24.76007766	4.11231793	0.29972366	13.72004	7.70E-43	3.73E-42	open	0.34242416	1.94E-05	GO:0005515	RNI-like superfamily protein
Sapur.006G2302000.1	415.2617552	2.96950808	0.21448623	13.71164	8.65E-43	4.18E-42	open	0.65452561	1.01E-20	GO:0006952;GO:0006468;GO:0005524;GO:0004672	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
Sapur.010G0512200.1	466.3218993	0.92240188	0.07068603	13.70551	9.94E-43	4.80E-42	open	0.68183344	9.31E-23	GO:0016567;GO:0006482	ARM-repeat superfamily protein
Sapur.014G0272500.1	1252.26924	0.65345454	0.04796241	13.66596	1.62E-42	7.81E-42	open	0.69324821	5.28E-24	GO:0005515	PQQ/BTB contain G-protein 1
Sapur.004G0118800.1	40.26963941	1.29147209	0.1797612	13.61428	3.29E-42	1.58E-41	open	0.58977292	4.40E-16	GO:0005975;GO:0004553	beta glucosidase 46
Sapur.016G0291900.1	2.58629984	1.49742588	0.33087682	13.50252	4.44E-42	2.12E-41	open	0.54730473	1.20E-13	GO:0007165;GO:0005515	Disease resistance protein (TIR-NBS-LRR class) family
Sapur.T053900.1	1025.252993	0.81313397	0.05905529	13.52986	6.04E-42	2.88E-41	open	0.52675531	2.52E-25	GO:0004554;GO:0016301;GO:0006662	ATJ3;ATCSH;ATCSH-like protein 4
Sapur.002G0760900.1	919.8619424	0.98247831	0.07984131	13.5317	7.32E-42	3.49E-41	open	0.62799725	1.47E-18	GO:0005524	Leucine-rich repeat protein kinase family protein
Sapur.002G0760900.1	18.36408042	1.61281122	0.12024172	13.41566	3.74E-41	1.76E-40	open	0.66660492	1.59E-21	GO:0006468;GO:0005524;GO:0004672	Leucine-rich repeat transmembrane protein kinase
Sapur.008G1928000.1	2509.08067	1.12138779	0.08346528	13.43528	3.76E-41	1.77E-40	open	0.62903671	1.12E-18	GO:0009051;GO:0004751	ribose-5-phosphate isomerase 2
Sapur.T035600.1	25.75185132	2.27773196	0.16952037	13.4169	4.81E-41	2.26E-40	open	0.68253082	8.46E-22		auxin response factor 11
Sapur.015W0700300.1	2.75272235	2.97289482	0.22149532	13.3769	8.25E-41	3.87E-40	open	0.53317328	6.54E-13	GO:0016021	TET11
Sapur.013G0005500.1	404.3595171	2.39901864	0.18032268	13.31117	1.99E-40	9.28E-40	open	0.53197836	8.06E-13		germin-like protein 10
Sapur.005G1195400.1	67.02559988	1.52226888	0.11661037	13.11115	1.96E-39	9.28E-39	open	0.61561329	1.78E-19		HSP20-like chaperones superfamily protein
Sapur.001G0300900.1	5.25654294	2.40332832	0.25591043	13.29623	2.43E-40	1.13E-39	open	0.51249479	2.06E-12	GO:0016021;GO:0004679;GO:0030247;GO:0004688;GO:0005524;GO:0004672	wall-associated receptor kinase-like protein, putative
Sapur.017G0980800.1	1.59271329	0.96200249	0.30902835	13.18245	2.93E-40	1.36E-39	open	0.62421258	4.80E-19		NA
Sapur.T008900.1	1.5954621	1.62976093	0.27337857	13.27751	3.13E-40	1.45E-39	open	0.65017202	6.21E-21	GO:0004518;GO:0006281;GO:0006289;GO:0005634;GO:0004519;GO:0003697	UVH3;UVR1
Sapur.005G1197000.1	891.6188093	0.92240188	0.07570549	13.16466	3.64E-40	1.69E-39	open	0.68347426	1.84E-17	GO:0005524;GO:0016616;GO:0006694;GO:0003854	GA13
Sapur.003G0647000.1	125.1850253	1.83086288	0.13828562	13.23975	5.17E-40	2.39E-39	open	0.52751826	1.32E-12		UGP-D-glucuronate 4-epimerase 3
Sapur.006G0730600.1	119.9879513	0.91940231	0.14496885	13.23845	5.26E-40	2.43E-39	open	0.5558813	2.28E-14		NA
Sapur.001G1907000.1	185.8279959	1.87655706	0.14224106	13.19277	9.66E-40	4.46E-39	open	0.56893734	9.94E-15	GO:0006468;GO:0004672	Leucine-rich repeat protein kinase family protein
Sapur.017G0809900.1	334.4812751	0.93185211	0.09190956	13.16082	1.47E-39	6.75E-39	open	0.67771542	1.89E-22	GO:0006355;GO:0003677	cycling DOF factor 3
Sapur.001G1461600.1	873.3948949	0.97344488	0.05506317	13.15188	1.66E-39	7.59E-39	open	0.68869753	2.11E-23	GO:0006486;GO:0005622	EN/TW/DUF562 family protein
Sapur.006G1545400.1	16.00738341	1.97182239	0.14996068	13.14673	1.78E-39	8.12E-39	open	0.62643696	1.72E-18		VQ motif-containing protein
Sapur.008G0545300.1	232.1532227	1.40329311	0.10739785	13.11719	2.63E-39	1.20E-38	open	0.55571161	1.42E-11	GO:0006468;GO:0005524;GO:0004672	CRK9/KT4 receptor 2
Sapur.016G1491000.1	2.92105267	0.84228093	0.20591043	13.29623	2.43E-40	1.13E-39	open	0.49807018	2.19E-11		wall-associated receptor kinase-like protein
Sapur.017G0980800.1	74.87831771	1.84087226	0.12493878	13.07346	4.67E-39	2.11E-38	open	0.52840742	1.12E-12	GO:0016788	GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.010G1581800.1	17.32595868	4.20601047	0.32418575	13.05006	6.35E-39	2.87E-38	open	0.50902842	9.95E-12	GO:0006508;GO:0004190	Eukaryotic aspartyl protease family protein
Sapur.004G0238300.1	267.3564446	0.87388662	0.06903124	12.66354	9.40E-37	4.08E-36	open	0.63717642	7.72E-21	GO:0005515	bromodomain 5
Sapur.012G0222300.1	14.72232821	0.48767247	0.26745663	13.03983	7.24E-39	3.28E-38	open	0.45712155	1.76E-09	GO:0004544;GO:0006468;GO:0004672	S-locus lectin protein kinase family protein
Sapur.006G0730300.1	3.22612982	4.91181194	0.37606588	13.02168	7.87E-39	3.55E-38	open	0.5527031	1.34E-14		NA
Sapur.010G1605500.2	7.32645569	2.18450483	0.16792723	13.00865	1.09E-38	4.91E-38	open	0.50017813	2.56E-11		actin-11
Sapur.005G0849800.1	717.6683747	0.98553283	0.07585203	12.99256	1.35E-38	6.05E-38	open	0.62425573	4.77E-19		SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
Sapur.T019029700.1	7.854317271	2.50463768	0.19208628	12.9685	1.82E-38	8.14E-38	open	0.54738042	1.06E-13		Plasma membrane choline transporter family protein
Sapur.006G0843000.1	47.20936769	1.73129169	0.21008535	12.94613	2.54E-38	1.13E-37	open	0.5079423	1.14E-11	GO:0003824	cyclostarterol synthase 1
Sapur.019G0101500.1	138.2319445	1.51398121	0.11243166	12.9393	2.71E-38	1.21E-37	open	0.66820174	2.38E-23	GO:0005515	C2 calcium/lipid phospholipid and GRAM domain containing protein
Sapur.001G1360600.1	985.8628827	0.62006074	0.04792615	12.93848	2.73E-38	1.22E-37	open	0.67388603	6.76E-22	GO:0003993	HAD superfamily, subfamily IIIB acid phosphatase
Sapur.001G0461600.1	6.07354554	1.96202598	0.16723463	12.92869	3.10E-38	1.38E-37	open	0.68869753	2.11E-23	GO:0008168;GO:0005622	EN/TW/DUF562 family protein
Sapur.006G1545400.1	617.6807002	0.78171835	0.06043955	12.8903	5.10E-38	2.27E-37	open	0.62503557	1.88E-18		VQ motif-containing protein
Sapur.006G0545300.1	1910.684898	0.62421201	0.12262028	12.87029	5.38E-38	2.40E-37	open	0.58179664	3.46E-15	GO:0006508;GO:0004190	C2 calcium/lipid phospholipid and GRAM domain containing protein
Sapur.010G0258000.1	230.5072566	2.24706529	0.17488339	12.84891	8.72E-38	3.86E-37	open	0.57388603	6.76E-22	GO:0003993	HAD superfamily, subfamily IIIB acid phosphatase
Sapur.010G0270200.1	18.04378953	1.89022005	0.14717664	12.84338	9.38E-38	4.13E-37	open	0.68869753	2.11E-23	GO:0008168;GO:0005622	EN/TW/DUF562 family protein
Sapur.010G1948800.1	552.1472522	0.76020637	0.05934064	12.81079	1.43E-37	6.28E-37	open	0.62505557	1.88E-18		Coiled-coil-binding beta-1%2C6-N-acetylglucosaminyltransferase family protein, putative
Sapur.017G0656000.1	161.2518187	0.94286017	0.33980259	12.7965	1.73E-37	7.54E-37	open	0.52352069	1.96E-12	GO:0016788	Duplicated homodomain-like superfamily protein
Sapur.005G1461000.1	169.5109006	0.95631723	0.07535157	12.72284	4.41E-37	1.92E-36	open	0.64588116	1.36E-20		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.010G0403000.1	29.31562218	2.26615527	0.17835645	12.69456	6.34E-37	2.76E-36	open	0.49332895	5.22E-11		myb-like DNA-binding domain protein
Sapur.003G0681000.1	722.2493794	0.87388662	0.06903124	12.66354	9.40E-37	4.08E-36	open	0.60274041	6.70E-17		Protein of unknown function (DUF679)
Sapur.012G0283900.1	39.38162299	2.27897601	0.18150653	12.55572	3.70E-36	1.58E-35	open	0.64369137	9.68E-20		stress up-regulated Nod 19 protein
Sapur.003G0500800.1	52.26889736	1.58821765	0.12607053	12.51186	4.43E-36	1.94E-35	open	0.58615648	1.87E-16		F-box family protein with a domain of unknown function (DUF296)
Sapur.004G0691900.1	96.34273114	1.33879148	0.10704158	12.50721	6.82E-36	2.90E-35	open	0.58396358	9.94E-16		
Sapur.004G0291000.1	14.34491668	1.48034875	0.27849941	12.49679	7.77E-36	3.30E-35	open	0.45168623	2.86E-09	GO:0006881;GO:0003677	AGLS7
Sapur.010G1823000.1	9.32206289	3.02358086	0.24154123	12.46626	1.14E-35	4.83E-35	open	0.52381864	1.86E-12	GO:0005515;GO:0006468;GO:0004672	Leucine-rich repeat protein kinase family protein
Sapur.005G1364600.1	40.23230893	1.51093331	0.12127827	12.45378	1.13E-35	5.84E-35	open	0.61732310	7.52E-18	GO:0016021	camphor resistance CrcB family protein
Sapur.004G0694900.1	4.39167079	2.21508353	0.2561882	12.45166	1.96E-35	8.00E-35	open	0.45168684	1.18E-09	GO:0016788	GDSL-like Lipase/Acylhydrolase family
Sapur.019G1100900.1	1983.936147	0.96379727	0.07762182	12.41813	2.08E-35	8.78E-35	open	0.62646405	1.71E-18	GO:0007165	CBL-interacting Serine/Threonine-kinase, putative
Sapur.011G1200001.1	5.048669	1.53948263	0.46613813	12.41611	2.14E-35	9.00E-35	open	0.44421654	1.57E-09	GO:0015114;GO:0005887	FAD-binding Berberine family protein
Sapur.012G0257100.1	34.00792815	2.30608802	0.18640817	12.39035	2.95E-35	1.24E-34	open	0.53872593	3.37E-13	GO:0003677;GO:0003700	basic leucine-zipper 70
Sapur.005G1775300.1	3445.81555	1.15847261	0.09355163	12.37242	3.68E-35	1.54E-34	open	0.64394263	1.30E-19		
Sapur.012G0500001.1	2.46397612	4.72508805	0.38327849	12.3542	4.62E-35	1.93E-34	open	0.49260505	4.37E-11	GO:0046872;GO:0030001	Copper transport protein family
Sapur.010G0260001.1	214.5320216	1.02418675	0.08198895	12.34672	5.07E-35	2.12E-34	open	0.60704121	1.20E-17	GO:0008168	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.013G1187000.1	16.4541335	2.8007248	0.22717348	12.32867	6.35E-35	2.65E-34	open	0.48020853	1.30E-10		
Sapur.003G0200300.1	806.4776152	0.84561123	0.06854809	12.32146	6.94E-35	2.89E-34	open	0.65168623	2.86E-09	GO:0006355;GO:0003700	AT2G36R domain transcription factor
Sapur.009G0493400.1	810.1153235	0.72881799	0.05916007	12.3068	8.33E-35	3.46E-34	open	0.63457618	4.61E-19	GO:0008270;GO:0003677	NA
Sapur.013G1195500.1	221.0863929	2.09591242	0.17047976	12.2942	9.73E-35	4.04E-34	open	0.56839398	8.18E-15	GO:0016747;GO:0008610;GO:0016020;GO:0006633	3-ketoacyl-CoA synthase 19
Sapur.005G1440000.1	55.33549527	1.72391932	0.14460782	12.2744	1.24E-34	5.16E-34	open	0.54238707	1.28E-13		Nucleotide-diphosphate-sugar transferase family protein
Sapur.001G1984000.1	28.18494213	1.47483348	0.09349369	12.21385	2.62E-34	1.08E-33	open	0.64560207	1.77E-19		NHL domain-containing protein
Sapur.001G1520000.1	415.9413445	0.86606328	0.07106048	12.16921	3.14E-34	1.29E-33	open	0.66891215	1.58E-21		Protein of unknown function, DUF1083
Sapur.018G0898800.1	235.6813086	0.78128462	0.06429422	12.15757	5.23E-34	2.14E-33	open	0.63498541	3.53E-20	GO:0005885;GO:0016021	Major facilitator superfamily protein
Sapur.005G1317000.1	189.1244066	0.82439793	0.06870575	12.11012	7.03E-34	2.87E-33	open	0.63750073	4.76E-21	GO:0005524;GO:0016020;GO:0009055	glutaredoxin family protein
Sapur.014G1220002.2	5.29533949	1.70524429	0.14084716	12.107	9.70E-34	3.95E-33	open	0.67495191	5.01E-20	GO:0016021;GO:0004190	SIGNAL PEPTIDE PEPTIDASE-LIKE 3
Sapur.006G0730600.1	1612.581294	1.02347234	0.08477517	12.06664	1.10E-33	4.50E-33	open	0.66883621	1.04E-21	GO:0005992;GO:0004348	Histacid dehydrogenase-like trehalose (HAD) superfamily protein
Sapur.016G1501500.1	643.1871696	0.48141577	0.09975621	12.04393	2.09E-33	8.46E-33	open	0.67153601	6.24E-22	GO:0005524;GO:0016491;GO:0006633;GO:0005506	fatty acid hydroxylase 1
Sapur.005G0880600.1	245.6375578	0.58188503	0.04810542	12.03771	2.32E-33	9.12E-33	open	0.67478232	5.21E-22	GO:0005275;GO:0006531;GO:0005524	seven in absentia of Arabidopsis 2
Sapur.007G0170300.1	175.2640661	1.20192319	0.10089591	11.9151	1.02E-32	4.07E-32	open	0.60502701	4.77E-17	GO:0004365;GO:0003700;GO:0003700	basic leucine-zipper 44
Sapur.005G1180600.1	407.8069418	0.80635108	0.06771525	11.90862	1.07E-32	4.27E-32	open	0.63183058	7.12E-19	GO:0008234;GO:0006508	sylem bark cysteine peptidase 3
Sapur.004G1290000.1	180.1017313	1.11876452	0.09413828	11.88683	1.36E-32	5.32E-32	open	0.60405384	5.51E-17		armadillo repeat only 1 protein
Sapur.006G0770200.2	16.12134663	1.61030438	0.13578847	11.86406	1.82E-32	7.24E-32	open	0.60391752	5.63E-17		PAR1 protein
Sapur.007G0880200.1	3.01688312	1.06434433	0.29164593	11.82463	2.91E-32	1.15E-31	open	0.61237046	1.07E-17		transmembrane protein, putative
Sapur.013G0946800.1	41.63834148	2.62241884	0.22116254	11.80391	3.73E-32	1.47E-31	open	0.43659715	1.09E-08		NA
Sapur.004G0995000.1	2.38388104	1.15605091	0.36400464	11.80325	3.76E-32	1.48E-31	open	0.67004111	3.96E-22	GO:0016788	GDSL-motif lipase 3
Sapur.014G0250500.1	684.2538543	0.01461577	0.08280162	11.79203	4.29E-32	1.69E-31	open	0.64334865	9.95E-20		Protein of unknown function, DUF617
Sapur.006G1663400.1	2.38344688	3.62831856	0.30773401	11.7937	4.34E-32	1.71E-31	open	0.56556271	1.98E-14		
Sapur.003G1052500.1	89.91005517	1.19595793	0.09851053	11.76881	5.65E-32	2.22E-31	open	0.54775787	1.13E-13	GO:0008270;GO:0005515	RING/U-box superfamily protein
Sapur.010G0320800.1	20.7647975	1.70399493	0.14855376	11.76051	6.24E-32	2.45E-31	open	0.52393941	6.75E-13		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.006G1758500.1	898.7535661	0.51744958	0.04403154	11.7519	6.31E-32	2.51E-31	open	0.64496065	7.78E-20		Transducin/WD40 repeat-like superfamily protein
Sapur.013G0018000.1	58.88884803	1.03376561	0.08839146	11.69661	1.33E-31	5.18E-31	open	0.62945406	2.36E-18	GO:0005515	receptor like protein 7
Sapur.008G1383000.1	1021.856459	0.73184932	0.10016687	11.64993	2.36E-31	8.90E-31	open	0.52544006	1.60E-12	GO:0008270;GO:0006810;GO:0005215	peptide transporter PTR3-A
Sapur.018G1110000.1	2.96850239	4.31463839	0.70715137	11.6393	2.60E-31	1.01E-30	open	0.46417261	9.22E-10		Pentatricopeptide repeat (PPR-like) superfamily protein
Sapur.010G0260001.1	205.7978834	0.76729964	0.06094916	11.6347	2.76E-31	1.06E-30	open	0.60496065	7.78E-20	GO:0004519;GO:0016787	RNH endonuclease 1
Sapur.016G2302000.1	132.234984	1.14044398	0.09814825	11.61954	3.28E-31	1.27E-30	open	0.62832358	1.28E-18	GO:0045454;GO:0015035;GO:0009055	Glutaredoxin family protein
Sapur.007G0203300.2	12.86668879	1.51429407	0.13074521	11.6	3.54E-31	1.37E-30	open	0.49226163	5.83E-11	GO:0008355	HEAT5 family protein
Sapur.016G1587000.2	2.06052007	0.03575026	0.34765569	11.60848	3.73E-31	1.44E-30	open	0.53669609	3.44E-13		NA
Sapur.004G0327000.1	633.2193066	0.45608822	0.03936407	11.60603	3.75E-31	1.45E-30	open	0.61552863	4.26E-20	GO:0051539;GO:0006464	ATLLC
Sapur.016G0745500.1	194.756233	1.35880697	0.11711602	11.60223	4.01E-31	1.55E-30	open	0.59182518	3.29E-16		Pectin lyase-like superfamily protein
Sapur.001G1061000.1	8.07399979	4.47277426	0.38402238	11.5754	5.49E-31	2.12E-30	open	0.37935755	9.40E-07	GO:0005515	Transducin/WD40 repeat-like superfamily protein
Sapur.005G1492000.1	92.66659913	1.05835725	0.09136865	11.5678	6.09E-31	2.35E-30	open	0.64547678	7.12E-20	GO:0015114;GO:0009186	ribonucleotide reductase 1
Sapur.008G0499900.1	9.25777919	1.83930337	0.15938804	11.5425	8.03E-31	3.08E-30	open	0.60215996	7.31E-17		hypothetical protein
Sapur.009G0915000.1	105.6148893	1.18164962	0.10236187	11.5403	8.12E-31	3.09E-30	open	0.64744430	7.67E-20	GO:0005515	DNA-binding bromodomain-containing protein
Sapur.008G1671000.2	75.1771539	0.78366603	0.06291188	11.53454	8.84E-31	3.38E-30	open	0.65054768	2.94E-20	GO:0016161;GO:0003772	beta-amylase 3
Sapur.018G0898800.1	117.6437374	1.15485153	0.10019782	11.5269	9.51E-31	3.63E-30	open	0.59752763	1.68E-16	GO:0004364;GO:0005524;GO:0004672	Protein kinase superfamily protein
Sapur.001G0790600.1	354.5674616	0.57605764	0.05019993	11.47527	1.76E-30	6.67E-30	open	0.62382834	2.61E-18	GO:0016020	CAAX amino terminal protease family protein
Sapur.019G0463400.1	3.20824129	2.28488892	0.19648309	11.47053	1.88E-30	7.08E-30	open	0.63870962	2.01E-19		Remorin family protein (DUF828)
Sapur.019G0683000.1	3.71761984	2.25836258	0.28428184	11.46173	2.05E-30	7.79E-30	open	0.57532218	3.16E-15	GO:0007165;GO:0015035;GO:0043531	disease resistance protein (TIR-NBS-LRR class), putative
Sapur.014G0291800.1	1.72867798	4.08287815	0.30168445	11.44809	2.40E-30	9.10E-30	open	0.56189039	1.91E-14		NA
Sapur.T017600.1	0.55181774	2.01975615	0.17684685	11.43094	3.29E-30	1.24E-29	open	0.63870042	7.46E-16		NA
Sapur.007G0271000.1	80.24118821	1.22963304	0.10785029	11.40112	4.13E-30	1.55E-29	open	0.5809873	1.50E-15		peptide upstream ORF protein
Sapur.001G0390600.1	1009.424287	0.46375425	0.04251571	11.37871	5.34E-30	2.01E-29	open	0.67130006	5.07E-21		dehydration-induced protein, putative
Sapur.T005500.1	28.80156882	1.16545283	0.10523631	11.36758	6.06E-30	2.28E-29	open	0.63897823	2.16E-19		
Sapur.T125400.1	476.4814007	0.62478161	0.05649154	11.05605	3.94E-30	2.60E-29	open	0.63467664	4.6E-19		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.016G1545000.1	10.46274658	1.46378586	0.12706873	11.30542	1.23E-29	4.60E-29	open	0.59480357	2.12E-16		
Sapur.010G0260001.1	316.4162264	0.42875137	0.03813949	11.2489	2.98E-29	9.16E-29	open	0.62838198	1.78E-20		Protein of unknown function (DUF789)
Sapur.005G0805500.1	4.89466988	0.57639353	0.40757361	11.22927	2.93E-29	1.08E-28	open	0.44389757	6.88E-09		Calcium-binding EF-hand family protein
Sapur.010G0880500.1	21.18833213	1.41626423	0.17074514	11.22754	2.98E-29	1.11E-28	open	0.31452848	8E-05		hypothetical protein
Sapur.011G1245500.1	668.1163855	0.36423193	0.03245476	11.22595	3.04E-29	1.13E-28	open	0.66230321	3.71E-21	GO:0005515	transducin/WD40 repeat-like superfamily protein
Sapur.003G0312300.1	27.84863896	1.86779946	0.34079523	11.21716	3.35E-29	1.24E-28	open	0.40506574	1.42E-07		hypothetical protein
Sapur.019G0956005.1	52.1812422	1.35205152	0.12009470	11.17448	5.44E-29	2.00E-28	open	0.61873611	6.68E-18		ion channel protein, putative
Sapur.001G0800800.1	940.6236845	1.22191744	0.10952597	11.16814	5.84E-29	2.15E-28	open	0.51727193	4.04E-12	GO:0005975;GO:0004553	Cellulase (glycosyl hydrolase family 5) protein
Sapur.016G1824001.1	2.35393874	4.61056459	0.40609503	11.1369	6.18E-29	2.26E-28	open	0.50931994	6.11E-12		transmembrane protein, putative
Sapur.010G0864600.1	37.69767297	1.65042041	0.14941853	11.10583	1.18E-28	4.30E-28	open	0.50780029	1.13E-11		transcription factor R2R3-MYB2
Sapur.T091800.1	9.71365689	2.07284394	0.11451936	11.0267	1.28E-28	4.81E-28	open	0.48267351	1.12E-10		cystinosin, putative
Sapur.010G0903000.4	5.02257451	1.64497029	0.14874039	10.97945	1.58E-28	5.76E-28	open	0.43921954	4.62E-08		Protein of unknown function (DUF2741)
Sapur.010G0860100.1	61.95182636	1.71182435	0.15452376	10.97202	1.68E-28	6.05E-28	open	0.55720008	3.46E-14		HSP20-like chaperones superfamily protein
Sapur.010G1822000.1	6.46792155	2.95630326	0.26743783	10.95515	2.07E-28	7.53E-28	open	0.49405507	4.85E-11	GO:0005515;G

Sapur.006G028100.1	362.0953958	1.396166897	0.46799577	9.480048	2.54E-21	7.80E-21	cpm	0.56735234	9.43E-15	GO:0003333	
Sapur.001G191900.4	13.19510933	1.088567511	0.114856816	9.477605	2.60E-21	7.98E-21	cpm	0.68341752	6.11E-23	GO:0016787	
Sapur.006G188600.1	6.36832201	1.472834194	0.155541432	9.465609	2.92E-21	8.94E-21	cpm	0.51500833	8.02E-12		
Sapur.014G075800.1	29.46252001	1.007769729	0.106488002	9.463283	2.93E-21	8.97E-21	cpm	0.50482561	1.56E-11	GO:0006629	
Sapur.006G094300.1	5451.974866	0.496021333	0.052638347	9.426836	4.23E-21	1.29E-20	cpm	0.55508636	4.50E-14	GO:0016887;GO:0005524	
Sapur.005G003600.1	1873.634705	0.367900104	0.039075571	9.415574	4.71E-21	1.43E-20	cpm	0.6023769	7.08E-17	GO:0006468;GO:0004672	
Sapur.016G139300.1	5.790608677	2.301180895	0.244641091	9.406355	5.14E-21	1.57E-20	cpm	0.39763806	2.51E-07	GO:0006468;GO:0005524;GO:0004672;GO:0030246	
Sapur.7105300.1	35.97843898	0.825409992	0.087769034	9.404342	5.24E-21	1.59E-20	cpm	0.57397949	2.20E-15	GO:0055114;GO:0009186	
Sapur.016G058800.0	1270.874608	0.42373873	0.044880737	9.366876	5.62E-21	1.71E-20	cpm	0.59095956	3.91E-16		
Sapur.005G145500.1	31.36482257	0.588229157	0.062863182	9.360486	5.74E-21	1.75E-20	cpm	0.58885115	5.05E-16	GO:0055085;GO:0016020;GO:0006811;GO:0005216	
Sapur.017G041300.1	24.54092236	1.139007834	0.122085541	9.336529	9.95E-21	3.01E-20	cpm	0.58845894	5.34E-16	GO:0016787	
Sapur.005G318800.1	688.2618833	0.7108173	0.076135825	9.335451	1.13E-20	3.40E-20	cpm	0.57753248	2.41E-15	GO:0005911	
Sapur.012G059900.1	7.49596807	1.680369313	0.180762212	9.297049	1.44E-20	4.34E-20	cpm	0.50973533	9.21E-12	GO:0003682;GO:0006351;GO:0005634;GO:0003677	
Sapur.014G143000.1	725.8806768	0.6988225	0.075164429	9.297031	1.44E-20	4.35E-20	cpm	0.57212718	5.68E-15		
Sapur.016G162300.1	13.22272287	2.978899079	0.351375556	9.226575	2.79E-20	8.34E-20	cpm	0.47352072	3.77E-10	GO:0005544;GO:0005509	
Sapur.003G051500.1	857.1826289	1.340817766	0.151327575	9.196652	3.45E-20	1.01E-19	cpm	0.48960031	1.41E-10		
Sapur.7125700.1	348.185228	0.931200462	0.102015755	9.167216	4.85E-20	1.44E-19	cpm	0.56512218	1.26E-14		
Sapur.005G102100.1	121.7770561	0.657381437	0.071713532	9.166771	4.87E-20	1.46E-19	cpm	0.55022684	8.36E-14		
Sapur.010G031200.1	961.3995562	0.9144649	0.101492324	9.11373	7.96E-20	2.37E-19	cpm	0.56023954	2.51E-15		
Sapur.019G007700.1	735.201709	0.513802346	0.056380897	9.112572	8.05E-20	2.37E-19	cpm	0.56146601	1.18E-14	GO:0016491;GO:0008198;GO:0006725	
Sapur.003G141100.1	14.04976153	1.905382027	0.20964026	9.0862	1.05E-19	3.09E-19	cpm	0.52972798	3.04E-11		
Sapur.010G015700.1	885.9788887	0.383202907	0.042160653	9.045471	1.49E-19	4.36E-19	cpm	0.56410597	1.41E-14	GO:0008270;GO:0003677	
Sapur.012G025500.1	465.0155068	0.6032928	0.066385821	9.088212	1.58E-19	4.66E-19	cpm	0.57319184	1.32E-15	GO:0055114;GO:0020037;GO:0016705;GO:0005506	
Sapur.018G119900.1	2.682961798	2.862688777	0.315749186	9.003503	2.19E-19	6.37E-19	cpm	0.42385073	3.74E-08	GO:0005515	
Sapur.003G067500.1	10.56273441	1.087114	0.121117223	8.975027	2.83E-19	8.17E-19	cpm	0.54968204	3.08E-12		
Sapur.009G394800.1	638.2813506	0.537369575	0.059874027	8.975003	2.83E-19	8.24E-19	cpm	0.58296347	1.94E-15	GO:0019140;GO:0010264;GO:0005524	
Sapur.010G054500.1	538.6381279	0.428656563	0.047922377	8.94481	3.73E-19	1.08E-18	cpm	0.59861863	1.23E-16		
Sapur.005G107600.1	206.1051074	0.346461304	0.038751774	8.939284	3.90E-19	1.13E-18	cpm	0.56473826	2.16E-14		
Sapur.017G097600.1	13.93914905	1.343594888	0.150349881	8.936449	4.02E-19	1.16E-18	cpm	0.53814886	3.63E-13	GO:0006468;GO:0005524;GO:0004672	
Sapur.006G028200.1	229.0546611	1.2224874	0.12580045	9.621072	4.12E-19	1.19E-18	cpm	0.56631358	1.07E-14		
Sapur.006G018100.1	69.02027954	1.660852382	0.186687351	8.896456	5.77E-19	1.66E-18	cpm	0.46297028	1.01E-09	GO:0016758;GO:0008152	
Sapur.005G087500.1	5.981175676	2.168331313	0.180585858	8.878145	6.46E-19	1.86E-18	cpm	0.49701298	1.57E-11	GO:0006508;GO:0004252	
Sapur.009G139800.1	144.7915714	0.711363836	0.080240124	8.865438	7.02E-19	2.19E-18	cpm	0.52582823	5.12E-12		
Sapur.016G028300.1	0.995645538	3.00574482	0.351061269	8.83263	1.12E-18	3.20E-18	cpm	0.51860408	1.46E-12	GO:0000160	
Sapur.006G183800.1	20.55054845	2.026918866	0.2300277	8.811717	1.23E-18	3.52E-18	cpm	0.49010378	7.27E-11		
Sapur.016G039500.1	127.2988261	0.571812389	0.065246163	8.762138	1.55E-18	4.47E-18	cpm	0.56273706	5.04E-14		
Sapur.016G153500.1	2.066373508	3.590507209	0.408246652	8.794946	1.43E-18	4.08E-18	cpm	0.37769214	1.06E-06		
Sapur.009G281000.1	401.0675589	0.723349022	0.082470428	8.769798	1.79E-18	5.09E-18	cpm	0.50779689	1.54E-11	GO:0055515;GO:0016459;GO:0005524;GO:0003774	
Sapur.001G050000.1	4281.276882	0.688882225	0.079776168	8.63555	3.56E-18	9.96E-18	cpm	0.56612997	1.26E-11	GO:0006508;GO:0016787;GO:0006070;GO:0005618;GO:0005975;GO:0004553	
Sapur.012G019900.1	114.6521151	1.235067477	0.141136551	8.750869	2.12E-18	6.01E-18	cpm	0.52329122	2.56E-12	GO:0005515	
Sapur.009G028600.1	2434.029686	0.54205369	0.062037902	8.735889	2.35E-18	6.68E-18	cpm	0.54204371	2.98E-12		
Sapur.7000600.1	9.023142621	0.933006709	0.107075137	8.722269	2.73E-18	7.72E-18	cpm	0.54883413	9.93E-14	GO:0005515;GO:0006468;GO:0004672	
Sapur.016G049200.1	405.1970368	0.672605149	0.077184848	8.71469	2.93E-18	8.27E-18	cpm	0.56203124	1.86E-14		
Sapur.014G081100.1	297.2531385	0.482309892	0.055431246	8.701598	3.27E-18	9.25E-18	cpm	0.54207616	2.16E-13		
Sapur.016G081500.1	1.477126175	3.506487427	0.402561686	8.69027	3.52E-18	9.97E-18	cpm	0.42688431	4.02E-08		
Sapur.008G030100.1	1.7332022	2.618876618	0.301558639	8.684667	3.81E-18	1.07E-17	cpm	0.51122297	7.84E-12		
Sapur.001G054000.1	2.509812916	2.397082211	0.276131371	8.672058	4.24E-18	1.20E-17	cpm	0.47973456	2.06E-10		
Sapur.010G123600.1	10.18001748	1.069330164	0.123072318	8.668053	4.40E-18	1.24E-17	cpm	0.54758767	1.16E-13		
Sapur.018G095200.1	129.8438661	0.465037862	0.053833736	8.63513	4.93E-18	1.39E-17	cpm	0.57820749	2.20E-15		
Sapur.016G243000.1	665.3603797	0.5111209	0.059092932	8.641429	5.05E-18	1.42E-17	cpm	0.53933258	3.16E-13		
Sapur.012G059000.1	105.9505932	1.352466886	0.145883269	8.611334	7.22E-18	2.03E-17	cpm	0.47970277	2.86E-10	GO:0005515	
Sapur.018G112900.1	2.991606421	2.116477159	0.2477186	8.545157	7.60E-18	2.13E-17	cpm	0.32501751	1.36E-05	GO:0005515	
Sapur.012G020000.1	40.76248903	1.038382801	0.121230312	8.565373	1.08E-17	3.00E-17	cpm	0.55011658	2.06E-11	GO:0005515	
Sapur.003G219100.1	212.6492813	0.7147	0.083496176	8.560107	1.10E-17	3.05E-17	cpm	0.52867728	5.08E-12		
Sapur.006G069000.1	5023.286818	0.817807892	0.094833166	8.552783	1.20E-17	3.34E-17	cpm	0.54154768	2.42E-13	GO:0055114;GO:0020037;GO:0016705;GO:0005506	
Sapur.006G088700.1	63.31263027	0.875407446	0.102346184	8.547109	1.21E-17	3.47E-17	cpm	0.51583818	1.84E-12		
Sapur.7152600.1	446.9581338	1.039169622	0.121658496	8.541694	1.32E-17	3.68E-17	cpm	0.52867196	1.34E-12		
Sapur.006G081900.1	6.869834689	1.892069372	0.220450025	8.541207	1.33E-17	3.69E-17	cpm	0.50853809	2.15E-11	GO:0005509	
Sapur.010G085000.1	2018.877827	0.4181723	0.048971439	8.537754	1.35E-17	3.80E-17	cpm	0.56413027	1.46E-13	GO:0006468;GO:0005524;GO:0004672	
Sapur.7132200.1	1.080559166	2.566473859	0.301534124	8.511382	1.73E-17	4.76E-17	cpm	0.51262564	6.70E-12	GO:0005681;GO:0000398;GO:0000387	
Sapur.019G020400.1	491.1931024	0.7	0.085184431	8.496884	1.96E-17	5.26E-17	cpm	0.52083229	2.87E-12	GO:0006468;GO:0004672;GO:0005524	
Sapur.019G020000.1	649.9478027	0.486273154	0.057437164	8.466154	2.56E-17	6.99E-17	cpm	0.55580693	4.16E-14	GO:0005515;GO:0006468;GO:0004672	
Sapur.005G028700.1	1.260419098	2.450024407	0.28887926	8.48494	2.79E-17	7.66E-17	cpm	0.51767324	1.81E-12	GO:0016758;GO:0008152	
Sapur.009G185900.1	0.72316286	2.760326659	0.326870016	8.444542	3.05E-17	8.39E-17	cpm	0.52657949	1.56E-12	GO:0043565;GO:0003700;GO:0003700	
Sapur.004G047000.1	148.2108044	0.6103142	0.052629964	8.42039	3.73E-17	1.02E-16	cpm	0.51702051	1.46E-12	GO:0008270;GO:0009972;GO:0004126	
Sapur.009G081600.1	28.07263533	0.821068175	0.125180137	8.40276	4.36E-17	1.19E-16	cpm	0.40889926	1.06E-07		
Sapur.003G274000.1	3.978517593	2.526051325	0.3017788	8.402109	4.37E-17	1.20E-16	cpm	0.46256516	1.26E-09	GO:0005544;GO:0005509	
Sapur.011G007200.1	4.52897241	2.047389382	0.244215052	8.383551	5.14E-17	1.40E-16	cpm	0.44680841	4.52E-09		
Sapur.004G105400.1	154.2996684	0.354737272	0.042319591	8.382258	5.19E-17	1.42E-16	cpm	0.53982724	5.24E-14	GO:0004872	
Sapur.007G052600.1	87.9472607	0.574325684	0.06924659	8.367767	5.87E-17	1.60E-16	cpm	0.52491176	1.70E-12	GO:0016791	
Sapur.005G193400.1	95.8254658	0.815811377	0.097510036	8.366453	5.94E-17	1.62E-16	cpm	0.47384073	4.43E-10		
Sapur.7017800.1	3.586403896	2.0793235	0.248602088	8.363608	6.12E-17	1.66E-16	cpm	0.44425136	5.60E-09		
Sapur.005G010000.1	92.72680539	2.278077917	0.272720624	8.35482	6.56E-17	1.79E-16	cpm	0.44191728	6.87E-09	GO:0005515;GO:0006468;GO:0005524;GO:0004672	
Sapur.006G088500.1	927.3533168	0.763609734	0.091682529	8.332519	7.93E-17	2.16E-16	cpm	0.48897572	1.91E-11	GO:0005524;GO:0003677	
Sapur.010G078800.1	18.16263112	1.139309152	0.138239854	8.241539	1.70E-16	4.57E-16	cpm	0.52715638	1.29E-12	GO:0016829;GO:0006520	
Sapur.016G201100.1	1918.063943	0.503605207	0.072089461	8.234707	1.80E-16	4.85E-16	cpm	0.51615841	2.27E-12		
Sapur.002G009600.1	9.253653388	1.306375027	0.1587424	8.229528	1.88E-16	5.04E-16	cpm	0.52834795	1.55E-12		
Sapur.003G075400.1	310.6953871	0.291656114	0.035633649	8.19327	2.54E-16	6.80E-16	cpm	-0.55681975	3.75E-14	GO:0005525	
Sapur.006G162200.1	12.15661737	0.967502087	0.118206452	8.185206	2.28E-16	8.55E-16	cpm	0.48834107	8.70E-11	GO:0008270;GO:0005515	
Sapur.002G170400.1	2825.979018	0.69031659	0.084161736	8.158349	3.40E-16	9.05E-16	cpm	0.50094961	2.36E-11	GO:0016747;GO:0008152	
Sapur.015G030500.1	394.7885268	0.325338323	0.039951685	8.15449	3.54E-16	9.41E-16	cpm	-0.57437372	1.52E-15		
Sapur.7091200.1	9.403878652	2.980047545	0.367459605	8.111497	5.00E-16	1.33E-15	cpm	0.37487614	1.32E-06	GO:0016788	
Sapur.7017200.1	1.345498642	2.75680843	0.340124988	8.107026	5.24E-16	1.39E-15	cpm	0.4032055	3.62E-07		
Sapur.005G067700.1	544.0735567	0.326454884	0.040510574	-8.0584	7.73E-16	2.04E-15	cpm	-0.56293457	1.67E-14		
Sapur.7000100.1	16.94586388	0.878898202	0.109152362	8.037302	9.18E-16	2.42E-15	cpm	0.51752718	3.91E-12		
Sapur.006G049400.1	2.9640183	1.533931788	0.191455176	8.012172	1.13E-15	2.96E-15	cpm	0.49092568	6.68E-11		
Sapur.003G083800.1	41.34568603	0.761439803	0.095000458	8.020745	1.12E-15	2.96E-15	cpm	0.48047053	1.02E-10		
Sapur.010G091000.1	313.5398656	0.294905669	0.036898127	-7.99872	1.26E-15	3.30E-15	cpm	-0.55764014	3.26E-14	GO:0006872;GO:0030001;GO:0055114;GO:0005506;GO:0000801;GO:0016532;GO:0005507	
Sapur.006G040300.1	220.1274955	0.552567947	0.069288699	7.974864	1.53E-15	3.99E-15	cpm	0.51279461	6.63E-12		
Sapur.004G005200.1	42.88837389	-0.5416316	0.068090657	-7.95616	1.66E-15	4.48E-15	cpm	0.54573481	1.45E-13	GO:0016811;GO:0016021;GO:0006672	
Sapur.001G144000.1	1.037751604	2.939106415	0.369528822	7.953659	1.83E-15	4.73E-15	cpm	0.47340861	8.31E-10	GO:0016021	
Sapur.009G040800.1	1275.505824	0.4778329	0.054754147	7.943151	1.87E-15	5.46E-15	cpm	0.55601763	7.91E-14		
Sapur.019G091600.1	8.332721207	0.87431733	0.110308273	7.926098	2.26E-15	5.88E-15	cpm	0.46423763	9.12E-10		
Sapur.010G061000.1	12.29638378	1.034837227	0.130859163	7.904765	2.68E-15	6.97E-15	cpm	0.48173993	1.90E-10		
Sapur.018G091900.1	929.7644867	0.341301909	0.043195053	-7.87153	3.50E-15	9.07E-15	cpm	-0.56353148	1.55E-14		
Sapur.006G188200.1	12.32007035	1.186610169	0.15088193	7.863695	3.72E-15	9.63E-15	cpm	0.4999026	2.02E-10		
Sapur.006G182500.1	14.69752284	1.679060806	0.215508859	7.838699	4.51E-15	1.17E-14	cpm	0.37643029	1.18E-06		
Sapur.005G188500.1	9.461244881	1.355280613	0.174096653	7.81345	4.75E-15	1.22E-14	cpm	0.26393634	0.00752466	GO:0016020;GO:0015696;GO:0008519;GO:0072488	
Sapur.7039700.1	576.2127569	0.86940007	0.111416716	7.822452	5.18E-15	1.33E-14	cpm	0.50036581	2.51E-11		
Sapur.003G123000.1	79.79252945	0.441480386	0.056515491	7.811671	5.64E-15	1.45E-14	cpm	0.51890486	3.31E-12		
Sapur.010G160000.1	311.9883081	0.368763865	0.047240387	7.805713	5.90E-15	1.52E-14	cpm	0.51491136	2.32E-12		
Sapur.002G001200.1	44.27848131	1.118005324	0.143123789	7.801155	6.13E-15	1.58E-14	cpm	0.50303431	1.89E-11		
Sapur.005G056200.1	0.79933558	3.074888865	0.39600736	7.760768	8.64E-15	2.21E-14	cpm	0.50503778	2.56E-11		
Sapur.002G145600.1	190.8314115	0.990064823	0.127456458	7.774929	7.55E-15	1.94E-14	cpm	0.50471799	1.58E-11		
Sapur.005G139800.1	211.8090226	0.864989523	0.092739253	7.766665	8.04E-15	2.06E-14	cpm	0.49427171	4.74E-11		
Sapur.013G049000.1	5.39635065	2.015455663	0.25956276	7.764589	8.18E-15	2.10E-14	cpm	0.43960234	8.55E-09		
Sapur.008G206300.1	712.2493486	0.262280437	0.033768514	7.758659	8.52E-15	2.18E-14	cpm	0.51735425	5.81E-12		
Sapur.001G191900.2	43.25959057	0.724768133	0.093405546	7.753369	8.54E-15	2.18E-14	cpm	0.61523309	8.27E-17	GO:0016787	
Sapur.012G028000.1	43.73829996	1.505028889	0.19429319	7.752565	9.03E-15	2.30E-14	cpm	0.44852253	5.31E-09	GO:0055114;GO:0016491	
Sapur.003G037700.1	11.52051363	0.811727369	0.104738866	7.715445	1.21E-14	3.07E-14	cpm	0.36338002	2.53E-06	GO:0055085;GO:0016021	
Sapur.017G041600.1	1.264927611	3.769181538	0.489206309	7.703794	1.33E-14	3.36E-14	cpm	0.37649431	1.18E-06		
Sapur.005G116500.1	207.3424677	0.336438247	0.043692639	7.69931	1.41E-14	3.56E-14	cpm	0.50041929	5.31E-11		
Sapur.006G095300.1	285.8000239	0.327703845	0.042602822	-7.67585	1.64E-14	4.17E-14	cpm	-0.54854906	1.27E-13		
Sapur.006G000400.1	1.135037705	2.828673237	0.42213185	7.667926	1.75E-14	4.46E-14	cpm	0.46203174	1.73E-10		
Sapur.010G030200.1	405.1215429	0.365017248	0.047802979	7.654666	1.94E-14	4.90E-14	cpm	0.50909539	9.04E-12	GO:0006351;GO:0005634;GO:0003677	
Sapur.016G028200.1	473.3272386	0.567409347	0.074355	7.630966	2.31E-14	5.62E-14	cpm	0.51680203	1.56E-12	GO:0055114;GO:0020037;GO:0016705;GO:0005506	
Sapur.010G086200.1	1.085190713	3.003944403	0.381504544	7.611821	2.70E-14	6.80E-14	cpm	0.37145888	1.67E-06		
Sapur.013G043000.1	2.407513468	1.803171344	0.237211826	7.593145	3.08E-14	7.54E-14	cpm	0.44683729	4.29E-09		
Sapur.016G212800.1	3778.383858	0.386798905	0.050912707	7.597296	3.02E-14	7.60E-14	cpm	0.49055874	6.94E-11	GO:0055114;GO:0009055	
Sapur.002G018300.1	62.40468811	0.802329775	0.105819378	7.582527	3.19E-14	8.51E-14	cpm	0.45771503	1.67E-09	GO:0006355;GO:0003700	
Sapur.018G077000.1	11.55501003	0.705501088	0.09806849	7.57624	3.58E-14	8.79E-14	cpm	0.50184329	1.77E-11		
Sapur.7139200.1	267.1341886	0.945437664	0.125430768	7.537526	4.79E-14	1.20E-13	cpm	0.50063815	2.46E-11		
Sapur.005G074000.1	1.582315127	2.643663324	0.350482219	7.507699	5.64E-14	1.50E-13	cpm	0.38183093	7.30E-07		
Sapur.001G160900.1	41.48079182	0.85705867	0.114523281	7.483093	7.26E-14	1.80E-13	cpm	0.43861301	9.15E-09		
Sapur.018G000400.1	71.31489944	0.611585623	0.08178277	7.48209	7.31E-14	1.82E-13	cpm	0.49353902	1.02E-11		
Sapur.008G097100.1	24.08073122	1.29031084	0.17259447	7.475969	7.66E-14	1.90E-13	cpm	0.41482673	6.61E-08		
Sapur.013G028000.1	43.41672177	0.664843182	0.089016614	7.464578	8.87E-14	2.20E-13	cpm	0.47824694	2.51E-10	GO:0005515	
Sapur.008G140300.1	0.902012531	2.938709888	0.39488205	7.461994	9.02E-14	2.45E-13	cpm	0.43986117	8.22E-09		
Sapur.005G163500.1	3722.802021	0.495880541	0.054639947	7.430629	1.08E-13	2.67E-13	cpm	0.52133278	2.61E-12		
Sapur.005G182500.1	209.4434684	0.554382435	0.076136992	7.281453	1.24E-13	3.05E-13	cpm	0.47372052	1.02E-08		
Sapur.005G155600.1	147.133381	0.841963301	0.115795005	7.412843	1.24E-13	3.05E-13	cpm	0.47527436	3.18E-10		
Sapur.007G052600.1	1311.953854	0.325011275	0.045065159	7.40751	1.28E-13	3.17E-13	cpm	-0.6484251	1.24E-10		
Sapur.013G133800.1	263.2332673	0.586715057	0.07921837	7.381003	1.57E-13	3.86E-13	cpm	0.52907155	1.05E-12		
Sapur.013G051100.1	391.1472869	0.276825009	0.037416667	7.34651	1.78E-13	4.36E-13	cpm	-0.55464114	4.6E-14		
Sapur.7138400.1	264.7795524	0.757422464	0.103360495	7.329128	2.13E-13	5.66E-13	cpm	0.48209505	8.81E-11	GO:0005524	
Sapur.016G042100.1	846.0827523	0.364073723	0.05611443	7.31483	2.16E-13	5.96E-13	cpm	0.51377818	1.58E-12	GO:0016779;GO:0004631;GO:0003677;GO:0004652;GO:0005634	
Sapur.001G114800.1	26.25579817	1.070596912	0.146855447	7.290141	3.10E-13	7.53E-13	cpm	0.4241221	3.11E-08		
Sapur.005G208800.1	4.302610085	1.854865202	0.34871676	7.263446	3.71E-13	9.15E-13	cpm	0.38798631	5.16E-07	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	
Sapur.016G241000.2	4.293080737	1.210780876	0.16672227	7.261826	3.82E-13	9.26E-13	cpm	0.47151771	4.57E-10	GO:0016788;GO:0006886;GO:0006505	
Sapur.003G189900.1	948.8746668	-0.20517876	0.028264453	-7.25925	3.89E-13	9.43E-13	cpm	-0.52653808	1.41E-12		
Sapur.006G162500.1	29.16556605	0.912152292	0.125784427	7.25669	3.98E-13	9.64E-13	cpm	0.43847515	2.36E-09	GO:0006508;GO:0004185	
Sapur.7105400.1	14.82188847	0.890604197	0.123477771	7.212668	5.49E-13	1.32E-12	cpm	0.48435293	1.30E-10		
Sapur.017G056400.1	48.77873633	0.5148535	0.07696529	7.20176	5.95E-13	1.43E-12	cpm	0.51774054	7.6E-13		
Sapur.014G080800.1	1385.078807	0.79578345	0.110785461	7.183104	6.81E-13	1.64E-12	cpm	0.48336737	1.41E-10		
Sapur.018G079100.1	0.86883901	1.854121336	0.44459	7.17027	7.08E-13	1.70E-12	cpm	0.39136564	4.01E-07		
Sapur.003G061100.2	1.997387328	1.858152254	0.258968866	7.156336	7.14E-13	1.72E-12	cpm	0.48471585	1.25E-10		
Sapur.018G000100.1	1.868621889	2.846051303	0.39664682	7.17484	7.24E-13	1.74E-12	cpm	0.42028658	2.59E-08		
Sapur.010G172100.1	0.724684543	2.701535116	0.382146113	7.157863	8.13E-13	1.96E-12	cpm	0.44796358	4.03E-09		
Sapur.7030900.1	340.1790661	0.7855002	0.111566869	7.037165	1.09E-12	2.63E-12	cpm	0.49280506	1.40E-11		
Sapur.002G164600.1	20.92093629	0.836374823	0.117839657	7.097567	1.27E-12	3.03E-12	cpm	0.46145621	1.08E-09		
Sapur.006G142900.1	359.6750557	0.641663751	0.090483085	7.091462	1.32E-12	3.14E-12	cpm	0.45237573	2.48E-09		
Sapur.013G139200.1	834.4993642	0.498441092	0.070431061	7.079017	1.45E-12	3.45E-12	cpm	0.42245895	4.79E-08	GO:0006468;GO:0005524;GO:0004672	
Sapur.008G071100.2	49.94834303	0.585329885	0.082786128	7.070554	1.54E-12	3.67E-12	cpm	0.48897952	1.01E-10		
Sapur.5018800.1	736.8160179	0.38147415	0.05374601	7.0486	1.68E-12	4.00E-12	cpm	0.48507234	7.66E-11		
Sapur.017G045500.1	1571.756699	0.712741072	0.101138285	7.047194	1.83E-12	4.33E-12	cpm	0.51251247	6.80E-12	GO:0006355;GO:0003700	
Sapur.003G188800.1	1719.668664	0.224127359	0.031733564	7.065	1.85E-12	4.36E-12	cpm	0.48326802	1.47E-08		
Sapur.008G052300.1	40.75555509	0.628443902	0.089171297	-7.03961	1.93E-12	4.56E-12	cpm	-0.47527336	3.18E-10		
Sapur.003G092200.1	216.4078902	0.977406491	0.13905726	7.028327	1.98E-12	4.67E-12	cpm	0.4284824	1.24E-10		
Sapur.006G079900.1	451.5182956	0.317559793	0.045357	6.994726	2.66E-12	6.36E-12	cpm	0.48375351	1.38E-10		
Sapur.016G028700.1	196.7910881	0.476882228	0.068324379	6.979316	2.97E-12	6.98E-12	cpm	0.45780749	1.65E-09	GO:0005524	
Sapur.003G092800.1	20260.11614	0.294314406	0.042180642	6.973931	3.08E-12	7.22E-12	cpm	0.44811132	1.98E-09	GO:0016020;GO:0006810;GO:0005215	
Sapur.001G105200.1	788.739382	0.398717207	0.057280449	6.960712	3.39E-12	7.95E-12	cpm	0.47469874	3.37E-10		
Sapur.019G044400.1	439.3644401	0.5	0.072819058	6.86659	6.51E-12	1.52E-11	cpm	0.51328227	1.68E-12	GO:0005515	
Sapur.006G210000.1	267.1847529	0.278231128	0.040105548	6.93454	3.52E-12	8.31E-12	cpm	-0.49495356	3.19E-11	GO:0003676;GO:0031369;GO:0006413;GO:0005852;GO:0003743;GO:0003723	
Sapur.010G086300.1	11.21507219	0.8441766	0.121478829	6.945026	3.67E-12	8.61E-12	cpm	0.46364795	5.66E-10	GO:0008312;GO:0003824	
Sapur.005G113400.1	376.15843	0.280664475	0.040408504	6.94548	3.77E-12	8.83E-12	cpm	0.47381215	4.44E-10		
Sapur.013G201400.1	439.3644401	0.5	0.072819058	6.86659	6.51E-12	1.52E-11	cpm	0.51328227	1.68E-12	GO:0016627;GO:0016021;GO:0006629;GO:0005737	
Sapur.7032300.1	0.702059856	3.927837314	0.429038329	6.906365	4.97E-12	1.16E-11	cpm	0.43772565	9.88E-09		
Sapur.010G150000.1	134.5808875	0.627908925	0.091395674	6.87016	5.45E-12	1.27E-11	cpm	0.42302256	4.96E-08	GO:0006952	
Sapur.7145000.1	175.802779	0.37455328	0.054665258	6.851

Sapur.01C0209200.1	0.65098474	7.31069384	0.386099592	5.985164	2.18e-09	4.55E-09	cpm	0.42839504	2.18E-08	AT4G18125.1	Protein of unknown function (DUF679)	transmembrane protein, putative
Sapur.01B0109200.1	66.70126164	8.873176476	0.146142651	5.978518	2.25E-09	4.74E-09	cpm	0.31452163	5.37E-05			NA
Sapur.01J0201000.1	0.518852658	5.918516618	0.088267369	5.970793	2.36E-09	4.96E-09	cpm	0.46319471	1.17E-09			NA
Sapur.01K0404200.1	14.86851167	0.785970207	0.131934477	5.957321	2.56E-09	5.38E-09	cpm	0.38179403	8.06E-07	AT3G04470.1	Ankyrin repeat protein	ankyrin repeat protein 13C-B
Sapur.01G0209000.1	98.74149187	0.438281865	0.073868453	5.93328	2.97E-09	6.22E-09	cpm	0.45073716	3.14E-09	AT5G22310.1	transcription factor jumonji (jmjC) domain-containing protein	transcription factor, putative
Sapur.01G0209500.1	187.6143011	0.186766235	0.031546262	5.919195	3.24E-09	6.76E-09	cpm	0.38981496	4.50E-07	AT2G26682.1	ATSPK2,SPK2	SPK domain gene 2
Sapur.01B0111400.1	0.943305251	2.353838359	0.38193829	5.908051	3.62E-09	7.55E-09	cpm	0.35485491	5.39E-06	GO:0005515	receptor-like protein 9	receptor-like protein 9
Sapur.01G0221500.2	3.476351551	1.124581675	0.2152043	5.183323	4.05E-09	8.38E-09	cpm	0.37576901	1.24E-06	GO:0008270;GO:0009089	ATBCA1,ATSABP3.CA1.SABP	carbonic anhydrase 1
Sapur.01G0109400.1	15.62371475	0.812387801	0.138136703	5.879595	4.11E-09	8.57E-09	cpm	0.349869097	7.01E-06		Protein of unknown function, DUF547	NA
Sapur.01J0207800.1	0.880080612	2.087553006	0.355988885	5.865492	4.94E-09	1.03E-08	cpm	0.392388398	1.74E-07	GO:0016747	HXXXD-type acyltransferase family protein	echinocystin 5-aromatic acyltransferase, putative
Sapur.01G0130300.1	2994.673053	0.760388424	0.130611276	5.82174	5.82E-09	1.21E-08	cpm	0.42413264	3.10E-08	AT4G28960.1	Transmembrane amino acid transporter family protein	amino acid transporter, putative
Sapur.01J0111300.1	0.424452214	1.801936685	0.312541818	5.764142	6.24E-09	1.24E-08	cpm	0.46751398	6.96E-10			NA
Sapur.01G0133000.1	0.741118886	-0.057064638	0.354667711	5.799949	6.63E-09	1.37E-08	cpm	0.45179788	1.83E-07			NA
Sapur.01G0249100.1	42.10610656	0.528376882	0.091266491	5.79098	7.04E-09	1.45E-08	cpm	0.44938836	3.88E-09		Uncharacterized protein	NA
Sapur.00G0501000.1	16.65437168	1.526021362	0.265195851	5.754318	8.70E-09	1.79E-08	cpm	0.432953017	1.49E-08	AT3G54070.1	Ankyrin repeat family protein	ankyrin repeat protein
Sapur.00G0146300.1	8.113293952	1.152204025	0.201145266	5.730117	9.56E-09	1.97E-08	cpm	0.369476573	1.32E-06	AT3G46150.1	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.7D79300.1	2.656728253	1.369760307	0.240287671	5.700419	1.20E-08	2.46E-08	cpm	0.360026571	3.62E-06			NA
Sapur.00B0209000.1	375.3057631	0.224467449	0.037266172	5.666155	1.49E-08	2.97E-08	cpm	0.399153029	2.24E-07			EE1G2/EHBP1 protein amino-terminal domain protein
Sapur.5H0708800.1	2183.775024	0.404897665	0.071258447	5.684265	1.68E-08	3.36E-08	cpm	0.397419711	2.47E-07	MIF2	mini zinc finger 2	2'-HO protein dimerization region protein
Sapur.15W0G0240.0	396.1528865	-0.2414262	0.042863021	-5.63265	1.77E-08	3.60E-08	cpm	-0.43151419	1.42E-08	GO:0016491;GO:0008152	NADP(+)-binding Rossmann-fold superfamily protein	forewer young oxidoreductase
Sapur.06G0133000.1	868.8961138	0.148892122	0.026477943	5.624197	1.92E-08	3.91E-08	cpm	-0.42316759	3.30E-08	GO:0042176;GO:0042174;GO:0030234;GO:0000502	PAM domain (PfamPF) protein	26S proteasome non-ATPase regulatory subunit 3
Sapur.01G0117400.1	254.6485144	0.262408821	0.046858537	-5.60002	2.14E-08	4.33E-08	cpm	-0.428044636	2.24E-08	GO:0005515;GO:0006468;GO:0005524;GO:0004672	receptor-like protein kinase 2	LRR receptor-like kinase
Sapur.01K0207400.1	444.024541	0.253686238	0.045188092	-5.5648	2.62E-08	5.28E-08	cpm	-0.430041285	1.90E-08	GO:0004648;GO:0005524;GO:0004672	calmodulin-binding receptor-like cytoplasmic kinase 2	calmodulin-binding receptor-like cytoplasmic kinase
Sapur.01G0179800.1	696.15467	0.242312775	0.043576354	5.560648	2.69E-08	5.41E-08	cpm	0.403608143	1.59E-07			seed maturation protein PM23, putative
Sapur.01G0123300.1	0.963466309	2.028700104	0.365809584	5.54522	2.93E-08	5.90E-08	cpm	0.37678231	2.51E-06			NA
Sapur.01G0235100.1	68.6605267	-0.317317501	0.057272971	-5.54044	3.02E-08	6.06E-08	cpm	0.400808026	1.97E-07			hypothetical protein
Sapur.01G0219800.1	22.26155932	1.041631384	0.188406383	5.5287	3.23E-08	6.47E-08	cpm	0.43422808	1.31E-08	GO:0016758;GO:0008152	AtUGT85A3,UGT85A3	UDP-glucosyl transferase 85A3
Sapur.01J0288800.1	279.1160628	-0.153283939	0.027802293	-5.51478	3.46E-08	6.98E-08	cpm	-0.403126799	1.64E-07	GO:0031124	ESP1	hydroxyproline rich glycoprotein family protein
Sapur.01K0108800.1	485.3543633	0.392581276	0.071245309	5.510862	3.57E-08	7.16E-08	cpm	0.384082227	6.84E-07			alpha/beta-hydrolases superfamily protein
Sapur.01K0119700.1	17.64045226	0.784987665	0.139102626	5.647604	3.85E-08	7.69E-08	cpm	0.39738876	5.60E-08	GO:0005515	Transducin/WD40 repeat-like superfamily protein	WD40 domain protein
Sapur.01G0259000.2	9.552809395	0.616291098	0.112481484	5.479045	4.28E-08	8.54E-08	cpm	0.40062649	2.20E-07		RING membrane-anchor 3	zinc-RING finger protein
Sapur.00G0661200.1	14.64161536	1.557252466	0.28413572	5.481216	4.77E-08	9.42E-08	cpm	0.41306032	8.91E-08			NA
Sapur.00G0610000.2	33.80924698	0.770782551	0.141501579	5.447206	5.12E-08	1.02E-07	cpm	0.38383066	7.04E-07	GO:0005515	F-box family protein	F-box plant protein
Sapur.01J0111900.1	87.6780724	0.525857736	0.096751781	-5.44546	5.17E-08	1.03E-07	cpm	-0.42429404	3.06E-08	GO:0004045	Peptidyl-tRNA hydrolase family protein	peptidyl-tRNA hydrolase
Sapur.01G0301300.1	93.56150101	-0.436193381	0.080217235	-5.43765	5.40E-08	1.07E-07	cpm	-0.4305649	9.64E-08	GO:0006355;GO:0005739;GO:0003690	Mitochondrial transcription termination factor family protein	mTERF protein
Sapur.00G0264500.1	0.465105941	1.354188437	0.250133287	5.414398	6.15E-08	1.22E-07	cpm	0.448262739	3.50E-08			NA
Sapur.01T0115700.1	2327.64553	0.282184307	0.052176802	-5.40822	6.17E-08	1.26E-07	cpm	0.411875955	8.35E-08	GO:0006355;GO:0005634;GO:0003677;GO:0009725	DVL12,RTL12	auxin response factor
Sapur.01G0290300.1	292.2008382	0.210292946	0.038958076	5.402441	6.57E-08	1.30E-07	cpm	0.379873441	1.14E-06		AtRTA,ATARFB	auxin response factor B
Sapur.00G0130700.1	75.63746861	0.601581497	0.12063414	5.401908	6.58E-08	1.30E-07	cpm	0.348376318	1.98E-06		sequence-specific DNA binding transcription factors	Myb/SANT-like DNA-binding domain protein
Sapur.01B0243000.1	638.3219432	-0.249091986	0.045344271	-5.40115	6.62E-08	1.31E-07	cpm	-0.402080015	1.76E-07	GO:0003824;GO:0006470;GO:0004722	homology to ABI1	transmembrane protein, putative
Sapur.00G0290800.1	40.6526777	0.559455215	0.069949363	5.37975	7.46E-08	1.47E-07	cpm	0.40047505	9.61E-08		TIP1B	abscisic insensitive protein 18
Sapur.01T0108800.1	931.322625	1.028378858	0.191741191	5.36337	8.17E-08	1.61E-07	cpm	0.380981362	8.51E-07	GO:0006807;GO:0006542;GO:0004356	ATGLN1-1,ATGLR1,GLN1:1:1	TIP41 protein, putative
Sapur.01G0109100.1	59.51910103	0.587109124	0.112638366	5.305791	8.31E-08	1.64E-07	cpm	0.424357127	1.38E-08	GO:0005515	AtRLP43,RLP43	glutamine synthetase
Sapur.01J0119500.1	107.1142658	0.491969304	0.091940366	5.347525	9.17E-08	1.80E-07	cpm	0.306543245	9.43E-05			receptor like protein 43
Sapur.01J0202100.1	388.4664819	0.276314269	0.051673313	5.347266	9.19E-08	1.81E-07	cpm	0.38664762	4.55E-07			ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2)
Sapur.01G0229700.1	103.5352836	0.234633974	0.044038949	5.328116	9.92E-08	1.95E-07	cpm	0.390045894	4.43E-07			Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01G0288300.1	68.05428135	0.594227567	0.111537287	5.328669	9.92E-08	1.95E-07	cpm	0.390631292	4.34E-07	GO:0016567;GO:0004842	ChaC-like family protein	PPR containing plant protein
Sapur.01G0340000.1	175.2768718	0.296040017	0.056171658	5.270182	1.36E-07	2.67E-07	cpm	0.409323214	1.02E-07		RING-type E3 ubiquitin transferase	NA
Sapur.00G0115700.1	30.44215698	0.480305515	0.091543163	5.253648	1.49E-07	2.91E-07	cpm	0.369652072	1.89E-06		RING/U-box superfamily protein	U-box protein
Sapur.00G0147200.1	125.5322232	0.363226835	0.069501538	5.226166	1.73E-07	3.37E-07	cpm	0.365423277	9.36E-06		Protein of unknown function, DUF593	double-stranded RNA-binding motif protein
Sapur.01T0288800.1	236.8868558	0.252439906	0.048377471	5.216145	1.83E-07	3.55E-07	cpm	0.386246515	8.50E-07	GO:0005515	Oxiticoupestiphe/Phos/Rem3p family protein	VQ motif-containing protein
Sapur.00G0290600.1	1906.770564	0.295218182	0.057369939	5.211616	1.87E-07	3.64E-07	cpm	0.372641814	1.50E-06	GO:0016021	Auxin-responsive family protein	P61 domain protein
Sapur.01B0123000.1	262.6276634	0.165908001	0.032882239	5.164733	2.41E-07	4.66E-07	cpm	0.424355139	3.05E-08			auxin-induced in root cultures protein
Sapur.00G0115000.1	649.5341314	0.207902004	0.040273153	5.164027	2.42E-07	4.67E-07	cpm	0.404868401	1.07E-07	GO:0005085;GO:0016023;GO:0015299;GO:0006812	ATCHX20,CHX20	ATP-binding protein, putative
Sapur.01G0195500.1	10293.51566	0.186825651	0.036179161	5.146908	2.65E-07	5.11E-07	cpm	0.370904563	1.74E-06	GO:0016829;GO:0010333;GO:0080132	ATTPS4,TPS14	cation/H+ exchanger 20
Sapur.01G0197500.1	1923.501378	0.326489888	0.051933382	5.137532	2.78E-07	5.37E-07	cpm	0.363828852	2.46E-06	GO:0005975;GO:0009533	AtGH9B5,GH9B5	myrosinase-binding protein 1
Sapur.01G0233900.1	176.2885845	0.283218405	0.055146346	-5.13576	2.81E-07	5.42E-07	cpm	-0.424685465	2.56E-08	GO:0008170;GO:0006644	ATPMT,PLMT	terpene synthase 14
Sapur.01G0217300.1	37.57241459	0.633060279	0.123308587	5.134194	2.83E-07	5.46E-07	cpm	0.385348822	6.24E-07	GO:0005975;GO:0005553		gibberellin 2-oxidase 8
Sapur.01G0138800.1	480.3459324	-0.251957744	0.049173714	-5.12753	2.94E-07	5.65E-07	cpm	-0.42928712	1.92E-08		ATLCP2,LCP2	Glycosyl hydrolase superfamily protein
Sapur.01G0188200.1	128.12509	0.304679995	0.059433088	-5.12627	2.95E-07	5.68E-07	cpm	-0.401398574	1.89E-07	GO:0008270;GO:0005515		uncoupling protein 2
Sapur.00G0621300.1	738.8619197	0.242005267	0.047264197	5.120167	2.96E-07	5.69E-07	cpm	0.352760232	5.38E-06	GO:0005515	RING/U-box superfamily family protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.01B0501000.1	690.8309441	0.634813865	0.124952381	5.080423	3.77E-07	7.20E-07	cpm	0.314722992	5.96E-05	GO:0042545;GO:0030599;GO:0005618	Ribosome associated membrane protein RAMP4	ribosome associated membrane protein RAMP4
Sapur.01G0230500.1	87.62229774	0.333826663	0.066585812	5.01653	4.80E-07	9.17E-07	cpm	0.362681683	1.41E-06		Pectin lyase-like superfamily protein	pectinesterase
Sapur.01G0232500.1	42.9143841	-0.463301621	0.091407512	-5.06162	4.16E-07	7.94E-07	cpm	-0.423979756	3.14E-08		Erythronate-4-dehydrogenase family protein	NA
Sapur.01G0219700.1	21.58124328	0.750287307	0.150032426	5.000417	5.73E-07	1.09E-06	cpm	0.381802737	3.86E-07	GO:0016758;GO:0008152	AtUGT85A3,UGT85A3	plant/MG/11-3 protein, putative
Sapur.15W0G0100.0	59.90469257	0.640036589	0.127703421	-5.01425	5.32E-07	1.01E-06	cpm	-0.381628138	2.78E-07			UDP-glucosyltransferase family protein
Sapur.01J0139000.1	61.71412049	0.626861564	0.13321145	4.970703	6.68E-07	1.25E-06	cpm	0.318688767	1.24E-05	GO:0055114;GO:0050660;GO:0016491	FAD-binding Berberine family protein	hypothetical protein
Sapur.00G0503000.1	122.1750273	0.416817528	0.083981314	4.963218	6.93E-07	1.31E-06	cpm	0.341414342	1.23E-05	GO:0005515;GO:0006468;GO:0005524;GO:0004672	Leucine-rich receptor-like protein kinase family protein	reticulon oxidase, putative
Sapur.01G0203300.1	571.5592381	0.335661237	0.067698834	4.956751	7.17E-07	1.35E-06	cpm	0.364423091	8.81E-06	GO:0031225;GO:0016049;GO:0010215	ATSEB1,COB6,TSEB1	LRR receptor-like kinase
Sapur.01J0204700.1	830.2125107	0.175113879	0.035350029	4.95089	8.68E-07	1.63E-06	cpm	0.363192502	3.10E-06	GO:0016021	TOPP4	COBRA-like protein 7 precursor
Sapur.01G0118500.1	342.8086923	-0.262171965	0.053232412	-4.91664	8.80E-07	1.66E-06	cpm	-0.364457991	2.70E-06	GO:0003676		serine/threonine protein phosphatase 4
Sapur.00G0177200.1	164.9764121	0.210623837	0.042786828	4.924237	9.15E-07	1.72E-06	cpm	0.605507881	4.38E-07	GO:0003985		RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.01G0109500.1	0.428809127	2.152035821	0.437461919	4.911665	9.03E-07	1.70E-06	cpm	0.442583222	6.48E-09			Rho GTPase activation protein with PAK-box/PH-like domain
Sapur.01G0302700.1	2.820507153	1.201484674	0.245446664	4.894507	9.86E-07	1.84E-06	cpm	0.294691915	0.000181178			PLC-like phosphodiesterase superfamily protein
Sapur.01B0109800.1	6.497917504	0.996815699	0.204768272	4.866903	1.12E-06	2.10E-06	cpm	0.349049567	7.45E-05	GO:0006508;GO:0004190		Plant protease of unknown function (DUF239)
Sapur.01G0109100.1	0.355105871	1.685023895	0.350154547	4.791555	1.66E-06	3.12E-06	cpm	-0.360660809	1.53E-06	GO:0016491;GO:0000722		Eukaryotic aspartyl protease family protein
Sapur.01G0203000.1	0.543880209	2.367528841	0.497168654	4.859773	1.18E-06	2.19E-06	cpm	0.391120188	4.06E-07	GO:0016818;GO:0008270;GO:0003676;GO:0005524	BAMT,BMT4	beta-amylase
Sapur.01G0290100.1	0.593770118	1.581669589	0.325585544	4.859302	1.18E-06	2.20E-06	cpm	0.399892334	2.84E-07		GO:0051536;GO:0051539	chromatin remodeling complex subunit, putative
Sapur.01J0205800.1	1266.227557	-0.268145658	0.055146837	-4.85792	1.19E-06	2.21E-06	cpm	-0.373586974	1.46E-06			NA
Sapur.00G0145000.1	925.7032198	0.544705211	0.11258411	4.796624	1.61E-06	2.99E-06	cpm	0.36347896	2.88E-06			hypothetical protein
Sapur.00G0251100.1	1097.32622	0.107887291	0.0241203	-4.7755	1.78E-06	3.32E-06	cpm	-0.382988581	7.40E-06		Pentatricopeptide (PPR) superfamily protein	transcription factor, putative
Sapur.01J0127500.1	4.374806252	1.809763507	0.37917583	4.772835	1.82E-06	3.36E-06	cpm	0.307969481	8.72E-05	GO:0046983;GO:0008171	O-methyltransferase family protein	PPR containing plant protein
Sapur.01T0116200.1	2984.491612	0.210623837	0.042786828	4.762727	1.91E-06	3.52E-06	cpm	0.305280606	8.01E-05			caffeic acid 3-O-methyltransferase
Sapur.01G0127200.1	37.86883304	0.387667762	0.081665379	4.745865	2.08E-06	3.83E-06	cpm	0.383296009	7.16E-07	GO:0043565;GO:0003700;GO:0030717	ABF2,AREB1,ATAREB1	transmembrane protein, putative
Sapur.01G0109300.1	853.9609947	0.173181276	0.036501778	4.72654	2.28E-06	4.19E-06	cpm	0.387708238	1.36E-07			ABA-responsive element-binding factor 2
Sapur.00G0132200.1	23.19281998	1.599724452	0.339519876	4.718605	2.37E-06	4.37E-06	cpm	0.294315289	0.000182892	GO:0005515;GO:0006468;GO:0004672	Leucine-rich repeat protein kinase family protein	eukaryotic regulator protein
Sapur.00G0170300.1	0.305150871	1.685023895	0.356514547	4.715576	2.41E-06	4.48E-06	cpm	0.472092025	4.12E-10			NA
Sapur.01G0178900.1	177.4979863	-0.472102627	0.100456949	-4.69955	2.61E-06	4.79E-06	cpm	-0.374180757	1.38E-06	GO:0016757	FUCS5A	beta-galactosidase
Sapur.01G0203500.1	2279.373833	-0.234237427	0.050092334	-4.67611	2.92E-06	5.36E-06	cpm	-0.379261108	9.66E-07	GO:0016051;GO:0008250;GO:0006487	HAP6	1,2-alpha-L-fucosidase
Sapur.01G0109600.1	686.5658123	-0.211352431	0.045404718	-4.65134	3.26E-06	5.98E-06	cpm	-0.360640809	3.53E-06	GO:0016021;GO:0000722	RBX2	ribophorin II (RPN2) family protein
Sapur.01G0140700.1	152.6752633	0.32874224	0.071470321	4.614132	3.95E-06	7.19E-06	cpm	0.301120188	4.06E-07	GO:0016818;GO:0008270;GO:0003676;GO:0005524		F-box protein 1
Sapur.01G0204200.1	700.0918844	-0.354617336	0.076817243	-4.59734	4.28E-06	7.78E-06	cpm	-0.316609301	4.56E-06	GO:0006355;GO:0003700;GO:0005622	ATCSPB1,CSP1	autophagy-related protein
Sapur.01G0201000.1	2.238684177	0.746956916	0.162242336	4.591631	4.40E-06	7.99E-06	cpm	0.423011497	1.40E-08			Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain
Sapur.01G0266100.2	1.516807549	1.360691588	0.297127269	4.580358	4.64E-06	8.42E-06	cpm	0.319013081	4.80E-05	GO:0016301;GO:0007205;GO:0004143	ATCGK1,DGK1	exportin 1A
Sapur.01G0160800.1	353.6305009	0.293788459	0.064257442	4.572053	4.83E-06	8.75E-06	cpm	0.34703293	9.88E-06	GO:0008270;GO:0005515		diacylglycerol kinase 5
Sapur.01G0203100.1	14.98088829	0.568864827	0.124963311	4.549345	5.38E-06	9.72E-06	cpm	0.347781748	8.88E-06		RING/U-box superfamily family protein	RING/U-box superfamily protein
Sapur.07G0867000.1	924.5316152	0.164294421	0.036448551	-4.50757	6.56E-06	1.18E-05	cpm	-0.363234667	2.07E-06	GO:0005525		
Sapur.01G0109200.1	238.8209088	-0.173982324	0.039838125	-4.50666	6.58E-06	1.18E-05	cpm	-0.346228752	8.80E-06	GO:0005515	ARABARA,RABA4a	RAB GTPase homolog A4A
Sapur.01G0251500.1	0.647077876	2.260866453	0.504200067	4.484039	7.32E-06	1.31E-05	cpm	0.282918755	0.000330101			Glutathione S-transferase family protein
Sapur.01G0205500.1	874.6749802	0.180889558	0.040363182	4.481548	7.41E-06	1.33E-05	cpm	0.334432614	1.86E-05	GO:0006351;GO:0005634;GO:0003677		Transcription elongation factor (TFIIS) family protein
Sapur.01G0297000.1	1267.173473	0.224883059	0.050288278	4.471451	7.77E-06	1.39E-05	cpm	0.310852589	7.44E-05	GO:0005515	CINV2	cytosolic invertase 2
Sapur.01G0148900.1	332.9331111	0.878953944	0.196635824	4.469958	7.82E-06	1.40E-05	cpm	0.328619826	2.64E-05	GO:0016705;GO:0016117	LYC	cyclase/dehydrase family protein
Sapur.01G0188200.1	521.7208016	0.457102278	0.10257988	4.45664	8.16E-06	1.46E-05	cpm	-0.362735837	1.47E-06	GO:0005515;GO:0008324		capsophin/capsorubin synthase, chromoplast protein
Sapur.01G0118600.1	328.2118834	0.145327427	0.032768837	-4.43479	9.22E-06	1.64E-05	cpm	-0.388974331	5.54E-07	GO:0016592;GO:0003557;GO:0001104	ANP-dependent synthase and lyase family protein	acyl-CoA ligase auxin-conjugate synthetase 8 protein
Sapur.01G0279000.1	154.5631016	0.255404023	0.05775157	-4.42169	9.60E-06	1.71E-05	cpm	-0.402802007	1.51E-07	GO:0003700;GO:0005739;GO:0003690	TATA-binding related factor (TRF) of subunit 20 of Mediator complex	mediator of RNA polymerase II transcription subunit 20, putative
Sapur.01G0193800.1	590.2357346	0.169124278	0.038443882	-4.40004	1.08E-05	1.92E-05	cpm	-0.377593221	1.07E-06	GO:0005515	Transcription termination factor family protein	mTERF protein
Sapur.01G0173200.1	0.695073327	1.777061237	0.404407349	4.394402	1.11E-05	1.97E-05	cpm	0.313980051	4.45E-05	GO:0005515	Calcium-dependent lipid-binding (CaLB domain) family protein	synaptotagmin protein
Sapur.01G0266400.1	200.9855569	0.637722844	0.145453523	4.384375	1.16E-05	2.06E-05	cpm	0.317739962	5.00E-05	GO:0005515	ATPRLPR 1,PR1	pathogenesis-related protein 1a, putative
Sapur.01G0190200.1	4.786409079	0.931209192	0.152682321	4.348388	1.37E-05	2.42E-05	cpm	0.326892797	2.97E-05	GO:0005515	VFB2	VIER F-box protein 3
Sapur.01G0130500.1	2409.305868	-0.213885576	0.076218218	-4.34663	1.39E-05	2.46E-05	cpm	-0.303917566	9.76E-05	GO:0016788	GDSL-like Lipase/Hydrolase family protein	slip-2, putative
Sapur.01K0113900.1	447.9838435	-0.018708209	0.043587618	-4.33776	1.44E-05	2.54E-05	cpm	-0.374592919	1.67E-06	GO:0004018;GO:0005524;GO:0004812;GO:0000166;GO:0004831	tmb2768	Tyrosyl-tRNA synthetase, class Ib, bacterial/mitochondrial
Sapur.00G0175000.1	294.5875423	0.180404881	0.041664139	4.329107	1.51E-05	2.66E-05	cpm	0.318461639	1.30E-05	GO:0004648;GO:0005524;GO:0005515	CERK1,LYSM RLK1	chitin elicitor receptor kinase 1
Sapur.01G0117900.1	3485.700053	0.722396636	0.168231835	4.29346	1.76E-05	3.09E-05	cpm	0.346297692	8.61E-06	GO:0055114;GO:0050660;GO:0016491	FAD-binding Berberine family protein	NA
Sapur.01B0260400.1	661.9155414	0.178060049	0.041588469	4.280728	1.86E-05	3.26E-05	cpm	0.303983737	0.000108627	GO:0055114;GO:0016491;GO:0016705	Aldehyde oxidase 1	reticulon oxidase, putative
Sapur.01G0054500.1	8146.264212	0.640381663	0.149597343	4.280702	1.86E-05	3.27E-05	cpm	0.381347028	8.31E-07		ATNCED5,NCED5	9-cis-epoxycarotenoid dioxygenase 5
Sapur.01G0265400.1	564.7435	0.160988872	0.037655247	4.276966	1.87E-05	3.27E-05	cpm	0.391639437	3.93E-07	GO:0004648;GO:0004672	Protein kinase family protein	NA
Sapur.7I8400.1	0.28690905	1.574069851	0.369475825	4.260201	2.04E-05	3.57E-05	cpm	0.460760421	1.27E-09			NA
Sapur.00G0556000.1	1619.041036	0.345073882	0.081079051	4.263998	2.02E-05	3.84E-05	cpm	0.299078068	0.000181812	GO:0005515	Embryo-specific protein 3, (ATS3)	embryo-specific protein
Sapur.00G1168000.1	162.0398652	0.219568071	0.051740622	4.24363	2.20E-05	3.86E-05	cpm	0.331373871	4.06E-05			cytochrome P450 family protein, putative
Sapur.00G0162800.1	3277.476131	0.367505251	0.087271169	4.215852	2.49E-05	4.33E-05	cpm	0.335214188	1.72E-05	GO:0016740;GO:0009058	PSY	PHYTOENE SYNTHASE
Sapur.00G0274000.1	24.18034156	0.365464553	0.091539073	4.211083	2.54E-05	4.42E-05	cpm	0.328329229	2.62E-05	GO:0009058;GO:0003824	PECT1	phosphorylcholine cytidylyltransferase 1
Sapur.00G1681000.1	60.91942887	0.326506204	0.076139896	4.207635	2.58E-05	4.49E-05	cpm	0.579238845	1.78E-15	GO:0006355;GO:0005667;GO:0003700	ATE2FA,E2F3	ethanolamine-phosphate cytidylyltransferase
Sapur.00G0179500.1	4.978803824	0.514225193	0.122246453	4.206455	2.60E-05	4.52E-05	cpm	0.329491284	6.81E-05			transcription factor E2F
Sapur.01D0591000.1	76.57141188	-0.208202603	0.049729669	-4.20115	2.66E-05	4.61E-05	cpm	-0.351025273	3.84E-06		Uncharacterized protein family (UPF0497)	DNA topoisomerase 3-binding protein
Sapur.01G0109400.1	551.4784251	0.278211194	0.066211612	4.202485	2.68E-05	4.65E-05	cpm	0.294842777	0.000177669	GO:0006355;GO:0005634;GO:0003677	ATHB-13,ATHB17,HB17	DUF588 domain protein
Sapur.00B0245600.1	431.9491874	0.164603628	0.039695208	4.135228	3.55E-05	6.12E-05	cpm	0.290518362	0.000223349	GO:0008270;GO:0005515	RHC2A	Transcription factor (TFIIIC) family protein
Sapur.01G0109300.1	12.02573238	0.867249769	0.170071619	4.102422	3.82E-05	6.57E-05	cpm	0.279167808	0.000348372	GO:0000166;GO:0016301	ATRH4,RH42,PMA2	zinc finger (CCCH type) protein
Sapur.01C0118100.1	4.570718825	0.754976783	0.182971147	4.126287	3.68E-05	6.36E-05	cpm	0.247694246	0.001812944			ATP-dependent RNA helicase A/ATPase
Sapur.01G0285300.1	24.12053994	0.719264045	0.178653897	4.025803	4.68E-05	6.93E-05	cpm	0.325419986	3.28E-05	GO:0005515;GO:0006355;GO:0000700;GO:0003677	ATZIP4,ATZIP4.7,HB17	Transcriptocoptide repeat (TFIIS) family protein
Sapur.01G0171100.1	921.5047081	-0.024868366	0.059851078	-4.09129	4.29E-05	7.37E-05	cpm	-0.301933595	0.000112442	GO:0005515;GO:0000160	APRR7,PRR7	homeobox leucine zipper protein ATHB-4
Sapur.01G0140900.1	159.1999105	0.832093679	0.203975085	4.085319	4.44E-05	7.61E-05	cpm	0.32216185	3.88E-05		DDB2	pseudo-response regulator 7
Sapur.01T0204600.1	858.7938924	0.255017522	0.064886261	4.064081	5.72E-05	9.75E-05	cpm	0.294793606	0.000178097	GO:0006355;GO:0003700		damaged DNA binding 2
Sapur.00B0201300.1	41.12771474	0.528213523	0.132493799	3.987458	6.68E-05	0.000113402	cpm	0.274240408	0.000329654	GO:0004983;GO:0003677	AGL62	Basic-leucine zipper (bZI

Sapur.002G056100.1	846.034284	4.52837825	0.026892143	17.67614	6.40E-70	4.81E-69	cpm	0.809397246	1.16E-37		AT5G77220.1	Protein of unknown function (DUF300)	organic solute transporter ostalpha protein
Sapur.001G135700.1	1345.563287	0.787513828	0.04690885	17.53583	7.63E-69	5.63E-68	cpm	0.795483824	1.57E-35	GO:0005525;GO:0003924	AT5G58630.1	ADL1;CFL1;DL1;DRP2B	dynamin-like 2
Sapur.018G079500.1	9.870416664	1.149387802	0.178875779	17.50718	1.26E-68	9.26E-68	cpm	0.763920241	1.19E-27		AT4G28730.1	Family of unknown function (DUF566)	DUF566 family protein
Sapur.016G202100.1	1006.105845	0.928070904	0.053346179	17.41401	6.46E-68	4.70E-67	cpm	0.76409764	2.59E-31	GO:0055085	AT5G27020.1	YSL6	YELLOW STRIPE like 6
Sapur.019G116800.1	9271.913314	0.601483553	0.034844028	17.26327	9.06E-67	6.48E-66	cpm	0.8041737	7.60E-37	GO:0015194;GO:0003712	AT1G01230.1	TUDOR-like protein 1	tudor protein
Sapur.014G296600.1	934.7685492	0.538810828	0.031657032	17.02026	5.81E-65	4.06E-64	cpm	0.82772258	9.79E-41		AT4G02030.1	Vps11/Vps17 family (components of vesicular transport) protein	Fer-free-like protein
Sapur.003G094300.1	841.3117989	0.842419345	0.050005054	16.84668	1.11E-63	7.58E-63	cpm	0.785835424	3.63E-34	GO:0003131;GO:0016192;GO:0006886;GO:0030117	AT4G23440.1	Adaptin family protein	beta-adaptin-like protein
Sapur.002G036300.1	1022.983973	1.235257272	0.073570709	16.79001	2.89E-63	1.96E-62	cpm	0.738631374	2.45E-28	GO:0055015	SPI	Bego/BEACH domain; WD domain, G-beta repeat protein	WD repeat and FYVE domain protein
Sapur.004G058400.1	4228.427638	0.674167046	0.04018058	16.77793	3.54E-63	2.40E-62	cpm	0.78274817	9.66E-34	GO:0055114;GO:0015136;GO:0016651;GO:0016491	AT5G37510.1	C7GLEMB1467	NADH-ubiquinone oxidoreductase, putative
Sapur.012G051900.1	9569.923471	0.553602363	0.033048363	16.51139	3.29E-60	2.00E-59	cpm	0.779413363	1.29E-27	GO:0016887;GO:0000166	AHA11;HA11	H(+)-ATPase 11	plasma membrane H+-ATPase
Sapur.010G016300.1	2045.68554	0.492821293	0.030364666	16.08715	3.14E-58	1.97E-57	cpm	0.795438148	1.55E-35	GO:0031625;GO:0006511	AT1G13;AKR6;CUL1	cullin 1	CULLIN-like protein
Sapur.018G000600.1	1380.988597	0.7164844	0.045496817	15.74644	4.25E-58	2.66E-57	cpm	0.76087836	6.13E-32	GO:0016887;GO:0070163;GO:0005622;GO:0005871	AT4G00330.1A;KINESIN-13	P-loop containing nucleoside triphosphate hydrolases superfamily protein	kinesin motor domain protein
Sapur.016G184600.1	2049.377597	0.6476146 4	0.040623744	15.94178	3.25E-57	2.01E-56	cpm	0.773051174	2.55E-32	GO:0003127;GO:0008370;GO:0006888;GO:0006886	AT5G05320.1	Sec23/Sec24 protein transport family protein	protein transporter Sec23
Sapur.001G028900.1	2272.613875	0.717604208	0.045064654	15.97068	2.57E-57	1.84E-56	cpm	0.76108	1.16E-30	GO:0003131;GO:0016192;GO:0006886;GO:0030117	AT4G23440.1	Adaptin family protein	beta-adaptin-like protein
Sapur.017G065100.1	646.3354726	0.864634979	0.054607112	15.83372	1.82E-56	1.11E-55	cpm	0.75221224	1.20E-29	GO:0003924;GO:0005086	AT5G19380.2	EMB30;GNL;GNL1	sec7 domain-containing protein
Sapur.013G201500.1	367.992284	1.364151324	0.085189654	15.96184	1.67E-56	2.15E-55	cpm	0.72830784	1.38E-26	GO:0003767	AT5G05580.1	Calcineurin-like metallophosphoesterase superfamily protein	serine/threonine-protein phosphatase PP1
Sapur.016G041800.1	11.2971279	1.142541356	0.200852088	15.64605	3.54E-55	2.11E-54	cpm	0.685495054	4.02E-23	GO:0009790	GEA6-5	Late Embryogenesis Abundant 4-5	late embryogenesis abundant group 1 protein
Sapur.006G076200.1	1864.851177	0.583858884	0.03747082	15.58169	9.70E-55	5.76E-54	cpm	0.762033362	4.66E-31	GO:0003131;GO:0016192;GO:0006886;GO:0030117	AT4G28070.1	Adaptor protein complex AP-1, gamma subunit	AP-1 complex subunit gamma-2
Sapur.010G121700.1	1208.944965	0.780327887	0.054525276	15.52128	2.48E-54	1.47E-53	cpm	0.735237127	5.75E-28	GO:0016491	Bego/BEACH domain; WD domain, G-beta repeat protein	Purple acid phosphatase superfamily protein	inactive purple acid phosphatase;
Sapur.016G280400.1	551.2643881	0.826828912	0.040402891	15.49599	3.69E-54	2.17E-53	cpm	0.76014241	7.98E-31		AT4G27030.1		plant/P3/M23-340 protein
Sapur.014G006100.1	1279.931342	0.54 14885	0.034 9 5 7	15.44885	6.06E-54	3.56E-53	cpm	0.78114894	1.24E-33	GO:0006887;GO:0000166	AT1G10130.1	AtECA2;ECA2	endoplasmic reticulum-type calcium-transporting ATPase 3
Sapur.15WG0894000.3	9.892775175	-1.623902087	0.106016888	-15.4023	1.58E-53	9.21E-53	cpm	0.31124777	7.20E-05		AT4G27450.2	ADP-glucose pyrophosphorylase family protein	maintenance-1-phosphate guanylyltransferase
Sapur.001G029100.1	1657.508369	1.464862127	0.093008879	15.31133	4.72E-53	2.75E-52	cpm	0.757770551	1.54E-30		AB1;ELD1;XDB1	elongation defective 1 protein / ELD1 protein	SDL protein
Sapur.017G114600.1	943.587923	0.649931344	0.042494426	15.29451	8.32E-53	4.79E-52	cpm	0.75232653	6.88E-30	GO:0016020	AT5G54320.1	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein	NA
Sapur.010G137800.1	1001.104989	0.717604208	0.046864654	15.07868	1.61E-52	9.39E-52	cpm	0.761638301	1.28E-30		AT4G28300.1	Vps11/Vps17 family (components of vesicular transport) protein	vps11/vps17 family (component of vesicular transport) protein
Sapur.016G058000.1	464.450559	1.208835155	0.080409009	15.01832	5.57E-51	3.11E-50	cpm	0.736615301	4.07E-28		AT4G30190.1		NA
Sapur.012G082300.1	1657.518878	0.534297032	0.035649781	14.98949	8.60E-51	4.78E-50	cpm	0.779454638	1.67E-32	GO:0015937;GO:0005524;GO:0004594	AT2G21180.1	PTANKN2;PANK2	pantothenate kinase 2
Sapur.006G138800.1	751.672452	0.728749186	0.048664856	14.8849	1.01E-50	5.62E-50	cpm	0.761035552	1.02E-31	GO:0005515;GO:0006488;GO:0005524;GO:0004672	AT5G19320.1	protein kinase family protein / WD-40 repeat family protein	phosphoinositide-3 kinase, regulatory subunit 4, p150
Sapur.014G070000.1	1154.790435	0.862308173	0.058006148	14.85401	6.55E-50	3.59E-49	cpm	0.748415241	1.94E-29	GO:0048278;GO:0006887;GO:0005737	SEC10	exocyst complex component sec10	exocyst complex component Sec10
Sapur.011G160600.1	678.0868313	0.7 5 2 0 9 8 4	0.037236235	14.6165	2.20E-48	1.18E-47	cpm	0.761000037	4.24E-31				NA
Sapur.017G125900.1	1963.144274	0.688005769	0.044512641	14.36682	1.12E-46	5.79E-46	cpm	0.738809603	3.88E-28	GO:0016021		Endomembrane protein 70 protein family	transmembrane 9 family protein
Sapur.003G088800.1	4205.121866	0.481078733	0.03345657	14.34105	1.21E-46	6.27E-46	cpm	0.74328161	6.29E-29	GO:0016021	AT3MN1;TMN1	transmembrane 9	NA
Sapur.007G023200.1	647.725222	0.750650617	0.049596248	14.3008	2.16E-46	1.12E-45	cpm	0.738645348	8.08E-28	GO:0016192;GO:0006886	EMB2754	Vacuolar sorting protein 39	tubby-like F-box protein
Sapur.018G000300.1	1186.96797	0.862806089	0.059086028	14.26705	3.51E-46	1.81E-45	cpm	0.732668184	2.26E-27	GO:0016773;GO:0016779;GO:0004015;GO:0005536;GO:0004396;GO:0005617	AT4G19860.1	hexokinase 2	hexokinase
Sapur.005G158800.1	2372.652214	0.767284032	0.055001803	13.95016	3.14E-44	1.56E-43	cpm	0.73087027	1.69E-27	GO:0016773;GO:0016020;GO:0005524	AT3MPK20;MPK20	MAP kinase 20	MAP kinase
Sapur.011G208400.1	1278.977227	0.512689401	0.037 1 8 3 6 9	13.81896	1.51E-43	7.43E-43	cpm	0.718260602	4.32E-26			NAD domain-containing protein	NA
Sapur.001G185400.1	304.7223861	0.462003029	0.033672707	13.75575	3.11E-43	1.51E-42	cpm	0.732797599	1.05E-27	GO:0016020;GO:0008375	KLP7	Core-J/J-branching beta-1,6-N-acetylglucosaminyltransferase family protein	core-2/I-branching enzyme
Sapur.009G204900.1	2551.107721	0.686978898	0.050526446	13.56642	4.21E-42	2.01E-41	cpm	0.701818168	2.10E-25	GO:0016021;GO:0008270;GO:0055057;GO:0004022;GO:0006508	Rsh10	rTSH protease 10	ATP-dependent zinc metalloprotease FtsH
Sapur.005G088300.1	2319.461637	0.526 4 2 4 2 5	0.039 1 3 5 7 6	13.4218	4.55E-41	2.17E-40	cpm	0.715058104	2.12E-25	GO:0006487;GO:0000900;GO:0010191;GO:0080165	VPS25A;ZIP3	VPS25 homolog A	vacuolar protein sorting-associated protein
Sapur.003G021200.1	650.7147729	0.655092418	0.048939378	13.40285	5.82E-41	2.75E-40	cpm	0.721607104	1.76E-26	GO:0008324	AT5G17250.1	Alkaline-phosphatase-like family protein	phosphoglycerol/cardiolipin synthase
Sapur.014G142600.1	1739.242234	0.703324235	0.052626691	13.36423	9.98E-41	4.67E-40	cpm	0.711208194	1.68E-25		AT1G72750.1	Chaperone DnaJ-domain superfamily protein	auxilin-related protein, putative
Sapur.010G098800.1	2424.335992	0.502645316	0.037069892	13.33281	1.49E-40	6.95E-40	cpm	0.724623134	7.62E-27		AT5G25800.1	PDF1;PP2AA2;PR E5	serine/threonine protein phosphatase 2A regulatory subunit A, putative
Sapur.018G000500.1	1575.692002	0.513 6 3 5 6 4	0.038 1 1 7 6 1 1	13.2 4 5 6 4	4.79E-40	2.16E-39	cpm	0.76 5 0 5 2 3 2	1.20E-30		AT4G04630.1	Clathrin adaptor complexes medium subunit family protein	AP-2 complex subunit mu
Sapur.012G054700.1	1093.236808	0.57163926	0.043456159	13.18901	1.02E-39	4.66E-39	cpm	0.7293174	2.44E-27	GO:0016773;GO:0048015;GO:0004854	ATVPS34;PI3K;VPS34	vacuolar protein sorting 34	phosphatidylinositol 3-kinase
Sapur.006G081100.1	1270.427934	0.686832344	0.052078589	13.18494	1.07E-39	4.92E-39	cpm	0.725473813	1.26E-27	GO:0008080;GO:0006351;GO:0005634;GO:0003677	BAM1	BAM domain; TFIIS/CRSP70 double-like domain	BAM and TFIIS domain protein
Sapur.007G016600.1	157.7623922	0.791885955	0.060114241	13.17314	1.25E-39	5.74E-39	cpm	0.70078065	1.67E-24				transmembrane protein, putative
Sapur.005G085700.1	1347.76884	0.552 4 8 9 2 8 5	0.047374774	13.08173	1.98E-38	8.98E-38	cpm	0.72983663	1.52E-27	GO:0005509	AT3G08690.1	Calcium-binding EF-hand family protein	calcium-binding EF-hand protein
Sapur.011G169200.1	870.7871323	0.677899109	0.063730073	13.01466	1.01E-38	4.55E-38	cpm	0.721177348	1.72E-26	GO:0071805;GO:0016020;GO:0015079	KUP7	K+ uptake permease 7	oligomeric subunit 4
Sapur.005G189600.1	685.1374273	0.810041417	0.062381191	12.99132	1.37E-38	6.14E-38	cpm	0.69870255	2.60E-24	GO:0031179;GO:0015591;GO:0015078	VHA-A2	vacuolar proton ATPase A2	vacuolar proton ATPase a3
Sapur.008G139300.1	3133.68872	0.446842095	0.034292496	13.0661	1.96E-38	8.09E-38	cpm	0.712960846	1.14E-25	GO:0008168		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase PMT2, putative
Sapur.004G135300.1	4328.827409	0.513985693	0.048939378	13.48285	5.82E-41	2.42E-37	cpm	0.713235845	1.07E-25	GO:0030126;GO:0016192;GO:0006886;GO:0005198;GO:0030117	AT4G34550.1	coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	coatomer subunit gamma
Sapur.014G142600.1	1797.903858	0.703324235	0.052626691	13.37333	6.36E-39	2.82E-37	cpm	0.706688165	4.61E-25	GO:0015702;GO:0009058	AT1;CBL1;EMB2779;FBR11;LC	long-chain base biosynthesis protein 1a	long-chain base biosynthesis protein 1a
Sapur.006G184800.1	3868.460554	0.760176681	0.060495513	12.56583	3.25E-36	1.39E-35	cpm	0.695046637	5.44E-24	GO:0008270;GO:0008237;GO:0006508	APM1;ATAPM1	aminopeptidase M1	puromycin-sensitive aminopeptidase
Sapur.016G080100.1	68.64061111	0.739747986	0.085750929	12.56209	3.29E-36	1.41E-35	cpm	0.706052729	4.74E-25	GO:0006488;GO:0004672		Leucine-rich repeat protein kinase family protein	NA
Sapur.009G194200.1	2413.983465	0.829362282	0.066157071	12.53602	4.74E-36	2.02E-35	cpm	0.691619603	1.15E-23		AT5G17020.2		transmembrane protein, putative
Sapur.003G058000.1	616.0168461	0.671000326	0.053 6 3 8 3 2 5	12.52681	5.33E-36	2.27E-35	cpm	0.688123068	1.86E-23		AT5G05570.1		hypothetical protein
Sapur.009G245061.1	650.1563045	0.561863308	0.044885332	12.51775	5.97E-36	2.54E-35	cpm	0.695496266	5.13E-24	GO:0043565;GO:0003705;GO:0003700	AT2G40950.1	BZIP17	Basic-leucine zipper (bZIP) transcription factor family protein
Sapur.014G009200.1	104.4706273	0.191912388	0.018124651	12.4983	7.64E-36	3.25E-35	cpm	0.643833874	1.72E-19		AT4G26680.1		PIWM family methyltransferase
Sapur.003G080800.1	1064.920882	0.88 3 6 4 6 1 4 8	0.070114168	12.47422	1.03E-35	4.38E-35	cpm	0.703112026	1.01E-24	GO:0005525;GO:0003924	ADL1;CFL1;DL1;DRP2B	dynamin-like 3	dynamin-2A protein
Sapur.008G149300.1	844.756674	0.728399025	0.058487317	12.45397	1.33E-35	5.63E-35	cpm	0.675161136	3.11E-22		AT5G26400.1	eukaryotic translation initiation factor 4B1	eukaryotic translation initiation factor 4B
Sapur.014G141600.1	4897.029482	0.667074209	0.055 6 1 3 3 3 1	12.0 0 1 3 3	1.34E-35	5.88E-35	cpm	0.691218205	5.20E-24	GO:0016021	AT4G21610.1	Endomembrane protein 70 protein family	transmembrane 9 family protein
Sapur.003G138300.1	1303.040751	0.589276477	0.047344617	12.44665	1.46E-35	6.16E-35	cpm	0.68815646	2.34E-23	GO:0048391;GO:0005793			oligomeric subunit 4
Sapur.018G000400.1	7727.631474	0.793371925	0.064185182	12.36258	4.26E-35	1.78E-34	cpm	0.679869159	1.21E-22	GO:0016020;GO:0030136;GO:0016192;GO:0006886;GO:0005198		Clathrin, heavy chain	clathrin heavy chain
Sapur.005G059400.1	1937.284002	0.671821058	0.054375635	12.35519	4.57E-35	1.91E-34	cpm	0.689705133	1.71E-23	GO:0016887;GO:0005524;GO:0005085;GO:0042626;GO:0016021;GO:0006810	AC3G;AHAC0;CLTS;PED3;P	peroxisomal ABC transporter 1	ABC transporter D family protein
Sapur.012G040900.1	1526.818027	0.52 6 3 4 7 6 2	0.044 2 8 7 2 4 8	12.3 4 8 1 4	5.12E-34	2.14E-33	cpm	0.688869073	2.05E-23	GO:0003723;GO:0008380	AC;AEP;CASP	CCAAT-displacement/cleavage domain protein; alternatively spliced product	CASP carbon-rich protein
Sapur.008G101800.1	14664.12901	0.648145053	0.060376291	12.1271	7.58E-34	3.10E-33	cpm	0.674873013	3.42E-24	GO:0016887;GO:0006754;GO:0055524;GO:0005773;GO:0046034;GO:0015992;GO:0033117	AGMB3;CAP;GAR1	ATP synthase alpha/beta family protein	ATP synthase F1, beta subunit
Sapur.006G031300.1	830.4846035	0.610408188	0.053675537	12.11874	8.46E-34	3.45E-33	cpm	0.68517032	3.6E-23		AT5G23170.2	Protein of unknown function (DUF239); transmembrane	DUF2359 family protein
Sapur.15WG0797000.1	288.5419139	0.95095091	0.078587053	12.10061	1.05E-33	4.27E-33	cpm	0.66707597	1.45E-21				NA
Sapur.017G009600.1	1700.977954	0.690216889	0.057618891	11.97953	4.58E-33	1.84E-32	cpm	0.699122093	2.88E-24	GO:0004672;GO:0000166;GO:0016021;GO:0015914;GO:0005524;GO:0004012;GO:0000028	ALA2	aminophospholipid ATPase 2	phospholipid-translocating ATPase
Sapur.006G201900.1	1051.77932	0.8607467	0.040047435	11.96025	5.75E-33	2.31E-32	cpm	0.680042178	2.20E-22	GO:0008168	AT5G10220.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase PMT2, putative
Sapur.005G085700.1	7913.827904	0.510887138	0.04217761	11.95964	5.78E-33	2.32E-32	cpm	0.688060948	2.39E-23	GO:0008012	AC5G35830.1	ACO1	aconitase 1
Sapur.001G080800.1	2755.858516	0.399371122	0.03 4 3 2 1 0 2 2	11.6466	1.82E-31	7.88E-31	cpm	0.64274802	6.42E-24	GO:0006488;GO:0005524;GO:0004672	AT3G13670.1	Protein kinase family protein	casein kinase, putative
Sapur.T046600.1	405.6654717	0.484328848	0.041536997	11.66017	2.04E-31	7.90E-31	cpm	0.692619603	1.15E-23		AT5G17020.2	Sec23/Sec24 protein transport family protein	protein transporter Sec23
Sapur.006G170200.1	1756.920164	0.628310362	0.054117987	11.60403	3.93E-31	1.52E-30	cpm	0.688123068	1.86E-23		AT1G12910.1	aspartate aminotransferase family protein	vacuolar sorting receptor homolog 1
Sapur.008G084800.1	72.91764436	1.114897389	0.096485505	11.55568	6.93E-31	2.65E-30	cpm	0.645854587	6.67E-20	GO:0008312;GO:0008033;GO:0004812	AC1G60650.1	AC1B-1	ATP-citrate lyase B-1
Sapur.006G231100.1	2614.723215	0.605860319	0.048850575	11.54264	8.01E-31	3.07E-30	cpm	0.656045826	1.11E-20	GO:0003700;GO:0000568;GO:0048481;GO:0006520	AAT3;ASPC;ATAAT1	aspartate aminotransferase	aspartate aminotransferase
Sapur.012G089400.1	1667.476446	0.549232187	0.042048842	11.42235	3.23E-30	1.22E-29	cpm	0.694826295	6.98E-24	GO:0003127;GO:0008270;GO:0008189;GO:0006886	AT4G01830.1	Sec23/Sec24 protein transport family protein	protein transporter Sec23
Sapur.010G032100.1	70.38517562	0.779060888	0.068050349	11.41238	3.63E-30	1.37E-29	cpm	0.66314986	2.02E-21		AT5G27820.1	zinc ion binding	hypothetical protein
Sapur.006G137000.1	3.383016674	0.362526876	0.034050679	10.66073	1.56E-26	5.41E-26	cpm	0.627060455	2.01E-20	GO:0016020;GO:0005635	LA21	Protein of unknown function (DUF300)	organic solute transporter ostalpha protein
Sapur.004G167900.1	974.1192946	0.706618925	0.066441213	10.63525	2.04E-26	7.10E-26	cpm	0.628681728	1.02E-20	GO:0016192;GO:0006886;GO:0006906;GO:0030117;GO:0005737		Coatomer, beta subunit	coatomer subunit beta
Sapur.003G028000.1	1830.5127	0.514014276	0.032055507	10.43669	1.80E-25	6.11E-25	cpm	0.673435425	2.60E-20	GO:0008080;GO:0007165;GO:0005159	AT5G55130.1	Protein phosphatase 2C regulatory B subunit family protein	serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' protein-like
Sapur.002G142900.1	1499.369479	0.539258839	0.052388334	10.29349	7.54E-25	2.53E-24	cpm	0.651997664	2.27E-20	GO:0005515	SPI	Bego/BEACH domain; WD domain, G-beta repeat protein	WD repeat and FYVE domain protein
Sapur.013G093400.1	1243.715882	0.677001949	0.040606164	11.07755	1.61E-26	5.98E-26	cpm	0.679603821	2.30E-22	GO:0004648;GO:0005524;GO:0004672		Protein kinase family protein with ARM repeat domain	kinase domain protein
Sapur.007G080800.1	2717.812399	0.604372913	0.054884547	11.01163	3.36E-26	1.22E-25	cpm	0.673320591	9.50E-22		AT5G05590.1	Transducin/WD40 repeat-like superfamily protein	vacuolar protein
Sapur.008G139400.1	935.7947313	0.463384625	0.042182703	10.98542	4.49E-26	1.62E-25	cpm	0.668333387	1.14E-21	GO:0003127;GO:0008270;GO:0006886;GO:0006886	ERMO2;SEC24A	Sec23/Sec24 protein transport family protein	protein transporter Sec24-like protein
Sapur.014G012900.1	3155.638312	0.658154234	0.060565158	10.86681	1.66E-27	5.92E-27	cpm	0.641662193	1.37E-19	GO:0012012;GO:0005086	AT4G30860.1	SEC7-like guanine nucleotide exchange family protein	brefeldin A-inhibited guanine nucleotide-exchange protein
Sapur.009G180900.1	1155.660794	0.313187283	0.028781655	10.86274	2.16E-27	7.69E-27	cpm	0.676282007	2.08E-22	GO:0003824	CO:11	CTC-interacting domain 11	RNA-recognition motif 2 in plant thaliana CTC-interacting domain COB
Sapur.011G138700.1	533.7373683	0.597341222	0.055608498	10.73834	6.72E-27	2.37E-26	cpm	0.660634776	4.78E-21	GO:0005085	AT5G77631.1	Ras-interacting protein 1 family protein	UAA transport family protein
Sapur.006G103200.1	6621.202868	0.450580536	0.04234023	10.66482	1.49E-26	5.18E-26	cpm	0.66149159	4.10E-21	GO:0055524;GO:0009378;GO:0006310;GO:0006281	AT5G03340.1	ATRnm; AAA-type, CDC48 protein	cell division control protein
Sapur.016G248500.1	7714.887723	0.362526876	0.034050679	10.66073	1.56E-26	5.41E-26	cpm	0.657263056	8.81E-21	GO:0016020;GO:0005635	AT5G58250.1	Sec1 protein family protein	preprotein translocase, Sec1 subunit
Sapur.004G167900.1	974.1192946	0.706618925	0.066441213	10.63525	2.04E-26	7.10E-26	cpm	0.628681728	1.02E-20		AT5G15650.1		transmembrane protein, putative
Sapur.003G088800.1	1830.5127	0.514014276	0.032055507	10.43669	1.80E-25	6.11E-25	cpm	0.673435425	2.60E-20	GO:0005515	AT5G18800.1	transducin family protein / WD-40 repeat family protein	phosphoglycan A-2-mannosyltransferase
Sapur.002G142900.1	1499.369479	0.539258839	0.052388334	10.29349	7.54E-25	2.53E-24	cpm	0.651997664	2.27E-20	GO:0005515	AT5G46560.1	transducin family protein / WD-40 repeat family protein	transducin family protein
Sapur.T040200.2	18.67591574	0.801795651	0.086605486	-10.1865	8.10E-25	2.71E-24	cpm	-0.46806407	1.27E-08		AT5G66620.1	Protein of unknown function (DUF231)	gap transporter, putative
Sapur.009G038300.1	530.3844448	0.382464411	0.037277916	10.25954	1.07E-24	3.58E-24	cpm	0.668179441	1.18E-21	GO:0005515	AT5G12430.1	Heat shock protein DnaJ-domain family protein	DnaJ heat shock amino-terminal domain protein, putative
Sapur.001G154000.1	25.80733097	0.568833194	0.061322261	10.20589	1.10E-24	3.68E-24	cpm	0.607072342	2.61E-17		AT1G08110.1	D-fructose/mannose kinase family	growth regulator protein, putative
Sapur.014G116000.1	367.835235	0.490831087	0.048390462	10.14314	3.51E-24	1.17E-23	cpm	0.642045647	1.75E-19	GO:0016192;GO:0006904			Sec1 family containing protein
Sapur.006G064400.1	1787.479351	0.583381029	0.057501252	10.10751	5.14E-24	1.68E-23	cpm	0.656283113	4.06E-16	GO:0016887;GO:0004824	CAS1	cycloartenol synthase 1	cycloartenol synthase
Sapur.017G065200.1	1217.926585	0.577968894	0.057285519	10.08821	6.23E-24	2.04E-23	cpm	0.625675216	1.94E-18	GO:0003127;GO:0005086	AT5G13980.1	EMB30;GNL;GNL7	sec7 domain-containing protein
Sapur.014G068900.1	733.5317007	0.495630047	0.049313617	10.05051	9.14E-24	2.97E-23	cpm	0.648083861	6.52E-20		AT5G28350.1	Quinoprotein amine dehydrogenase, beta chain-like; RIC1-like guanyl-nucleotide exchange factor	quinoprotein amine dehydrogenase, beta chain-like/RIC1-like guanyl-nucleotide exchange factor
Sapur.005G156700.1	8794.296490	0.652806061	0.066551968	9.807224	1.05E-22	3.38E-22	cpm	0.601651394	1.20E-17	GO:0005515;GO:0003824	PLD;PLDLAH;HA1	phospholipase D alpha	phospholipase D alpha
Sapur.002G056900.1	37.3268907	0.731302104	0.074895589	-9.7666	1.24E-22	3.92E-22	cpm	0.410513861	9.27E-08		AT4G05460.1	ATPDK1;PDK1;SSE;SSE1	shrunken seed protein (SSE1)
Sapur.004G068200.1	10.93564571	1.267774207	0.130078524	-9.7602	1.91E-22	6.04E-22	cpm	0.557846424	1.98E-15				NA
Sapur.008G079400.1	2898.265152	0.761003333	0.078233715	9.733659	2.17E-22	6.82E-22	cpm	0.597159172	1.52E-16	GO:0005515	AT5G48090.1	calcium-dependent lipid-binding family protein	calcium-dependent lipid-binding family protein
Sapur.014G138000.1	885.6502093	0.386082383	0.039776008	9.70157	2.87E-22	8.00E-22	cpm	0.639356887	1.52E-16		AT5G67320.1	RING/C3H2C3H2-type (RING Finger) protein family	zinc finger; C3HC4-type (RING Finger) protein
Sapur.007G059300.1	142.3712366	0.762913999	0.059679776	9.68788	3.36E-22	1.05E-21	cpm	0.602841268	6.61E-17	GO:0055114;GO:0016616;GO:0051287;GO:0000287	AT4G35260.1	isocitrate dehydrogenase 1	NA
Sapur.013G080800.1	8713.803074	0.367133386	0.038047557	9.649197	4.95E-22	1.55E-21	cpm	0.633858517	4.01E-19	GO:0005515;GO:0016887;GO:0005524;GO:0019538	AT4G09320.1	CLPC homologue 1	ATP-dependent Clp protease ATP-binding subunit clpA-like protein
Sapur.010G039300.1	2587.614611	0.664103717	0.068565012	9.646366	5.08E-22	1.59E-21	cpm	0.574319247	3.72E-15	GO:0016887;GO:0005524;GO:0016020	AT5G15530.1	ABCG40;ATABCG40;ATPDR1	pleiotropic drug resistance, ABC transporter family protein, putative
Sapur.012G054100.1	677.1275536	0.364808303	0.038110405	9.567154	1.10E-21	3.41E-21	cpm	0.648888872	5.77E-20	GO:0005515	AT4G05540.2	WD-40 repeat family protein / beige-related	NA
Sapur.006G201300.1	1195.170742	0.636482052	0.038319274	9.538491	1.48E-21	4.56E-21	cpm	0.624747213	2.24E-18	GO:0016192;GO:0006886	AT5G18450.1	adaptin family protein	beta adaptin-like protein
Sapur.003G025200.1	1.172624952	3.362758542	0.352198851	9.493111	2.29E-21	7.02E-21	cpm	0.528802007	2.71E-12	GO:0005085;GO:0042626;GO:0016021;GO:0006810;GO:0005524;GO:0016887	AT2G12510.2	ATMRP6;ARM6	multidrug resistance-associated protein 6
Sapur.T005500.1	40.47103979	1.102 4 0 1 1 5 9	0.103047173	9.32495	1.06E-20	2.16E-20	cpm	0.58652612	4.95E-16	GO:0016020;GO:0015171;GO:0015193;GO:0015215	AT4G04510.2	cation-chloride cotransporter 1	cation-chloride cotransporter
Sapur.001G154600.1	1934.671544	0.583095469	0.062517966	9.325362	1.11E-20	3.34E-20	cpm	0.560286828	2.91E-16	GO:0016021	AT5G35160.2	Endomembrane protein 70 protein family	transmembrane 9 family protein
Sapur.006G184300.1	46.46081629	0.593297514	0.101219693	9.251302	2.22E-20	6.64E-20	cpm	0.59002 8 2 2 4	1.50E-16	GO:0005515;GO:0016020;GO:0022857	TMT2	tonoplast monosaccharide transporter2	hexose transporter
Sapur.001G121200.2	14.49263641	1.158269732	0.125636971	9.21902	3.00E-20

Sapur.03G0217600.2	10.57985485	0.65310154	0.11354023	5.752069	8.82E-09	1.81E-08	cpm	0.53209617	7.41E-13	GO:0006468;GO:0006772;GO:0005524	AT5G47750.1	D6PK2,PKS	D6 protein kinase like 2	Serine/Threonine kinase domain protein
Sapur.03G0296800.1	212.1389097	0.25315721	0.04405656	5.746177	9.13E-09	1.87E-08	cpm	0.447814227	4.06E-09	GO:0008270;GO:0019789	AT5G41580.1		RING/U-box superfamily protein	zinc finger MIZ domain protein
Sapur.03G1309900.2	11.25089165	-0.51464092	0.09054629	-5.7082	1.17E-08	2.36E-08	cpm	-0.61371316	9.58E-10	GO:0005515	AT4G27310.1	GTE4	Transcription factor group E4	global transcription factor group E4
Sapur.03G0622000.1	1684.54872	0.29188523	0.05214757	5.59658	2.19E-08	4.42E-08	cpm	0.37614079	9.42E-07	GO:0007165	AT4G28930.2	NINJA	novel interactor of JAZ	ninja-family protein mc610, putative
Sapur.03G1507000.1	76.37476328	-0.49155458	0.08707084	-5.58731	2.31E-08	4.65E-08	cpm	-0.43773812	9.90E-09	GO:0070572;GO:0005875	AT5G22140.2	RHD guanyl-nucleotide exchange factor 11	dynein light chain LC6, flagellar outer arm protein	dynein light chain LC6, flagellar outer arm protein
Sapur.03G0641300.1	200.3827319	-0.35849897	0.06428898	-5.58324	2.36E-08	4.76E-08	cpm	-0.38921729	4.70E-07	GO:0051603;GO:0005839;GO:0004298	AT5G21720.1	PBC1	proteasome beta subunit C1	NA
Sapur.03G0125800.1	2418.739818	-0.42021304	0.07229566	-5.56902	2.51E-08	5.06E-08	cpm	-0.44155677	7.12E-09		AT5G23880.1			NA
Sapur.03G1618000.1	5109.360897	0.24339391	0.04378967	5.557269	2.59E-08	5.21E-08	cpm	0.435482675	1.20E-08	GO:0055114;GO:0004471;GO:0051287	AT5G79750.1	ATNADP-ME4,NADP-ME4	NADP- malic enzyme 4	malic enzyme NAD(P)-binding domain protein
Sapur.03G0273700.1	-718.427831	0.37332927	0.06740784	5.541379	3.00E-08	6.03E-08	cpm	0.416058973	5.98E-08		AT5G23110.1		Zinc finger, C3HC4 type (RING finger) family protein	C3HC4-type RING finger protein
Sapur.03G1614100.3	53.05515	-0.38613234	0.06919479	-5.58209	3.14E-08	6.21E-08	cpm	-0.40703858	1.22E-07	GO:0006352;GO:0003746;GO:0016390	AT1G69532.1	ATTAF6,TAF6,TAFII59	TATA BOX-DIRECTED FACTOR II 5B	transcription initiation factor TFIID protein, putative
Sapur.03G0411100.1	113.7878075	-0.31434024	0.05710253	-5.49889	3.82E-08	7.64E-08	cpm	-0.3881321	2.26E-07					NA
Sapur.03G1445100.1	73.58159458	-0.38427135	0.07134619	-5.38106	3.96E-08	7.88E-08	cpm	0.400354596	2.96E-07	GO:0055114;GO:0009055;GO:0055114;GO:0046872;GO:0016491	AT4G34600.1	AKR2,AOX,ADIsemma,aldo	aldehyde oxidase 2	NA
Sapur.03G1319400.1	1181.876658	0.20796718	0.03794382	5.482302	4.20E-08	8.38E-08	cpm	0.406889918	1.24E-07		AT4G33390.1	NEF1	no exine formation 1	No exine formation protein
Sapur.03G0280100.1	633.3707077	0.37908164	0.06919267	5.479444	4.34E-08	8.64E-08	cpm	0.424284664	5.46E-09	GO:0055114;GO:0006555;GO:0004489				NA
Sapur.03G1291000.1	28.78808032	0.52181305	0.09588011	5.443489	5.22E-08	1.04E-07	cpm	0.380652936	8.75E-07	GO:0016020;GO:0008375	AT5G03520.1			core-2/I-branching beta-1|6-N-acetylglucosaminyltransferase-like protein
Sapur.03G1246400.1	57.53418818	0.42357887	0.07218874	5.41465	6.14E-08	1.22E-07	cpm	-0.41248424	7.01E-07	GO:0006508;GO:0009058	AT5G03970.1		Tyrosine transferase family protein	NA
Sapur.03G0320200.1	3303.513569	0.23742529	0.04432986	5.353856	8.52E-08	1.68E-07	cpm	0.38049841	8.88E-07	GO:0016021	AT5G08580.1		Transmembrane CLPTM1 family protein	cleft lip and palate transmembrane protein
Sapur.03G1394000.1	905.4984032	0.26981786	0.05040245	5.35327	8.64E-08	1.70E-07	cpm	0.40681899	1.23E-07	GO:0008270;GO:0055114	AT5G58410.1		HEAT/U-box domain-containing protein	E3 ubiquitin-protein ligase listerin, putative
Sapur.03G4580600.1	20.76152469	0.66261234	0.12375726	5.34116	9.08E-08	1.79E-07	cpm	0.394898484	1.75E-07	GO:0003886;GO:0006226;GO:0016021;GO:0006810;GO:0005524	AT5G25125.1	PGP11	P-glycoprotein 11	NA
Sapur.03G4113300.1	215.2354553	0.46035245	0.08261148	5.330449	9.80E-08	1.93E-07	cpm	0.398583731	2.35E-07	GO:0016021;GO:0015693;GO:0015095	AT5G26630.1		Protein of unknown function (DUF803)	magnesium transporter NIPA protein
Sapur.03G0231800.1	24.2453049	0.62264201	0.11692175	5.32511	1.07E-07	2.26E-07	cpm	-0.35450853	3.51E-06					hypothetical protein
Sapur.03G1182300.1	229.3908804	-0.44286785	0.08364134	-5.29483	1.19E-07	2.34E-07	cpm	-0.410497659	3.01E-08		AT3G13540.1	ATMYB5,MYB5	myb domain protein 5	Myb-like transcription factor 2, putative
Sapur.03G1410000.1	1105.560739	0.30158841	0.05691935	5.301292	1.21E-07	2.38E-07	cpm	0.408821197	1.06E-07	GO:0005515	AT5G22760.1		PHD Finger family protein	DNA binding and zinc finger protein, putative
Sapur.03G0251200.1	103.5286364	-0.32155993	0.06059545	-5.28364	1.27E-07	2.48E-07	cpm	-0.391386495	4.01E-07		AT5G18430.1		Calcium-binding EF-hand family protein	calcineurin B subunit (protein phosphatase 2b regulatory subunit)-like protein
Sapur.03G0622700.1	591.1831685	0.37908164	0.07125205	5.319249	1.40E-07	2.73E-07	cpm	0.402030745	1.76E-07	GO:0006355;GO:0003677	AT4G34410.1	anac078,NAC2	NAC domain containing protein 78	NAC transcription factor
Sapur.03G0131000.1	43.8270808	0.39662426	0.07626026	-5.2006	1.99E-07	3.85E-07	cpm	0.393905195	3.86E-07	GO:0045767;GO:0007049;GO:0006221	AT4G18132.1	ATER,ER	enhancer of rudimentary protein, putative	enhancer of rudimentary-like protein
Sapur.03G4286600.1	18.25224114	0.39956836	0.07715353	5.181175	2.23E-07	4.27E-07	cpm	0.449809773	3.65E-09		AT4G27140.3	SWEETIE	HEAT repeat-containing protein	NA
Sapur.03G0231100.2	24.55672239	0.60167233	0.08593783	-5.17888	2.23E-07	4.32E-07	cpm	-0.37920091	9.70E-07		AT4G20325.1			Vc27Bp family (RNase H2 complex component) protein
Sapur.03G0393200.1	67.11805876	0.34387021	0.06718065	-5.11781	3.09E-07	5.96E-07	cpm	-0.35127601	4.09E-07		AT5G39500.1			transmembrane protein, putative
Sapur.03G0225200.1	67.88667973	0.42488222	0.08621428	5.08053	3.58E-07	6.85E-07	cpm	0.375119796	1.26E-06	GO:0005515	AT5G04580.1	EIN4	Signal transduction histidine kinase, hybrid-type, ethylene sensor	NA
Sapur.TD47700.1	46.14329298	0.31148716	0.06123048	-5.08713	3.64E-07	6.96E-07	cpm	-0.38291049	7.44E-07	GO:0009165;GO:0004789;GO:0000287	AT5G46530.1		Phosphoribosyltransferase family protein	ribose-phosphate pyrophosphokinase
Sapur.03G1361800.2	3.658848426	0.76888245	0.15207574	-5.0565	4.27E-07	8.16E-07	cpm	-0.409017217	9.74E-08		AT5G79260.1			UPF0676 fatty acid-binding protein-like protein
Sapur.TD69200.1	113.5374294	0.41949141	0.08405683	4.990579	6.02E-07	1.14E-06	cpm	0.414903653	6.56E-08		AT5G47140.3	SWEETIE	HEAT repeat-containing protein	NA
Sapur.03G0102200.3	8.241816517	0.56168287	0.11292574	4.972328	6.62E-07	1.25E-06	cpm	0.612131181	1.87E-17	GO:0005515;GO:0008270	AT5G22630.1	RIN13	RPM1 interacting protein 2	E3 ubiquitin protein ligase RIN3
Sapur.03G0184900.1	412.8014615	0.17546378	0.03547021	4.946401	7.56E-07	1.43E-06	cpm	0.36262272	2.39E-06		AT3G06310.1			EEIG/EHBP1 protein amino-terminal domain protein
Sapur.03G0207300.1	108.5718159	-0.40364247	0.08203381	-4.92146	8.37E-07	1.58E-06	cpm	-0.447298448	3.01E-07					NA
Sapur.03G4245500.1	71.30318989	-0.24936282	0.05082144	-4.90851	9.18E-07	1.72E-06	cpm	-0.35429023	5.26E-06		AT3G15351.1			NA
Sapur.03T0242700.1	4081.597518	0.20708769	0.04232945	4.88768	1.02E-06	1.91E-06	cpm	0.35277286	5.86E-06		AT3G22730.1		26S proteasome regulatory complex, non-ATPase subcomplex, Rpn2/Psmd1 subunit	26S proteasome non-ATPase regulatory subunit
Sapur.03G0283300.2	4.56919613	-0.61124473	0.13181017	-4.87795	1.21E-06	2.01E-06	cpm	-0.444254584	5.61E-09		AT5G60550.1		hydroxyproline-rich glycoprotein family protein	hypothetical protein
Sapur.03G0310000.1	1872.226133	0.14322487	0.03041587	4.835662	1.33E-06	2.47E-06	cpm	0.363313384	2.91E-06	GO:0055114;GO:0004471;GO:0051287	AT3G13560.1	NAD-ME1	NAD-dependent malic enzyme	NAD-dependent malic enzyme
Sapur.03T0280000.1	1861.167836	0.21780307	0.04501704	4.838422	1.34E-06	2.50E-06	cpm	0.373113179	7.15E-06		AT3G05180.1	RPN1A,RPN1A	26S proteasome non-ATPase regulatory subunit S2 1A	26S proteasome non-ATPase regulatory subunit
Sapur.03G0941200.1	1264.845239	0.25446218	0.05279364	4.819709	1.44E-06	2.67E-06	cpm	0.38648851	5.76E-07		AT5G11700.2			transmembrane protein, putative
Sapur.03G0217600.1	232.3343677	0.52186171	0.10827743	4.817469	1.46E-06	2.71E-06	cpm	-0.344626297	9.88E-08	GO:0006355;GO:0003700	AT5G11260.1	SHN1,WIN1	Integrase-type DNA-binding superfamily protein	ethylene-responsive element-binding factor 1
Sapur.03G1417100.1	120.5985088	-0.28090459	0.05840335	-4.80993	1.51E-06	2.80E-06	cpm	-0.36363767	1.49E-06		AT2G39950.1	ELF4-L1	ELF4-like 1	NA
Sapur.03G1443000.1	115.0853876	0.32202882	0.06723872	4.79361	1.64E-06	3.04E-06	cpm	-0.36691624	2.26E-06					NA
Sapur.03G0620000.1	1661.97582	0.20936517	0.04369831	4.774089	1.81E-06	3.34E-06	cpm	-0.15205284	6.14E-06	GO:0016887;GO:0016021;GO:0006812	AT5G26330.1	MRAP2R2	phosphate deficiency response 2	cation-transporting ATPase, putative
Sapur.03G0767000.1	191.6297284	0.36365692	0.07452416	4.746365	2.13E-06	3.93E-06	cpm	0.375183571	7.12E-06	GO:0006468;GO:0005524;GO:0004672	AT5G37840.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.03G0603800.1	13.73854581	0.56429463	0.12297507	4.73693	2.14E-06	3.95E-06	cpm	0.368344017	2.07E-06	GO:0006355	AT5G70560.1	SNL4	SHQ1-like 4	paired amphipathic helix-like protein
Sapur.03G0248300.1	162.5204223	-0.18336876	0.03609177	-4.69945	2.61E-06	4.79E-06	cpm	-0.365452792	2.52E-06		AT5G53400.1		Ubiquitin domain-containing protein	ubiquitin domain protein
Sapur.03G2091000.1	24.27542534	0.49867202	0.07032458	4.69388	2.61E-06	4.79E-06	cpm	0.351938823	9.49E-06	GO:0055114;GO:0016787	AT3G28330.1		Uncharacterized protein family (UPF0497)	DUF588 domain protein
Sapur.03G1427200.2	5.22024603	0.56842486	0.12297056	4.622468	3.79E-06	6.91E-06	cpm	0.469286472	5.66E-10	GO:0016592;GO:0005737;GO:0001104	AT5G53325.2	GCT	RNA polymerase II transcription mediators	mediator of RNA polymerase II transcription subunit 13
Sapur.03T0180400.1	75.4673369	0.36365197	0.07892287	4.56017	4.96E-06	8.88E-06	cpm	0.302758635	2.00E-05	GO:0016614;GO:0008152	AT1G77210.1		Pyridoxal phosphate (PLP)-dependent transferase family protein	2|5|2-dihydro-5-methylene-2-phosphoglycerate phosphatase
Sapur.03G0647200.2	11.39427176	0.52876344	0.11589649	4.562269	5.06E-06	9.16E-06	cpm	0.742818526	8.36E-29		AT5G25730.1		Ubiquitin-like superfamily protein	large proline-rich protein bat3
Sapur.03G0341200.1	1021.164053	0.16369733	0.03602124	4.545078	5.09E-06	9.17E-06	cpm	0.393015777	1.64E-07	GO:0008270	AT5G62060.1		CW type Zinc Finger	CW type zinc finger protein, putative
Sapur.03G0222500.1	239.8596319	0.24119139	0.05298922	4.551757	5.12E-06	9.62E-06	cpm	-0.33611284	1.88E-05	GO:0006376	AT5G19420.1		Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain	regulator of chromosome condensation (RCC1) family with FYVE zinc finger protein
Sapur.03G0450200.1	784.2145205	0.15196546	0.11468783	4.524167	5.73E-06	1.03E-05	cpm	-0.361744107	3.24E-06		AT5G45430.1		WD-40 repeat family protein | beige-related	beige-related and WD-40 repeat protein
Sapur.03G1180800.1	136.913472	0.29280195	0.06428977	-4.53051	5.88E-06	1.06E-05	cpm	-0.341740076	1.18E-05		AT5G06700.1	TBR	Plant protein of unknown function (DUF828)	Pm5/Cas3p GDSL/SGNH-like acyl-esterase family protein
Sapur.03G0212200.1	251.8012467	0.36241881	0.07962953	4.527187	5.98E-06	1.08E-05	cpm	-0.36751765	2.08E-06		AT3G59180.1	MED33A,RFR1	RFR4-related 1	mediator of RNA polymerase II transcription subunit 33A
Sapur.03G4182800.1	243.7684892	-0.06886756	0.04426733	-4.44765	8.68E-06	1.56E-05	cpm	-0.376349165	2.00E-06	GO:0006457;GO:0003755;GO:0004013	AT5G04840.1		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.TD34200.1	231.2478806	0.09705877	0.04576039	-4.36416	1.28E-05	2.30E-05	cpm	-0.32200845	3.91E-05		AT5G23890.1			NA
Sapur.03G4297700.1	5.690458881	0.72365422	0.16737944	4.323372	1.47E-05	2.58E-05	cpm	0.351108253	5.49E-06	GO:0005524;GO:0016772	AT5G02120.1	AtFRGP,FRGP	L-fucokinase/GDP-L-fucose pyrophosphorylase	fucokinase/fucose pyrophosphorylase
Sapur.03W0161000.1	83.14559978	0.27942587	0.06490035	4.299556	1.71E-05	3.01E-05	cpm	0.315083222	5.85E-05		AT5G35935.1			Trm112p-like protein
Sapur.03T0145600.1	78.30776168	0.35231277	0.08050546	4.38015	1.76E-05	3.11E-05	cpm	0.45763111	2.07E-09		AT5G03151.1			transmembrane protein, putative
Sapur.03G0795900.1	248.3580611	0.29840924	0.07002959	4.259928	2.08E-05	3.64E-05	cpm	0.348829083	7.56E-06		AT5G07910.1	ATRNL,RNL	RNAdjacent	NA
Sapur.03G0290200.1	93.51250049	0.36239502	0.08491625	4.1756	2.97E-05	5.10E-05	cpm	-0.326798341	8.30E-05	GO:0008270	AT5G27125.1		Ran BINDING protein 2 zinc finger-like superfamily protein	RanBP2-type zinc finger protein
Sapur.03G0009000.1	1481.192403	0.20088979	0.04827137	4.161686	3.16E-05	5.47E-05	cpm	0.380022664	7.01E-07		AT3G17430.1		Nucleotide-sugar transporter family protein	sugar phosphate/phosphate translocator, putative
Sapur.03G0132000.1	1070.513239	0.20622203	0.04961215	4.15341	3.26E-05	5.64E-05	cpm	-0.3058938	1.08E-05	GO:0016491	AT1G51180.1	ATCLG1,CSL,ATCLG1,CSL,CLG1	Cellulose-synthase-like C1 glycosyltransferase family 2 protein	cellulose synthase-like C1 glycosyltransferase family 2 protein
Sapur.03G1124900.1	5127.286702	0.15162367	0.03653765	4.151072	3.31E-05	5.72E-05	cpm	0.306047673	9.72E-05	GO:0005975;GO:0004553	AT4G28720.1	ATGH9A1,DEC,GH9A1,IRX2	glycosyl hydrolase 9A1	membrane-anchored endo-1|3|4-beta-glucanase
Sapur.03G0281800.4	7.16141635	-0.48606787	0.11768778	-4.13016	3.63E-05	6.25E-05	cpm	0.27305678	7.71E-05		AT3G07080.1	RFP3	ROP interactive partner 3	interactor of constitutive active ROPs protein, putative
Sapur.03G0670200.1	36.12089312	0.50583058	0.10372248	4.112625	3.91E-05	6.73E-05	cpm	0.31261942	8.34E-05		AT5G77720.1	PPR1	pustelle protein 1	NA
Sapur.03G1315500.1	609.0003093	0.18157597	0.04216062	4.308823	3.98E-05	6.84E-05	cpm	0.312472188	6.77E-05	GO:0016192;GO:0006886	AT3G22860.1		Vacuolar sorting protein 39	vacuolar sorting protein 39 domain protein
Sapur.03G0134200.1	571.8720184	0.14885846	0.03626566	4.104047	4.05E-05	6.95E-05	cpm	0.313018026	6.56E-05		AT3G66991.1			hypothetical protein
Sapur.03G1387000.1	133.0308221	0.31035847	0.07606242	-4.08033	4.50E-05	7.71E-05	cpm	-0.33611284	1.88E-05	GO:0003676	AT3G14310.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1)-like protein
Sapur.03G0490100.1	67.16883017	0.28878831	0.07081623	-4.07802	4.54E-05	7.76E-05	cpm	0.315141703	8.21E-05	GO:0055114;GO:0016491;GO:0006633;GO:0005506	AT1G62290.1	SIH2	sphingoid base hydroxylase 2	SUR2 hydroxylase/desaturase, putative
Sapur.03G1138800.2	103.0028868	0.26979753	0.06618618	-4.07634	4.58E-05	7.84E-05	cpm	-0.29296335	0.00106493	GO:0005585;GO:0016021	AT4G46980.3	PHT4;3	phosphate transporter 4;3	anion transporter, putative
Sapur.03G0342400.1	632.6391666	0.14668599	0.03613508	-4.0445	5.24E-05	8.96E-05	cpm	-0.323735421	1.54E-05		AT5G58190.1	AHSBP,HSBP	heat shock factor-binding protein	heat shock factor-binding protein
Sapur.03G1175500.1	450.2814083	0.21206075	0.05245691	4.042352	5.29E-05	9.04E-05	cpm	-0.347579132	8.10E-06	GO:0008270;GO:0016168;GO:0019789;GO:0016925;GO:0005506;GO:0016049;GO:0005634	AT5G21523.1	ATSZI1,SZI1	DNA-binding protein with MIZ/SP-RING zinc finger, PHD-finger and SAP domain	DNA-binding protein with MIZ/SP-RING zinc finger protein
Sapur.03G0082200.1	1891.113203	0.56039563	0.04122918	4.03585	5.44E-05	9.29E-05	cpm	-0.39938475	4.43E-07	GO:0016021	AT4G04330.1	PMP22	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	peroxisomal membrane protein PMP22
Sapur.03G0842000.1	94.77514617	0.30681598	0.07777762	3.963449	6.74E-05	1.15E-04	cpm	0.31518253	5.76E-05		AT4G15170.1	PYD	PYD	sodium- and lithium-tolerant protein
Sapur.03G0811000.1	2062.476138	0.16453041	0.04166871	3.948704	7.88E-05	1.34E-04	cpm	0.301503009	2.00E-05	GO:0005886;GO:0016020;GO:0006811;GO:0005216	AT1G67420.1	ATCNGC5,CNGC5	cyclic nucleotide gated channel 5	cyclic nucleotide-gated ion channel protein, putative
Sapur.03G2077800.1	1214.684767	0.18328564	0.04704045	3.92979	8.00E-05	1.36E-04	cpm	0.32513388	5.26E-05		AT5G58420.1		RING/FYVE/PHD zinc finger	NA
Sapur.03G1125800.1	766.4694913	0.18188294	0.05050018	3.942603	8.06E-05	1.00E-03	cpm	0.299241925	0.00104582	GO:0008270;GO:0005515;GO:0005524	AT5G05130.1		Helicase protein with RING/U-box domain	DNA repair protein rad5
Sapur.03G0093700.1	1256.53083	0.22954769	0.05829768	3.937476	8.26E-05	1.01E-03	cpm	0.32601614	2.99E-05		AT5G61160.1	TIC	time for coffee protein	time for coffee protein, putative
Sapur.03G1838800.1	325.4225141	0.21876171	0.05618019	-3.89393	9.86E-05	0.00015576	cpm	-0.28057956	0.00371835		AT5G13340.1			arginine and glutamate-rich 1 protein
Sapur.03G0267300.1	1060.628861	0.16875424	0.04852629	3.88954	0.00010207	0.00016841	cpm	0.328827028	2.02E-05		AT5G23120.1		Enhancer of polycomb-like transcription factor protein	enhancer of polycomb-like transcription factor protein, putative
Sapur.03G0220900.1	160.464276	0.27367021	0.07052198	-3.88065	0.00010619	0.00017469	cpm	-0.27471268	0.00497841		AT5G27640.1		ARM repeat superfamily protein	NA
Sapur.03G0982300.1	10.67088204	0.46580316	0.12000583	3.882147	0.00010625	0.00017469	cpm	0.315658226	1.57E-05	GO:0016021;GO:0006810;GO:0005215	AT4T4G14	ATATH2,ATH2	ABC2 homolog 2	NA
Sapur.03G2300901.1	1462.203578	0.18802458	0.04852076	3.875111	0.00010676	0.00017862	cpm	-0.33417648	1.88E-05		AT4G31160.1	DCAF1	DDB1- CUL4 associated factor 1	DDB1- and CUL4-associated factor-like protein
Sapur.03G1121200.2	6.05887897	-0.47000975	0.12106649	-3.81793	0.00012474	0.00207442	cpm	-0.56736275	9.75E-15	GO:0005975;GO:0004553	AT5G22860.1		Glycosyl hydrolase superfamily protein	glucan endo-1|3|2-beta-D-glucosidase
Sapur.03G0862000.1	1688.029192	0.15243296	0.04025622	3.78666	0.00015002	0.00246667	cpm	0.276316267	0.00443667		AT5G60690.1	DEX1	defective in exine formation protein (DEX1)	defective in exine formation protein
Sapur.03G0209900.1	55.76615581	-0.36453461	0.07000726	-3.77868	0.00015659	0.00256873	cpm	-0.294366413	0.00182426					transmembrane protein, putative
Sapur.03G0180900.1	5.073121389	-0.47685481	0.1267026	-3.76305	0.00016754	0.00278262	cpm	-0.32229815	2.18E-05	GO:0016020;GO:0008375	AT5G16530.1		Core-2/I-branching beta-1|6-N-acetylglucosaminyltransferase family protein	core-2/I-branching enzyme
Sapur.03G0284000.1	1794.103206	0.19200781	0.05176385	3.720855	0.00019549	0.00327624	cpm	0.282270406	0.00341378		AT3G21790.1		Insulinase (Peptidase family M16) family protein	insulin-degrading enzyme, putative
Sapur.03G0180900.1	331.8196629	0.17181661	0.04708343	-3.6181	0.00027975	0.00457474	cpm	-0.268604054	0.00669774		AT3G21410.1			NB1A-interacting nuclear protein NIP30 NeNa-Nip30-N: amino-terminal domain protein
Sapur.03G1439300.1	139.8599428	0.40281800	0.11057863	3.64282	0.00029668	0.00480379	cpm	0.304010158	0.00104954		AT3G24600.1		DNA binding zinc ion binding DNA binding	NA
Sapur.03G1424200.1	215.5007272	0.25069843	0.07000237	3.61483	0.00030542	0.00489397	cpm	-0.264733212	0.00804459		AT5G07180.1	AtMYB6,MYB6	myb domain protein 6	MYB-like transcription factor 6, putative
Sapur.03G0615500.1	142.5192294	0.31858388	0.08819571	3.612278	0.00030519	0.00494098	cpm	-0.279607511	0.00401257	GO:0055114;GO:0003824;GO:0006164;GO:0003938	AT5G76470.1		Aldolase-type TIM barrel family protein	NA
Sapur.03G1525400.1	1342.502261	0.34277015	0.09368825	3.55208	0.00037551	0.00596115	cpm	-0.30553208	9.86E-05	GO:0005515	AT3G03880.1	DegP7	DegP protease-like protein	DegP protease-like protein
Sapur.03G1564800.1	6.571799823	0.70768833	0.19709593	3.543189	0.00039519	0.00626961	cpm	-0.279105807	0.00480153	GO:0016424;GO:0008152;GO:0055114;GO:0030976;GO:0006099;GO:0004591	AT5G57530.1		2-oxoglutarate dehydrogenase, E1 component	2-oxoglutarate dehydrogenase, E1 component
Sapur.03G0467000.1	129.8219049	0.33125767	0.09426894	3.513944	0.00044556	0.00701443	cpm	0.28221942	0.00996762	GO:0016020;GO:0009075;GO:0003840;GO:0000148	AT5G06490.1	ATGLD7,atgsl7,gsl7	glucan synthase-like 7	callose synthase
Sapur.03G0251800.1	26.76064767	0.24860217	0.07153664	3.477588	0.00050573	0.00800204	cpm	0.484859576	1.33E-10	GO:0016567;GO:0008047	AT5G65110.1	ATPVB1,PVB1	plant U-box 15	ported leaf protein, putative
Sapur.03G4130100.1	-480.365739	-0.31434024	0.06161886	-3.44301	0.00057587	0.00930203	cpm	-0.279360161	0.00395281	GO:0005622;GO:0003779;GO:0030042;GO:0015629	AT5G16700.1	ADF5,ATADF5	actin depolymerizing factor 5	actin-depolymerizing factor 5
Sapur.03G1451500.1	78.81227374	0.35431904	0.10352845	3.420688	0.00063406	0.00996681	cpm	0.284163004	0.00300033					NA
Sapur.03G0841200.1	0.96851774	-0.90018161	0.26415435	-3.40931	0.00065126	0.01030503	cpm	-0.474235905	3.52E-10	GO:0006303;GO:0015986	AT4G09650.1	ATP0	ATP synthase delta-subunit gene	ATP synthase F1, delta subunit
Sapur.03T0628200.1	31.06204795	0.10329932	0.0987135	3.37362	0.00073115	0.01147763	cpm	0.279243839	0.00458932	GO:0016773;GO:0048015;GO:0048854	AT1G07270.1	ATVPS34,PI3K,VPS34	vacuolar protein sorting 34	phosphatidylinositol 3-kinase
Sapur.03T0277400.1	21.92356334	0.38453661	0.11423609	3.366157	0.00076234	0.01200603	cpm	-0.27231007	0.00550616	GO:0005515;GO:0006488;GO:0005524;GO:0004672	AT5G10030.1		Leucine-rich receptor-like protein kinase family protein	inactive receptor kinase, putative
Sapur.03G0888300.1	531.9064663	0.19037856	0.05657856	3.364663	0.00077238	0.01217777	cpm	-0.265836603	0.00789192		AT5G60360.1	ATPDIL5-1	protein disulfide isomerase family protein	NA
Sapur.03G1129000.1	432.7790178	0.15770574	0.04769109	3.268052	0.00097581	0.01531667	cpm	-0.246649697	0.01845245		AT2G26930.1		Ubiquitin-associated/translation elongation factor EF1B protein	ubiquitin-associated/TS-N domain protein, putative
Sapur.03G0471000.1	730.8548632	0.15614497	0.04813117	3.244222	0.00117772	0.01846744	cpm	-0.22962788	0.03825537	GO:0007165	AT4G18700.1	ATWA-6,CYP412,SnRK3.8.WA	CBL-interacting protein kinase 12	CBL-interacting Serine/Threonine-kinase
Sapur.03G0180200.1	291.6881834	0.19646155	0.06061533	3.241009	0.00118724	0.01862946	cpm	-0.247983972	0.02232619		AT4G39180.1			mediator of RNA polymerase II transcription subunit 28, putative
Sapur.03T0088000.2	0.36804147	1.21754293	0.38412762	3.169628	0.00152288	0.02369641	cpm	0.54859	1.30E-14	GO:0005885;GO:0016020	AT5G04690.1	MSL2	MSCS-like 2	mechanosensitive channel of small conductance-like protein
Sapur.03G0291000.1	521.1188713	0.12102224	0.07139385	3.143166	0.00167313	0.02587753	cpm	0.264152293	0.00881368	GO:0016021;GO:0005886	AT5G61450.1	ATMEK1,MEK1	MAPKK domain-containing protein / MAK3 domain-containing protein	NA
Sapur.03G0209300.2	3.830979534	-0.40402048	0.13188509	-3.0653	0.00219549	0.03340504	cpm	-0.345313363	1.31E-05	GO:0003001;GO:0006338	AT5G43500.2	ARPA,TRP49	actin-related protein 9	actin-related protein
Sapur.03T0100800.1	0.521608237	0.52184397	0.17408931	-3.00177	0.00271785	0.04166828	cpm	0.297507668	0.01032561		AT5G17461.1		O-fucosyltransferase family protein	GDP-fucose O-fucosyltransferase family protein
Sapur.03T0044400.2	1.816278313	-0.56983609	0.19117399	-2.98075	0.00287561	0.04377381	cpm	0.359157666	3.85E-06	GO:0006402;GO:0016021;GO:0006

Sapur.0040G0300.1	127.5583497	8.168016353	0.19024739	42.93366	0	0	cpm	0.91188911	7.976-62		ATG32G5180.1		Protein of unknown function (DUF3368)
Sapur.0040G0600.1	656.7652369	6.560016266	0.17006129	56.21514	0	0	cpm	0.86398027	5.046-48		ATG5G3230.1		sodium/calcium exchanger family protein / calcium-binding EF-hand family protein
Sapur.0040G0820.1	419.1154589	5.968291991	0.11347525	52.59703	0	0	cpm	0.80689131	3.10E-37	Dag97	ATG5G3270.1	Dag97	DnaJ protease 7
Sapur.0042G0770.1	12534.35327	12.05499031	0.23795187	55.35775	0	0	cpm	0.85156212	2.53E-45		ATG8G8730.1		Late embryogenesis abundant protein (LEA) family protein
Sapur.0042G0800.1	7282.146813	11.12545581	0.14629859	83.8676	0	0	cpm	0.90341447	1.46E-58		ATG8G8730.1		Late embryogenesis abundant protein (LEA) family protein
Sapur.0042G0920.1	1484.984006	12.61854398	0.25073219	50.32686	0	0	cpm	0.83882591	8.88E-43		ATG8G8730.1		Late embryogenesis abundant protein (LEA) family protein
Sapur.0043G0880.1	169.8798154	8.544866611	0.19614136	43.56484	0	0	cpm	0.88982707	1.20E-54		ATN1G9090.1		RNA-binding protein
Sapur.0061G1740.1	75.14517444	5.787451865	0.14453526	40.04189	0	0	cpm	0.84996565	1.46E-45	QDD8950	ATR2G5220.1	RD2	Adenine nucleotide alpha hydrolases-like superfamily protein
Sapur.0061G1840.0	88.10410808	3.056329087	0.07631881	39.07707	0	0	cpm	0.90909834	7.96E-61		ATG3B5080.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.0061G1940.1	1155.352865	5.767845306	0.09305678	54.5716	0	0	cpm	0.87377034	2.18E-50	GQ466961.GD0331178.GD0159991.GD0161747	ATG11150.1	emb2448.TUF.TUFF.VHA-E1	vacuolar H+-ATPase subunit E1
Sapur.0052G0830.0	2549.746144	17.78615565	0.17290246	68.13362	0	0	cpm	0.9049231	2.19E-59		ATG5E6860.1		Glycoprotein membrane precursor GPI-anchored
Sapur.0052G0930.1	455.0431929	8.278622211	0.13483368	61.39894	0	0	cpm	0.88110301	2.84E-52		ATG6E8630.1		
Sapur.0052G0945.0	404.6263154	11.44698871	0.25389056	45.07303	0	0	cpm	0.87642072	4.69E-51		ATG13570.1	NF-Y87	nuclear factor Y, subunit B7
Sapur.0054G0450.1	416.5013784	3.972861624	0.08198026	48.45915	0	0	cpm	0.88108026	6.92E-58	GD0005225	ATG1G2160.1	AtRABH1a.RABH1e	Rab/Ras-related small GTPase
Sapur.0056G0820.1	171.6768056	7.464991668	0.15832631	47.02312	0	0	cpm	0.87233402	4.96e-50	GD0038242.GD0060470.GD0047722	ATG1G4730.1		Protein phosphatase 2C family protein
Sapur.0056G0860.1	159.9287207	2.931000031	0.08127544	47.7323	0	0	cpm	0.87827207	2.18E-50		ATG3G6130.1		hypothetical protein
Sapur.0056G0940.0	2701.834992	7.182718879	0.09120931	77.06008	0	0	cpm	0.85072309	3.76E-45	GD0008168	ATG5G3570.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.0059G0910.0	107.177532	4.391764276	0.10436188	42.08074	0	0	cpm	0.87213846	5.54E-50		ATG7B4840	LCV3	like CCV 3
Sapur.0061G1280.1	1869.06875	5.460631009	0.10307489	42.46385	0	0	cpm	0.91003564	1.29E-63		ATG9D3640		Late embryogenesis abundant protein, group 6
Sapur.0061G1840.0	120.1857835	3.071607499	0.07105792	43.22682	0	0	cpm	0.90595154	9.81E-60	GD0468872	ATG6E8830.1		Zinc finger C-x8-C-x5-C-x3-H type family protein
Sapur.0051G1500.1	365.75567	4.672836337	0.09089623	28.16996	0	0	cpm	0.86629093	5.00E-52	GD0372.GD0003676	ATG2F7620.1	PAB3	polyadenylate-binding protein, animal type 1, 2, 3, 4 family protein
Sapur.0051G1560.0	1475.116142	11.8359275	0.21249285	55.70024	0	0	cpm	0.8893335	7.34E-45		ATG2F7230.1		MA3 domain-containing protein
Sapur.0051G1570.0	304.687324	2.742663429	0.07291657	37.61666	0	0	cpm	0.87877589	1.16E-51	GD0163013.GD0035324	ATG2G8230.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.0062G0920.0	119.6282099	3.388012992	0.08899162	38.11422	0	0	cpm	0.91032586	1.64E-61	GD0081338.GD0006470	ATG8I8593.1		dual specificity phosphatase-domain protein
Sapur.0062H0450.0	201.1815662	5.771882406	0.11136181	51.83019	0	0	cpm	0.90810409	1.74E-60	GD0469961.GD0469931.GD0159986.GD0000275	ATG1G1610.1	ATRABA40.RABA40	RAB GTPase family 5
Sapur.0062R0800.0	4784.960046	11.86451242	0.15241043	77.84359	0	0	cpm	0.83451588	6.72E-42	GD0060508.GD0042552	ATG3G6230.1		Subtilisin-like serine endopeptidase family protein
Sapur.0063G1500.0	549.7089134	5.405439027	0.09884274	57.60121	0	0	cpm	0.89248938	1.84E-55		ATG3J8180.1		transmembrane protein, putative
Sapur.0063G1560.1	185.3185041	3.724281534	0.09182627	40.76362	0	0	cpm	0.8970878	4.83E-57	GD0064681.GD0060472	ATG3G8290.1	CPK20	calcium-dependent protein kinase 20
Sapur.0063Z0300.0	2185.473007	8.472384657	0.14079174	56.55798	0	0	cpm	0.87325697	9.21E-50	GD0055114.GD0166146.GD0066994.GD0003854	ATG7B5730.1	ATRHM1.RHM1.ROL1	rhamnose biosynthesis 1
Sapur.0070G0480.0	1309.545513	10.07904547	0.11260055	54.88452	0	0	cpm	0.8101039	2.22E-36	GD0081698	ATG3G9170.1		S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.0072G0120.0	959.6594018	2.457754186	0.06144681	39.99888	0	0	cpm	0.88773518	4.32E-54	GD0454564.GD0150105.GD0006642	ATG5G3100.1	ATTHK HL.ATTRK1.TRX1	thioredoxin H-type 1
Sapur.0072G0170.0	157.9763102	6.095395527	0.13019704	46.81668	0	0	cpm	0.86269003	2.22E-52	GD0003761	ATG6E8670.1	AGL11.BC16	AGAMOUS-LIKE11.AGL11 protein
Sapur.0074G0700.1	624.1994798	3.241820339	0.16177436	57.14795	0	0	cpm	0.84974936	6.04E-45		ATG6F2681.1		
Sapur.0075G0280.1	2020.466452	4.88891932	0.08839436	58.24716	0	0	cpm	0.84316151	1.28E-43	GD0055160.GD0468771.GD0000166	ATG7I4540.1	ACA2	calcium ATPase 2
Sapur.0075G0130.0	2808.423433	1.619605527	0.03905612	41.46355	0	0	cpm	0.92811969	1.01E-68	GD0550852.GD0057541	ATG7G5G0.1	ATVDAC2.VDAC2	voltage-dependent anion channel 2
Sapur.0075G0880.0	115.8988855	1.511622494	0.03966973	36.7824	0	0	cpm	0.90604543	2.53E-57		ATG7G3410.1	MGT2.MRS2-1	magnesium transporter 2
Sapur.0075G0300.1	4583.723788	11.71308288	0.17057444	68.66966	0	0	cpm	0.86388553	5.06E-48		ATG8G9550.1		GDP dissociation inhibitor family protein / Rab GTPase activator family protein
Sapur.0076G1120.0	132.4771507	3.307008968	0.12983934	40.87998	0	0	cpm	0.89392008	1.21E-55		ATG9H9150.1	ATGDX2.GDX2	gamete expressed 2
Sapur.0080G0450.1	416.3479424	4.705008086	0.07069675	49.08328	0	0	cpm	0.90810489	1.74E-60	GD0469961.GD0469931.GD0159986.GD0000275	ATG1G1650.1		ATP synthase subunit 9, mitochondrial
Sapur.0080G0700.0	82.5023012	5.225665512	0.11887091	43.95758	0	0	cpm	0.86429812	1.32E-48		ATG3G6550.1		ATP synthase subunit beta
Sapur.0080G0720.0	941.9169663	6.514071771	0.10050859	74.75236	0	0	cpm	0.87791993	1.94E-51		ATN8P1.NRP1	nodulin-related protein 1	hypothetical protein
Sapur.0082G0510.0	291.9252088	7.928291642	0.14963031	52.9788	0	0	cpm	0.86008123	1.81E-47		ATO6F5E-2.ATOEP16-5	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	translocase of inner membrane protein
Sapur.0082H0520.1	191.1225727	3.058403899	0.07023338	43.3105	0	0	cpm	0.87154481	9.07E-58	GD0015743		Aluminum activated malate transporter family protein	aluminum activated malate transporter
Sapur.0083G1720.0	189.2477986	7.784804802	0.14864058	52.49125	0	0	cpm	0.90163312	2.68E-58		ATG0370.1	Bax inhibitor-1 family protein	transmembrane BAX inhibitor motif protein
Sapur.0083J0800.1	352.972765	5.731074248	0.08615862	58.19513	0	0	cpm	0.87521222	7.18E-49	GD0468872	ATG4I4680.1	Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator repeat protein
Sapur.0083G1420.0	336.7123867	4.490073875	0.07648157	58.76061	0	0	cpm	0.91018904	3.26E-61		ATG1G7420.2	2n-dependent exoribonucleases superfamily protein	NGE2n-peptidase family protein
Sapur.0084G1440.0	271.5897291	5.660100259	0.12468047	43.04682	0	0	cpm	0.85823758	9.38E-47	GD0002333	ATG4D7180.1	LHT1	lysine/histidine transporter
Sapur.0086J0600.1	249.9709188	8.345691126	0.13605624	61.30574	0	0	cpm	0.90679657	5.04E-60		ATG6E7780.1		Chaperone DnaJ-domain superfamily protein
Sapur.0090G0930.0	617.6025913	7.86147302	0.13579021	57.89325	0	0	cpm	0.85305186	1.23E-45	GD0165751.GD0160220	ATG5D7650.1		Protein of unknown function (DUF604)
Sapur.0090G2220.0	132.6384966	8.84607287	0.07969976	48.10625	0	0	cpm	0.91015723	2.41E-61		ATG5D4230.1		
Sapur.0092H1500.0	1051.767611	9.026171123	0.16729212	53.97485	0	0	cpm	0.86409546	4.73E-48	GD0457251	ATG2B4690.1		RmlC-like cupins superfamily protein
Sapur.0093H0280.0	121.6496003	7.837667897	0.10203758	41.3307	0	0	cpm	0.86540621	2.24E-48	GD0055375.GD0004553	ATG6I8320.1	Glycosyl hydrolase family protein with chitinase activity	hydrolyzing O-glycosyl compounds hydrolase, putative
Sapur.0094G0830.1	106.5128048	3.24656299	0.08236004	39.3946	0	0	cpm	0.89117641	4.45E-55	GD0055114.GD0200037.GD0060879.GD0004601	ATG4R5730.1	Peroxidase superfamily protein	peroxidase
Sapur.0094G0880.0	906.8807863	9.077259166	0.16004465	55.63464	0	0	cpm	0.75362479	4.78E-30		ATG3H3790.1	RNA-binding protein	14-related protein 6 LA RNA-binding domain protein
Sapur.0095G0700.1	310.5523332	11.47438516	0.26178855	43.83074	0	0	cpm	0.82588687	2.06E-40		ATG5B9680.2	Cytathionine beta-synthase (CBS) protein	Cystathionine beta-synthase family protein
Sapur.0096G0780.1	387.9713132	5.018446448	0.08317347	61.19209	0	0	cpm	0.90728704	3.41E-60	GD0055375.1	ATG6D5570.1	SBF (S-Glycoprotein binding protein) family protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.0096G1280.0	226.4145425	1.541151616	0.03938072	18.12474	0	0	cpm	0.93090104	1.09E-69	GD0055115	ATG6F1580.1	F-box/RNI-like superfamily protein	F-box/LRR protein
Sapur.0100Z0780.1	626.9274733	3.018852509	0.08090946	37.51757	0	0	cpm	0.88281246	9.65E-53	GD0060950	ATG1J5910.1	ATDOT1.DT1	drought-induced 21
Sapur.0101G0180.1	74.30994688	7.084556645	0.18608293	38.46113	0	0	cpm	0.83042654	6.76E-53	GD0080833	ATG7F5L.EPT5	isopentenyltransferase 5	cytokinin biosynthetic isopentenyltransferase
Sapur.0102G0270.0	446.7609043	3.496379594	0.09198236	38.01534	0	0	cpm	0.85945737	5.05E-47	GD0161787.GD0081152	ATG1J5780.1	IAR3.IR3	peptidase M20/M25/M40 family protein
Sapur.0102H0480.1	5231.761230	11.60224994	0.19950397	68.18024	0	0	cpm	0.89067986	1.31E-59		ATG4J1560.1	UNE15	Late embryogenesis abundant protein (LEA) family protein
Sapur.0105G2960.0	79.99076954	3.048888807	0.07581785	40.21603	0	0	cpm	0.9034909	6.58E-59	GD0081152.GD0081824	ATG2J3880.1		AMP-dependent synthetase and ligase family protein
Sapur.0105Z0870.0	6449.869967	13.02154252	0.17088668	76.16015	0	0	cpm	0.88437928	3.23E-53		ATG4J1560.1	UNE15	Late embryogenesis abundant protein (LEA) family protein
Sapur.0105H0190.0	269.7059617	5.278714997	0.08138112	43.36226	0	0	cpm	0.90811819	1.76E-60		ATG5J8200.1		Class I glutamine amidotransferase-like superfamily protein
Sapur.0105H0240.0	2291.144865	5.114705197	0.10174147	57.27162	0	0	cpm	0.88882065	2.43E-54		ATO6F5E-2.ATOEP16-5	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	translocase of inner membrane translocase, subunit Tim17/22
Sapur.0105I1500.0	2343.545547	2.026461143	0.05470326	38.62078	0	0	cpm	0.91986867	6.93E-65	GD0055224	ATG6D6580.1	GAL1.GALK	Galactose/galactokinase family protein
Sapur.0105J3600.1	91.61829355	5.102245645	0.09950786	51.27847	0	0	cpm	0.91783973	4.58E-64				
Sapur.0105J4060.0	707.5162277	12.17561169	0.25642476	47.4822	0	0	cpm	0.85169502	2.46E-45	GD0167788	ATG6E6990.1		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.0105J5900.0	1496.534691	3.739085832	0.02443288	42.32211	0	0	cpm	0.93527423	6.14E-72		ATG9I3970.1		Mitochondrial substrate carrier family protein
Sapur.0106G1780.1	1202.573817	7.025486466	0.09142764	76.84219	0	0	cpm	0.90370502	5.56E-59	GD0160221	ATG2E8805.1	Low temperature and salt responsive protein family	stress-induced hydrophobic peptide protein
Sapur.0106J1770.0	92.6953044	6.614325506	0.17037841	38.82137	0	0	cpm	0.7997293	3.60E-36		ATG1H9960.1		hypothetical protein
Sapur.0106J8100.0	2820.425421	3.212811284	0.06874761	46.70608	0	0	cpm	0.86011542	2.46E-48	GD0055114.GD0166491	ATG1E0570.1	SDP6	FAD-dependent oxidoreductase family protein
Sapur.0110G2740.0	5024.167904	11.20453831	0.13842846	80.71067	0	0	cpm	0.85353117	9.84E-45	GD0055114.GD0166021	ATG7F9L.STP1	sugar transporter 1	hexose transporter
Sapur.0110H0180.0	193.4124669	5.354897979	0.11543707	55.04282	0	0	cpm	0.89257602	1.77E-55		ATK0C6.ATTPK2.KCDC17K2	Ca2+- and calmodulin-dependent rectifying K+ channel 4	outward rectifying potassium channel protein
Sapur.0112G0930.0	2869.931326	6.763835874	0.09455983	50.37888	0	0	cpm	0.87364527	7.31E-50	GD0008168	ATG3G3170.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	dehydration-responsive family protein
Sapur.0112G0980.0	118.1501962	8.610097612	0.22427091	38.39418	0	0	cpm	0.90502364	2.02E-59		ATG3B360.1	VQ motif-containing protein	VQ motif protein
Sapur.0112G7030.0	1254.894829	2.217291482	0.07748514	41.54645	0	0	cpm	0.87705865	2.22E-51		ATG4B5380.1	KING1	SNF1-related protein kinase regulatory subunit gamma
Sapur.0116G0720.0	764.709929	3.858330727	0.09703054	39.77042	0	0	cpm	0.8217837	1.06E-39		ATG5A7480.1		Protein of unknown function (DUF3249)
Sapur.0116G0750.0	451.5472491	9.981859937	0.19024102	50.09943	0	0	cpm	0.87309767	9.95E-50		ATG5J7120.1		Plant protein of unknown function (DUF639)
Sapur.0120G0930.0	293.9954921	4.153564076	0.09135715	45.46816	0	0	cpm	0.87783742	1.37E-42	GD0064702.GD0047722	ATG9T160.1		Protein phosphatase 2C family protein
Sapur.0120J0200.1	295.5202037	5.454367267	0.12067224	41.16984	0	0	cpm	0.86960045	1.26E-49	GD0055080.GD0160120.GD0068111.GD0005216	ATCNGC18.CNGC18	cyclic nucleotide-gated channel 18	cyclic nucleotide-gated ion channel protein, putative
Sapur.0121G0200.1	917.8197768	2.347656463	0.13829161	69.72419	0	0	cpm	0.90349025	6.56E-59	GD0160220.GD0165471.GD0159992	ATG2J7310.1	VAG2.VATG2.VHA-G2	vacuolar ATP synthase subunit G2
Sapur.0121G1300.1	990.7210382	12.68872395	0.25725479	49.36248	0	0	cpm	0.85761705	1.40E-46	GD0055114.GD0166491	ATG2D8020.1	NO34	NAD(P)H dehydrogenase B4
Sapur.0126G0140.0	86.02272246	6.874164774	0.15207635	45.20195	0	0	cpm	0.93195507	3.64E-70		ATG6D4600.1	DUO1	myb-like HTH transcriptional regulator family protein
Sapur.0126G0180.0	137.1779692	5.292331324	0.08423875	38.57409	0	0	cpm	0.87834707	6.05E-49	GD0069733	ATG4B4200.1		SAUR-like auxin-responsive family protein
Sapur.0142G0750.0	1362.916342	7.484431422	0.14275209	52.42957	0	0	cpm	0.91350004	2.02E-62		ATG4G4140.1		Late embryogenesis abundant protein
Sapur.0143G0700.1	531.2347037	11.35149669	0.24502107	46.3341	0	0	cpm	0.90021203	2.62E-58		ATG6G6300.1		Chaperone DnaJ-domain superfamily protein
Sapur.0143H1000.1	831.7040569	10.95434287	0.20841003	51.5563	0	0	cpm	0.87845683	6.52E-50		ATG1E0385.1	KING1	SNF1-related protein kinase regulatory subunit gamma
Sapur.0160Z0790.1	638.2622283	6.960888031	0.11770315	59.13935	0	0	cpm	0.8153815	1.57E-38		ATG5E6280.1		Protein of unknown function (DUF3249)
Sapur.0160Z0820.1	533.3877961	6.408328987	0.12034606	51.95606	0	0	cpm	0.85224951	1.82E-45		ATG2E6250.1		Plant protein of unknown function (DUF639)
Sapur.0161G0100.1	495.8120525	11.25070193	0.25634553	43.88878	0	0	cpm	0.83803708	1.25E-42		ATG2J7730.2		NAD(P)-linked oxidoreductase superfamily protein
Sapur.0161G1800.1	416.8139448	3.995974287	0.09423184	42.45077	0	0	cpm	0.89344855	9.51E-56	GD0055085	ATG1J1320.1		Nucleotide-sugar transporter family protein
Sapur.0161H1300.0	1564.747907	6.180530859	0.10767030	57.40237	0	0	cpm	0.80819052	1.80E-37	GD0160887.GD0055134.GD0160220	ATG2G9940.1	ATPDR1.PDR1	pleiotropic drug resistance 1
Sapur.0161L0200.1	2801.686479	7.373169651	0.05996515	19.57523	0	0	cpm	0.89796419	3.95E-57		ATG6D6420.2	UBQ10	polyubiquitin 10
Sapur.0161R0900.1	611.9390071	5.554814834	0.12554981	44.24403	0	0	cpm	0.77254906	2.30E-32	GD0060508.GD0040190	ATG0320.1		Eukaryotic aspartyl protease family protein
Sapur.0162H0400.1	2146.843963	3.771725587	0.06837606	54.36506	0	0	cpm	0.87832085	8.37E-52	GD0055114.GD0166230	ATG4K2120.1	GAPC.GAPC-1.GAPC1	glyceraldehyde-3-phosphate dehydrogenase family protein
Sapur.0162J7200.1	136.7512711	10.40208193	0.25093438	40.96759	0	0	cpm	0.85107775	6.04E-47	GD0082891	ATG6D8890.1	PDF2	protodermal factor 2
Sapur.0170Z0200.1	580.4588034	6.352867121	0.10028187	63.25648	0	0	cpm	0.86318074	2.36E-48	GD0055115	ATG2E8880.1		6-like type zinc finger protein with CCT domain
Sapur.0172G0410.0	744.1089866	5.241176178	0.08679495	58.44342	0	0	cpm	0.89479039	3.74E-56		ATG5B6820.2		Cytathionine beta-synthase (CBS) protein
Sapur.0180Z0900.1	179.09334	5.256851408	0.10403849	50.54006	0	0	cpm	0.88843507	2.74E-54		ATG8E2320.1		Protein of unknown function (DUF616)
Sapur.0182H0600.1	165.8962179	9.931760923	0.15419941	39.0893	0	0	cpm	0.85804882	2.53E-47	GD0055509	ATG3G6260.1		calcium-binding EF-hand family protein
Sapur.0183G0700.1	81.43855649	6.784064968	0.17018869	39.86703	0	0	cpm	0.83293487	7.23E-41		ATG1J9330.1	PIRL6	plant intracellular Ras-group-related LRR 6
Sapur.0186J1400.1	255.2548647	8.30508664	0.17008131	43.82962	0	0	cpm	0.83344621	2.12E-42	GD0055224	ATG6J6130.1	ARA4,ATGAL1,GA1	arabinose kinase
Sapur.0192G2220.0	1269.60769	10.38328553	0.16568776	62.63862	0	0	cpm	0.82645123	3.69E-40	GD0164936.GD0055134.GD003774.GD0055115	ATG4E1J0	MYS1	Myosin family protein with DII domain
Sapur.0192K0830.0	3422.192924	10.48481852	0.21418621	48.95025	0	0	cpm	0.85744606	1.40E-46				
Sapur.0192K0840.0	3167.751955	12.20100133	0.17795768	68.57118	0	0	cpm	0.86482188	3.04E-48		ATG1G2160.1		pfkB-like carbohydrate kinase family protein
Sapur.0194G0520.1	586.6673224	3.070466622	0.06467829	44.06487	0	0	cpm	0.85374611	2.01E-47		ATG1G7480.1		alpha/beta-Hydrolases superfamily protein
Sapur.0196G0850.1	413.0152014	6.681915871	0.10668458	62.64308	0	0	cpm	0.89423617	5.56E-56		ATG4G7870.1	LBD27,SCP	LOB domain-containing protein 27
Sapur.0196U3770.1	2126.703545	10.13561989	0.21139178	48.00445	0	0	cpm	0.86260254	3.31E-47	GD0048957	ATG4J7380.1		Plant invertase/pectin methylesterase inhibitor superfamily protein
Sapur.0196V4210.0	199.8955513	5.050632673	0.07189957	42.53089	0	0	cpm	0.90357936	4.26E-59	GD0038324.GD0060470.GD0047722	ATG5J7920.1	AHG1	Protein phosphatase 2C family protein
Sapur.0152G0530.0	80.0027734	4.49861377	0.09459235	47.39431	0	0	cpm	0.90962875	5.16E-61	GD0064682.GD0055234.GD0064672	ATG7E6730.1	ATMPK15,MPK15	MAP kinase 15
Sapur.0152K0200.1	248.3950513	7.688615649	0.24810245	41.68672	0	0	cpm	0.91191744	5.52E-62	GD0160221	ATG1B5120.1	TET1	tetraspanin1
Sapur.0152K0500.1	387.3717774	1.732715484	0.04153713	41.69821	0	0	cpm	0.92409737	1.23E-66	GD0055114	ATP2G1.PK3	serine/threonine protein kinase 3	Serine/Threonine kinase domain protein
Sapur.0152L0360.1	2892.163980	13.02349283	0.21534476	60.46814	0	0	cpm	0.82982525	2.29E-42				late embryogenesis abundant group 2 protein
Sapur.0190I0900.1	311.2155464	8.364121316	0.15425952	54.21203	0	0	cpm	0.87351526	3.31E-51	GD0163013.GD0035324	ATG2F4480.1	URL5	uridine kinase-like 5
Sapur.0162J7200.1	98.49868163	2.327122	0.06805164	27.4663	3.82E-067	1.95E-305	cpm	0.86293107	9.88E-49	GD0055115.GD0050696	ATG6G3180.1	ASG1	ASF-DEpendent factor GTPase-activating protein AGD12
Sapur.0063R0400.0	3873.673083	4.498754232	0.12075864	37.40363	3.41E-306	1.97E-304	cpm	0.88229399	1.50E-53	GD0160220.GD0068183.GD0052215	ATG6D4170.1	ATTIP1.3,GAMMA-TIP3,TIP3	tonoplast intrinsic protein 1.3
Sapur.0162G0600.1	234.7757147	4.891774897	0.07788757	42.12312	1.64E-301	4.94E-297	cpm	0.91285171	2.38E-62		ATG5D5610.1		Nucleotide/sugar transporter family protein
Sapur.0120G6300.1	63.79236694	4.424273118	0.11912563	37.13062	6.47E-302	3.66E-300	cpm	0.84752898	1.72E-44		ATG5D2J0.1	OLD5,OS,SUFE3	quinolinate synthase
Sapur.0120H6280.1	97.53948798	8.794169492	0.22769874	39.95675	5.67E-299	3.16E-297	cpm	0.93712232	9.38E-73	GD003677	ATG2N6550.1	ABI3,SIS10	AP2/EREBP transcriptional factor family protein
Sapur.0152R0400.1	72.75675424	3.267229886	0.10118315	36.82337	7.81E-297	4.38E-295	cpm	0.86971992	2.04E-49		ATG4H1J0.1		DNAse I-like superfamily protein
Sapur.0030G5600.0	138.2157283	2.093328497	0.08445284	36.64418	5.67E-294	3.08E-292	cpm	0.88606356	1.27E-53	GD0039051.GD0060696.GD0074743.GD0000287	ATG3Z4480.1	Pkp3	plastidial pyruvate kinase 3
Sapur.0036J1500.0	56.79659582	2.267122	0.06013661	36.38653	6.95E-292	3.72E-288	cpm	0.90201964	1.80E-58				
Sapur.0110G2750.0	595.7819535	2.100762493	0.0578705	36.30109	1.55E-288	8.24E-287	cpm	0.89985845	9.72E-58	GD0055115	ATG1J1920.1		ARM repeat superfamily protein
Sapur.0120J4100.1	191.9557114	3.127626264	0.09166018	38.29127	2.22E-288	1.18E-286	cpm	0.85464761	2.56E-45	GD0055115	ATS1F0.NTMC2T2.2.NTMC	Calcium-dependent lipid-binding (CaLB domain) family protein	calcium-dependent lipid-binding protein
Sapur.0120G7010.0	146.5194858	2.431488566	0.06710516	34.23461	1.77E-287	9.32E-286	cpm	0.91860297	2.22E-64		ATG1G1730.1	ATVIT1,VIT1	vacuolar iron transporter 1
Sapur.0120H6400.1	2830.63773	3.283361377	0.06013691	36.21087	1.51E-287	7.93E-286	cpm	0.86347025	2.57E-48	GD0055114.GD0166491	ATCDM11-PM2.CDM11-PM	CDM11 calcium-dependent membrane 2	cell activation protein CDM11-PM1
Sapur.0120R5200.1	739.9794283	8.323301137	0.10560655	36.20326	5.41E-287	2.83E-285	cpm	0.82981783	4.15E-41	GD0055115	ATG2F6180.1	Phototropic-responsive NPH3 family protein	BTB/POZ domain protein
Sapur.0120J8500.1	118.6215278	9.337788381	0.25813854	36.17638	1.41E-286	7.47E-285	cpm	0.83408683	3.93E-42		ATG4H8B0.1		polypyrimidine tract-binding-like protein, putative
Sapur.0006J9900.1	2600.726972	5.254562259	0.03468267	36.17457	1.53E-286	7.98E-285	cpm	0.90030176	0.00909058	GD0008483.GD0006230	ATG5J1L54	ASPG1,YLS4	aspartate aminotransferase 3
Sapur.0120Z2100.1	786.0327501	2.307667989	0.06670709	36.12557	9.00E-286	4.66E-284	cpm	0.91825281	2.19E-63		ATG4G1730.1		Reticulon family protein
Sapur.0121J7500.1	50.75679798	3.011832265	0.13274527	35.93818	2.28E-282	1.13E-280	cpm	0.82264594	1.14E-41		ATG4H6G1.1	LCV3	like CCV 3
Sapur.0105J0500.0	101.2836632	7.947516626	0.22178236	35.83542	3.10E-281	1.56E-279	cpm	0.75491554	1.94E-30	GD0055085.GD0468771.GD0000003.GD0160200	ATG4D6320.1	ZIP7	zinc transporter 7 precursor
Sapur.0051T1200.1	92.10518008	2.264164997	0.05819973	36.3575	1.98E-280	9.93E-279	cpm	0.91891859	6.61E-65		ATG2D5G0.1		Pl

Sapur.15WG022300.1	975.1923065	1.486766118	0.016015191	28.7843	3.37E-182	8.66E-181	cpen	0.873646011	7.31E-50	GO:0005515	AT1G80680.1	transducin family protein / WD-40 repeat family protein	66 kDa stress protein
Sapur.01G0025900.1	37.83667914	0.053710009	0.106127993	28.77384	4.54E-182	1.17E-180	cpen	0.8616287	2.10E-47		AT1G17950.1	ATMYB52,BWS2,MYB52	R2R3-Myb transcription factor MYB52, putative
Sapur.01G0221300.1	1152.125054	1.367114422	0.047538721	28.7002	5.09E-182	1.30E-180	cpen	0.873264992	9.06E-50		AT5G66490.2		plant/P24A02-2 protein
Sapur.01G0423800.1	905.4667889	1.173882116	0.040889993	28.69852	3.98E-181	1.01E-179	cpen	0.90122579	3.64E-58		AT1G53580.1	ETHEL,GLX2-3,GLY3	glyoxalase II 3
Sapur.01G0506300.1	348.3773008	1.866491994	0.065057863	28.68837	3.98E-181	1.01E-179	cpen	0.890721164	6.06E-55	GO:0016021,GO:0006886,GO:0005783	AT5G45730.1	B-cell receptor-associated 31-like	B-cell receptor-associated-like protein
Sapur.00B0263000.1	245.5062205	1.610284805	0.12596625	28.66073	1.18E-180	2.97E-179	cpen	0.835631511	3.83E-42	GO:0005975,GO:0004553	AT5G65630.1	AT1GH4,2,XDR2	endo-1%2C4-beta-glucanase
Sapur.01G0274400.1	872.0084066	0.904094293	0.03104053	28.60648	5.58E-180	1.40E-178	cpen	0.90520716	7.77E-58	GO:0055114,GO:0016616,GO:0006694,GO:0003854	AT1G53110.1	UGDH-like family	UDP-glucuronic acid decarboxylase 1
Sapur.01G0308300.1	3692.202414	0.869317012	0.03038707	28.60158	6.42E-180	1.61E-178	cpen	0.899950002	9.34E-58	GO:0005525,GO:0005524	AT4G14830.1	ATL1C,ATL1,DL1C,DRP1C	dynamin-related protein 1C
Sapur.01G0270400.1	31.19863438	6.96874764	0.24413361	28.54243	3.49E-179	8.71E-178	cpen	0.859423912	5.14E-47				transmembrane protein, putative
Sapur.02G0426700.1	2026.130301	1.09327612	0.03673863	28.51468	4.18E-179	1.01E-176	cpen	0.888794265	2.24E-54	GO:0016787	AT4G36760.1	APP1,ATAPP1	aminopeptidase P1
Sapur.00G0111500.1	28.80692715	5.530353722	0.19438704	28.45056	4.80E-178	1.19E-176	cpen	0.81286038	1.81E-38	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT5G20860.1		Plant invertase/pectin methylesterase inhibitor superfamily
Sapur.01G0137000.1	8261.01108	1.136197026	0.04196809	28.31743	2.11E-176	5.13E-175	cpen	0.83798181	1.28E-42	GO:0017934,GO:0042545,GO:0009507	AT2G37930.1	Phosphoglycerate/bisphosphoglycerate/phosphoenolpyruvate family protein	cytoplasmic phosphoglycerate
Sapur.00G0196500.1	161.013016	2.272231326	0.080319261	28.29077	4.62E-176	1.12E-174	cpen	0.820717149	1.62E-39	GO:0046565,GO:0008270,GO:0006355,GO:0003700	AT5G35830.1	GATA12	GATA transcription factor 12
Sapur.01W0215400.1	19.10108863	4.961417738	0.16728522	28.2836	5.95E-176	1.44E-174	cpen	0.836407006	2.39E-44				
Sapur.01G0251100.1	551.0054427	1.257806046	0.04456796	28.20386	5.23E-175	1.26E-173	cpen	0.88792065	3.84E-54		AT4G03320.1		Cytathionine beta-synthase (CBS) family protein
Sapur.01G0280600.1	1350.315075	0.940984207	0.03345122	28.15576	1.98E-174	4.74E-173	cpen	0.867440776	5.94E-47	GO:0005515	AT5G11330.1	PIRH9	plant intracellular Ras-group-related LRR protein
Sapur.01T0125800.1	278.3350881	2.29625753	0.08164865Z	28.13364	5.04E-174	1.20E-172	cpen	0.893469957	9.35E-56		AT5G65840.1	ATPADI6,PADI6	polyamine oxidase 6
Sapur.15WG0796600.1	45.54522724	2.797967012	0.275633332	28.10965	7.47E-174	1.78E-172	cpen	0.72883799	1.85E-21	GO:0006468,GO:0006672	AT4G11350.1		Protein kinase superfamily protein
Sapur.00G0122900.1	2965.451629	1.814287541	0.044217399	28.0856	7.70E-174	1.83E-172	cpen	0.876341061	1.81E-47	GO:0005773,GO:0055991,GO:0015978	AT5G47220.1	ATVHA-C4,VHA-C4	ATPase, V1 complex, subunit C protein
Sapur.00T0023300.1	98.5445608	2.122439817	0.146682467	28.10452	8.63E-174	2.05E-172	cpen	0.73711023	3.59E-28				NA
Sapur.01G0217600.1	56.75105974	4.651223407	0.302491839	28.07685	1.14E-173	2.45E-172	cpen	0.875155146	2.00E-53	GO:0005516,GO:0046872,GO:0000166	AT2G41560.1	ACA4	autoinhibited Ca(2+)-ATPase, isoform 4
Sapur.01G0278700.1	250.5342833	1.529743259	0.054801184	27.91426	1.79E-171	4.19E-170	cpen	0.88116754	2.73E-52				hypothetical protein
Sapur.01G0266400.1	22.66659517	7.240297612	0.470365754	27.91271	1.87E-171	4.38E-170	cpen	0.821841341	1.04E-32		AT4G32060.1		calcium-binding EF hand family protein
Sapur.00G0645500.1	61.20113349	3.682717604	0.132001945	27.89896	2.75E-171	6.41E-170	cpen	0.786957501	2.53E-34	GO:0008270,GO:0005515	AT5G19910.1	RING/U-box superfamily family	zinc-RING finger protein
Sapur.00G0134000.1	4931.922956	0.963157332	0.03416256	27.88216	4.39E-171	1.02E-169	cpen	0.891829798	2.38E-55	GO:0005886,GO:0016021,GO:0033178,GO:0016820,GO:0015991,GO:0005524	AT5G18520.1	ATPase, V1 complex, subunit B protein	V-type protein ATPase subunit B
Sapur.01G0661300.1	767.3096564	2.377221177	0.085510017	27.8005	4.26E-170	9.87E-169	cpen	0.798837439	4.72E-36		AT5G56340.1		hypothetical protein
Sapur.00B0137500.1	3717.764399	0.881005154	0.031707298	27.78556	6.48E-170	1.49E-168	cpen	0.901462287	3.05E-58	GO:0005385,GO:0005741	AT2G01280.1	ATVDAC1,VDAC1	voltage-dependent anion-selective channel 1
Sapur.01G0164700.1	1549.196605	2.267818891	0.052832057	27.76859	1.04E-169	2.38E-168	cpen	0.899372623	2.16E-57	GO:0005525	AT4G26060.1	ARA-1,ARA1,ATRABA,ATRABA1	RAB GTPase homologs Ba1
Sapur.00G0605800.1	40.11626971	3.429307461	0.123755028	27.71365	4.79E-169	1.09E-167	cpen	0.84897657	8.70E-45	GO:0004871,GO:0003677	AGL62	AGAMOUS-like 62	MADS box protein
Sapur.00G0124200.1	27.80330207	3.552227502	0.110604442	27.63876	3.81E-168	8.61E-167	cpen	0.832743132	2.20E-43		AT2G19210.1	ubq10-conjugating enzyme 23	NA
Sapur.01G0231500.1	107.9081546	2.645067516	0.095029343	27.57287	2.35E-167	5.28E-166	cpen	0.814585116	1.85E-38	GO:0004857	AT4G04940.1		Plant invertase/pectin methylesterase inhibitor superfamily protein
Sapur.01G0269300.1	900.0648973	1.551230194	0.033926445	27.54559	2.58E-167	5.78E-166	cpen	0.89398095	1.18E-55	PDI-like 6-2	AT3G08420.1	ATPDIL8,ATPDIL5-2,PDIL8,PDI	protein disulfide isomerase-like protein, putative
Sapur.01G0179900.1	26.8664682	4.146185912	0.152770044	27.53135	1.22E-166	2.70E-165	cpen	0.75590918	2.51E-30	GO:0008270,GO:0005515	AT5G08139.1		RING/U-box superfamily protein
Sapur.01G0270300.1	366.0137058	1.642127277	0.059869792	27.4282	1.26E-166	2.79E-165	cpen	0.860269465	3.16E-47	GO:0004689,GO:0016307	AT5G60860.1	Phosphoglycerate/bisphosphoglycerate/phosphoenolpyruvate family protein	Phosphoglycerate mutase-like 4-kinase family protein
Sapur.00G0179800.1	25.8198339	4.112337799	0.150113316	27.39489	3.16E-165	6.95E-164	cpen	0.759862887	8.58E-31	GO:0008270,GO:0005515	AT5G08139.1	RING/U-box superfamily family	RING/U-box superfamily protein
Sapur.T1E0100.1	24.73856524	4.398132103	0.161000133	27.3684	6.52E-165	1.43E-163	cpen	0.846280641	4.44E-36	GO:0005488,GO:0003008,GO:0000387	AT5G45850.2		ARM repeat superfamily protein
Sapur.00G0189500.1	72.14975234	1.412315334	0.051895687	27.21641	4.37E-163	9.49E-162	cpen	0.88024518	4.79E-52		AT4G32750.1		transmembrane protein, putative
Sapur.00G0270500.1	482.686297	1.515088862	0.05569381	27.19974	6.54E-163	1.41E-161	cpen	0.875132475	7.79E-50		AT4G28180.2	ORP2C	OSBP(oxysterol binding protein)-related protein 3C
Sapur.01B0204900.1	534.3491499	1.365267732	0.05123777	27.07505	4.24E-161	9.21E-160	cpen	0.893454245	9.41E-56		AT2G30130.1		transmembrane protein, putative
Sapur.01G0291100.1	272.7920319	1.893385332	0.069975085	27.05799	3.08E-161	6.54E-160	cpen	0.818061491	4.52E-39	GO:0005085,GO:0016021	AT5G09215.1		Auxin efflux carrier family protein
Sapur.01G0601100.1	5049.889314	0.856126327	0.040103373	26.97918	2.58E-160	5.48E-159	cpen	0.885447242	1.88E-53	GO:0055114,GO:0016614,GO:0016491,GO:0006694,GO:0003854	AT4H4M1,RHM1,RDL1	rhamnose biosynthesis 1	rhamnose biosynthesis enzyme, putative
Sapur.01G0251300.1	436.999326	1.128771345	0.041910421	26.933	9.02E-160	1.90E-158	cpen	0.868225677	4.89E-49	GO:0007034	AT5G23880.1	VPS20.1	SNF7 family protein
Sapur.00G0203300.1	141.1843037	2.290000188	0.086318826	26.91814	1.16E-159	2.45E-158	cpen	0.816882012	3.51E-37	GO:0046872,GO:0030001	AT1G68020.1		Heavy metal transport/detoxification superfamily protein
Sapur.01W0279300.1	232.3953455	2.104173539	0.078179453	26.9142	1.50E-159	3.15E-158	cpen	0.85208328	5.14E-45		AT3G12640.1	ATMYB3,MYB3	myb domain protein 3
Sapur.01G0181900.1	24.26073875	7.803160269	0.292766568	26.86526	5.60E-159	1.17E-157	cpen	0.674368323	4.12E-22	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G37370.1	CYP81E8	cytochrome P450, family 81, subfamily D, polypeptide 8
Sapur.00G0413200.1	13.08612136	6.675705769	0.248695727	26.81461	2.38E-158	4.94E-157	cpen	0.872812801	3.78E-50	GO:0003561,GO:0003705,GO:0003700	AT5G44460.1	AtbZIP67,DPBF2	Basic-leucine zipper (bZIP) transcription factor family protein
Sapur.00G0285100.1	131.1386228	1.885556502	0.070797989	26.54375	2.16E-155	4.19E-154	cpen	0.796885453	1.87E-40	GO:0016020,GO:0008375	AT5G10180.1		Cox4b-1(Cytochrome c 1,6-N-acetylglucosaminyltransferase family protein
Sapur.01G0149500.1	1518.776012	0.851612576	0.032088431	26.53955	3.39E-155	6.91E-154	cpen	0.893944035	6.75E-56	GO:0030133,GO:0030136,GO:0016192,GO:0006886,GO:0005198	AT4G40060.1		Clathrin light chain protein
Sapur.15WG0122300.1	2316.205304	1.805666655	0.068228245	26.46553	2.42E-154	4.92E-153	cpen	0.812497212	3.72E-38		AT4G48530.1	KING1	SNF1-related protein kinase regulatory subunit gamma 1
Sapur.00G0188200.1	16.44457513	6.568797964	0.248883273	26.39966	1.28E-152	2.80E-152	cpen	0.889397419	3.50E-54		AT2G30130.1	AGL51,BOU12,PCX1	Leunrey-type peroxidases (LOB) domain family protein
Sapur.00G0260900.1	187.2842201	0.788384728	0.026695531	26.37132	2.92E-153	5.90E-152	cpen	0.903091526	6.73E-58		AT5G21370.1		NA
Sapur.01G0601200.1	1776.240966	1.023588497	0.044111246	26.3183	4.76E-153	9.58E-152	cpen	0.868792148	5.82E-49	GO:0016491	AT4G26630.1		Oxidoreductase family protein
Sapur.00G0417600.1	176.1918807	1.407847927	0.053492083	26.12373	1.01E-152	2.05E-151	cpen	0.871572941	7.62E-50	GO:0009058,GO:0003824	AT2G38670.1	PECT1	phosphorylethanolamine cytidylyltransferase 1
Sapur.00G0230600.1	141.5216163	2.298388185	0.054177208	26.27004	4.19E-152	8.34E-151	cpen	0.878257622	7.9E-51		AT5G22240.1	NEG66	F-box family protein
Sapur.00G0111700.1	550.3978077	0.921027113	0.031610962	26.2329	1.12E-151	2.22E-150	cpen	0.894989303	1.24E-56	GO:0008299	AT3G46330.2	GPPS,GPS1	geranyl diphosphate synthase 1
Sapur.00G0413300.1	2310.092968	0.901403889	0.03705741	26.14864	1.02E-150	2.08E-149	cpen	0.872045411	4.66E-50	GO:0008234,GO:0006508	AT4G39090.1	RD19,RD19A	Papain family cysteine protease
Sapur.00G0109100.1	1510.006513	0.76027581	0.029105129	26.12516	1.89E-150	3.69E-149	cpen	0.908909686	1.78E-60		AT2G24320.1	NAPRT2	nicotinate phosphoribosyltransferase 2
Sapur.00G0136100.1	291.3586088	1.863107521	0.073164961	26.1149	2.35E-148	4.52E-147	cpen	0.885038315	8.92E-53		AT5G66330.1		RNI-like superfamily protein
Sapur.01T0007100.1	240.8034243	2.209521469	0.084699417	25.99455	7.51E-148	1.13E-147	cpen	0.831755234	1.14E-37	GO:0016773,GO:0005975,GO:0005524,GO:0004835,GO:0005516,GO:0004396,GO:0003617	AT4G37840.1	HKL3	hexokinase-like 3
Sapur.01B0098500.1	212.5454548	1.852310988	0.071502955	25.90538	5.79E-148	1.11E-146	cpen	0.794081776	2.45E-35		AT5G05010.1	AAPB,ATAAPB	amino acid permease 8
Sapur.00B0180000.1	497.2182676	1.592146194	0.05253493	25.8025	8.08E-148	1.55E-146	cpen	0.908083871	1.87E-60		AT5G15060.1		Uncharacterized conserved protein UCP031088, alpha/beta hydrolase
Sapur.00T0117700.1	22.90267699	7.145284693	0.276591866	25.8342	3.66E-147	6.97E-146	cpen	0.738768738	2.25E-28	GO:0020247,GO:0006468,GO:0005524,GO:0004672	AT5G07600.1		Protein kinase superfamily protein
Sapur.01G0425400.1	1493.015673	0.678719394	0.026253086	25.81201	3.88E-147	7.38E-146	cpen	0.899092967	1.87E-57		AT5G07170.1	ATSEC12,STL2P	SEC12P-like 2 protein
Sapur.00B0073700.1	36.8053313	8.586318068	0.333378339	25.75518	2.82E-146	5.35E-145	cpen	0.686858516	1.05E-22				NA
Sapur.00G0283300.1	912.8617973	1.548366129	0.059854969	25.66572	2.82E-145	5.31E-144	cpen	0.743808976	5.82E-28		AT2G44680.1		Leucine-rich repeat (LRR) family protein
Sapur.00G0260600.1	1166.928675	2.515185277	0.09811793	25.63431	6.33E-145	1.19E-143	cpen	0.838278208	2.17E-42	GO:0071949	AT5G58440.1	SQE1,SE1	FAD/NAD(P)-binding oxidoreductase family protein
Sapur.T0E7000.1	321.3917944	3.717667435	0.145419108	25.56519	3.72E-144	6.93E-143	cpen	0.754592634	1.36E-30		AT3G09500.1		Integral membrane HRF1 family protein
Sapur.15WG0151800.1	1688.082717	1.577664623	0.10087635	25.5326	5.14E-144	9.55E-143	cpen	0.855015134	5.90E-47		AT5G52420.1		plant/K2M67-17 protein
Sapur.00B0269600.1	1558.136684	1.345237965	0.052673796	25.53904	7.22E-144	1.35E-142	cpen	0.84210809	2.06E-42	GO:0006508,GO:0004185	AT3G04310.1	CYP_SCP1,49	SERINE CARBOXYPEPTIDASE-LIKE 49
Sapur.00G0142700.1	18.07658825	5.268891625	0.195218569	25.51086	1.49E-143	2.76E-142	cpen	0.841881937	2.28E-43	GO:0003924	AT4G09510.1	CYN2	cyclophilin 2
Sapur.01T0081200.1	10659.40256	1.774352446	0.066800466	25.42055	1.50E-142	2.75E-141	cpen	0.851028892	3.27E-45	GO:0020244,GO:0016866	AT2G22330.1	ATRGP1,RGP1	reversibly glycosylated polypeptide 1
Sapur.00G0238400.1	18.26227577	5.027860573	0.27760163	25.35144	7.83E-142	1.43E-140	cpen	0.689319399	3.94E-22	GO:0005802	AT4G24280.1	AIR12,AIR12	auxin-responsive family protein
Sapur.01G0222300.1	1499.378973	0.72441751	0.028595865	25.32357	1.76E-141	3.20E-140	cpen	0.890797943	1.73E-55		AT5G19180.1		Invasion (Peptidase family M16) protein
Sapur.00B0072100.1	973.2668772	0.884668833	0.034941134	25.23171	1.84E-141	3.34E-140	cpen	0.827275212	2.41E-46	GO:0016192,GO:0016021	AT3G61250.1	ATGPL,ATVTI11,VTI11	SNARE-like superfamily protein
Sapur.01G0192400.1	1832.154604	0.909042782	0.035690285	25.28337	4.87E-141	8.83E-140	cpen	0.88012265	5.16E-52	GO:0055114,GO:0016831,GO:0008299	AT5G42550.1	GHMP kinase family protein	mevalonate diphosphate decarboxylase
Sapur.01G0184300.1	37.70318176	3.808904169	0.149468647	25.23757	1.55E-140	2.80E-139	cpen	0.59192416	2.84E-16				NA
Sapur.01G0247700.1	1341.573386	0.731645183	0.02909507	25.14671	1.54E-139	2.74E-138	cpen	0.891678284	2.77E-55	GO:0046961,GO:0031178,GO:0191991,GO:0016747	AT4G11150.1	emb2448,TUF,TUFF,VHA-c1	vacuolar ATP synthase subunit E1
Sapur.T0D4700.1	386.4882555	0.757908893	0.030208347	25.0863	7.02E-139	1.24E-137	cpen	-0.902369941	1.54E-58	GO:0043565,GO:0003705,GO:0003700	AT4G26640.2	AHBP/OCS/WRKY20	WRKY family transcription factor family protein
Sapur.01G0189400.1	572.6518869	0.972609074	0.038816365	25.05825	1.42E-138	2.51E-137	cpen	0.873056495	1.01E-49	GO:0016757,GO:0016021	AT5G25020.1	ATXT2,XT2,XRT2	UDP-xylosyltransferase 2
Sapur.00G0111900.1	725.0537306	1.069708925	0.042603836	25.05595	1.50E-138	2.65E-137	cpen	0.88802123	1.32E-53	GO:0046981	AT1G11510.1	emb2448,TUF,TUFF,VHA-c1	vacuolar ATP synthase subunit E1
Sapur.01G0423000.1	142.9424611	2.055287882	0.082075565	25.02147	2.15E-138	3.79E-137	cpen	0.771834551	5.62E-32		AT1G61810.1	ATCE11,CE11	carboxypeptidase 11
Sapur.01G0101700.1	1622.621819	1.45623885	0.05828217	24.9663	1.42E-137	2.48E-136	cpen	0.864036402	4.67E-48		AT5G72100.1		late embryogenesis abundant domain-containing protein / LEA domain-containing protein
Sapur.01G0220200.1	647.3016124	1.782481572	0.071190574	24.92734	1.76E-137	6.54E-136	cpen	0.88025633	4.77E-52		AT5G47540.1		
Sapur.00G0152600.1	66.41942868	3.943766277	0.078037895	24.90836	6.04E-137	1.05E-135	cpen	0.80634547	3.51E-37	GO:0005634	AT3G10370.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	CCR4-associated factor, putative
Sapur.00G0230700.1	2885.789026	2.317464602	0.092882054	24.87617	1.35E-136	2.31E-135	cpen	0.87904778	9.92E-52	GO:0005524,GO:0042626	AT2G28730.1	ATNAP7,NAP7	vacuolar ATP synthase subunit a2, putative
Sapur.15WG0134600.1	11.41138677	6.907880961	0.278158184	24.83526	3.99E-136	6.89E-135	cpen	0.762915516	3.63E-31	GO:0005887,GO:0045245,GO:0030599,GO:0005618	AT4G26220.1		Plant invertase/pectin methylesterase inhibitor superfamily
Sapur.00T0260800.1	18.81631988	3.742767269	0.150932587	24.82479	4.84E-136	8.34E-135	cpen	0.823682271	1.31E-39		AT5G66570.1	ATGWD,ATEDR1,EDR1	Phosphoglucan, water dikinase, chloroplastic
Sapur.00G0142200.1	1547.920527	1.087151315	0.043910844	24.7565	2.64E-135	4.51E-134	cpen	0.868820798	1.34E-49	GO:0006122,GO:0005750,GO:0005743	AT3G27230.1	ATUCP1,UCP1	ubiquinol-cytochrome C reductase UQCRH/QCR6-like family protein
Sapur.00G0191800.1	818.2376872	1.163861933	0.047112219	24.70404	9.68E-135	1.61E-133	cpen	0.86677978	1.08E-48	GO:0046854,GO:0005737,GO:0003934	AT3G02730.1		GTP cyclohydrolase I
Sapur.01G0203400.1	1073.681594	1.211808085	0.04914488	24.65692	2.32E-134	3.86E-133	cpen	0.860600384	4.90E-47	GO:0005515	AT1G80680.1	transducin family protein / WD-40 repeat family protein	66 kDa stress protein
Sapur.00B0207400.1	255.4704914	1.515052445	0.061884747	24.48195	2.50E-132	3.84E-131	cpen	0.80034918	2.90E-36		AT5G51460.1	Pectin lyase-like superfamily protein	pectate lyase
Sapur.00G0510000.1	218.6752324	1.375329361	0.056238093	24.45947	6.51E-132	1.08E-130	cpen	0.80097326	1.01E-37		AT5G22620.1		transferring glycosyl group transferase family protein
Sapur.01G0210900.1	15.57615498	4.885806631	0.28201509	24.4143	1.21E-131	1.99E-130	cpen	0.6853833	4.11E-23		AT5G09290.1	TAC1	telomerase activator1
Sapur.01G0272100.1	580.7154877	0.760376472	0.02904357	-24.1553	1.09E-131	1.84E-130	cpen	-0.883761251	1.61E-52		AT5G67027.2MB64	embryo defective 2737	
Sapur.00G0657600.1	35.96515972	3.432888056	0.141348354	24.28531	2.80E-130	4.58E-129	cpen	0.72692457	4.39E-27		AT2G01300.1		NA
Sapur.00G0289100.1	536.9092005	0.853316464	0.03517928	24.25649	3.65E-130	5.22E-129	cpen	0.88663778	9.32E-54		AT5G51580.1		transmembrane protein, putative
Sapur.01G0267000.2	18.12663324	4.124771479	0.170318052	24.21865	1.44E-129	2.33E-128	cpen	0.791457578	5.82E-35	GO:0007165,GO:0005515,GO:0043531	AT5G17680.1	disease resistance protein (TIR-NBS-LRR class), putative	TIR-NBS-LRR resistance protein, putative
Sapur.01G0211800.1	4610.424628	0.856358564	0.035288592	24.21752	1.44E-129	2.36E-128	cpen	0.878053882	6.51E-51	GO:0004724,GO:0005886,GO:0006629,GO:0004045	AT5G60760.1	GSPD6	glucose-6-phosphate 1-dehydrogenase
Sapur.01B0235300.1	433.339226	1.931300168	0.079618384	24.19679	2.40E-129	3.89E-128	cpen	0.906709515	5.40E-60	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT5G25830.1	GATA12	GATA transcription factor 12
Sapur.00G0115300.1	821.4287165	0.770706479	0.031853524	24.19522	2.49E-129	4.03E-128	cpen	0.88004776	5.40E-52		AT5G19140.1		ubiquinone biosynthesis protein COQ9
Sapur.01G0284800.1	98.69451386	2.284497402	0.08628627	24.18008	3.61E-129	5.83E-128	cpen	0.78594502	5.32E-34		AT1G18930.1	Family of unknown function (DUF736)	transmembrane protein, putative
Sapur.00G0245400.1	46.75138306	3.159737641	0.130123521	24.12969	1.24E-128	1.99E-127	cpen	0.753491587	4.97E-30		AT3G45480.2		hypothetical protein
Sapur.15WG0102800.1	392.1173944	0.666002425	0.027387876	24.05761	4.14E-128	6.62E-127	cpen	0.719107051	3.01E-27		AT2G47240.1	Calcineurin-like metallo-phosphoesterase superfamily protein	component of high affinity phosphate transporter
Sapur.01G0165900.1	45.24751118	1.995819328	0.081316078	24.00929	2.22E-127	3.52E-126	cpen	0.851003857	1.20E-45		AT2G01310.2		Tesmin/TSO1-like CXC domain-containing protein
Sapur.00G0178100.1	730.4120277	1.365978187	0.02708845	23.96412	3.17E-127	5.01E-126	cpen	0.884763	2.91E-52	GO:0046872	AT3G44310.1	Ankyrin repeat family protein	zinc finger protein, putative
Sapur.01G0081400.1	1526.781235	1.220148846	0.050815428	23.99431	3.19E-127	5.03E-126	cpen	0.844469773	7.14E-44	GO:0016021,GO:0006886,GO:0007165	AT3G03160.1		erwinia induced protein
Sapur.01G0840500.1	531.1649154	0.966831744	0.040387116	23.92569	5.12E-127	8.05E-126	cpen	0.891539932	2.08E-55	GO:0046932,GO:0016021,GO:0006621	AT5G25040.1	ERO2B	endoplasmic reticulum retention defective 2B	ER lumen protein retaining receptor
Sapur.01G0121500.1	24.11040275	2.910765029	0.121488384	23.95937	7.38E-127	1.16E-125	cpen	0.851017068	8.75E-38				NA
Sapur.01G0250400.1	200.2873556	1.427867985	0.059673363	23.94164	1.13E-126	1.77E-125	cpen	0.830393817	3.27E-41		AT3G15310.1		Hum1, putative
Sapur.T0D4700.1	679.6205958	0.804624688	0.033768804	23.91679	1.28E-126	1.98E-125	cpen	0.888162589	2.58E-54	GO:0055114,GO:0016616,GO:0051287,GO:0000287	AT4G26260.1	IDH-I,IDH1	isocitrate dehydrogenase 1
Sapur.00T0251400.1	2385.568822	1.17779882	0.049414136	23.83498	1.45E-125	2.22E-124	cpen	0.872901304	3.59E-50		AT5G51160.1	GMDU,MUR1,MUR_1	NAD(P)-binding Rossmann-fold superfamily protein	GDP-mannose 4%2C6-dehydratase
Sapur.01G0125900.1	1318.710092	0.982387853	0.053049276	23.80791	2.77E-125	4.28E-124	cpen	0.879270846	1.42E-51	GO:0016746,GO:0008152	AT4G26910.1		Dihydrolipoamide succinyltransferase
Sapur.01G0236600.1	248.3514442	1.231613106	0.05174226	23.80285	3.12E-125	4.82E-124	cpen	0.84170837	2.48E-43	GO:0005524	AT4G29590.1	NSF	AAA-type ATPase family protein
Sapur.01G0280300.1	2.188013212	3.352861376	0.0988855	23.76358	1.89E-125	2.92E-124	cpen	0.867311504	2.40E-48		AT4G34960.1		NA
Sapur.01G0264800.1	1500.404052	0.620485927	0.026145566	23.76015	8.62E-125	1.33E-123	cpen	0.875492855	8.07E-51	GO:0005789	AT5G45140.1	PVA12	plant VAP homolog 12
Sapur.01G0266200.1	29.38074015	3.259382863	0.139127471	23.75662	1.12E-124	1.73E-123	cpen	0.848861513	6.92E-23		AT2G22860.1	Leucine rich repeat (LRR) family protein	
Sapur.01G0889000.1	4712.769184	5.666437957	0.06117643	23.6685	5.61E-124	8.68E-123	cpen	0.753491587	4.97E-30		AT4G13120.2	ENBGT78,RP1,HMGCLMVK	hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-methylglutaryl coenzyme A synthase	3-hydroxy-3-methylglutaryl coenzyme A synthase
Sapur.01G0233000.1	609.4182231	0.911735398	0.040290363	23.61509	6.42E-123	9.64E-122	cpen	0.862667633	4.68E-48		AT4G24360.1	prolyl oligopeptidase family protein	dipeptidyl peptidase IV, putative
Sapur.00G0113800.1	925.1267551	0.537661633	0.023850076	23.48577	5.70E-122	8.58E-121	cpen	0.892038378	2.08E-55	GO:0016746,GO:0008152	AT5G60620.1	GPAT9	glycerol-3-phosphate acyltransferase 9
Sapur.01T0202700.1	231.8930157	0.942164193	0.040103	23.47587	7.02E-122	1.07E-120	cpen	0.864035874	9.50E-48	GO:0016791	AT4G14130.1	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	magnesium-dependent phosphatase
Sapur.01G0214500.1	227.5050969	0.811532154	0.034520618	23.4486	1.37E-121	2.03E-120	cpen	0.854582223	4.26E-46		AT4G37470.1	Protein of unknown function (DUF3481)	DUF3481 domain protein
Sapur.01G0243500.1	422.2118996	0.552650977	0.023548061	23.44393	1.52E-121	2.26E-120	cpen	0.887583316	4.78E-54	GO:0016020,GO:0008375

Sapur.03G0808000.1	738.1219258	0.59232267	0.02886279	20.52201	1.37E-93	1.46E-92	cpsn	0.86020829	3.44E-47		AT2G26640.1	UBP19	ubiquitin-specific protease 19
Sapur.005G0120300.1	14.91428316	1.627401291	0.176807196	20.51614	1.51E-93	1.63E-92	cpsn	0.725376014	6.36E-27	GO:0008544,GO:0006468,GO:0004672	AT4G21190.1	B120	S-locus lectin protein kinase family protein
Sapur.012G0296300.1	241.3563938	1.227178765	0.058881072	20.50108	2.07E-93	2.17E-92	cpsn	0.818529123	1.29E-42		AT5G60920.1		
Sapur.003G0608000.1	101.7400095	1.502975327	0.073132425	20.49857	2.24E-93	2.35E-92	cpsn	0.82178664	1.06E-39				
Sapur.006G0944400.1	44.58576619	1.813665882	0.088609042	20.46691	4.56E-93	4.25E-92	cpsn	0.832454359	8.17E-40	GO:0005515	AT5G14570.2		Calcium-dependent lipid-binding (CaB domain) family protein
Sapur.007G0499900.1	176.0982797	-1.351570854	0.066035483	-20.4673	4.21E-93	4.40E-92	cpsn	-0.880836377	1.34E-52	GO:0005515	AT5G27185.1		Phototropic-responsive NPH3 family protein
Sapur.010G0394600.1	5107.1396	0.714384383	0.034908894	20.46422	4.49E-93	4.69E-92	cpsn	0.848392233	1.16E-44	GO:0055085,GO:0005741	AT1G04C1,VDAC1		voltage-dependent anion channel 1
Sapur.007G0850100.1	2305.214506	0.753852011	0.036930073	20.41296	1.28E-92	1.31E-91	cpsn	0.845050077	5.41E-44	GO:0020965,GO:0016651	FRO1		NADH-ubiquinone oxidoreductase 18 kDa subunit
Sapur.004G0631400.1	264.1245984	1.046094388	0.051232884	20.41045	1.35E-92	1.40E-91	cpsn	0.788741274	1.42E-34	GO:0005515	AT5G03440.1		ARM repeat superfamily protein
Sapur.012G0227200.1	72.61797539	1.233992629	0.060513088	20.38987	2.12E-92	2.21E-91	cpsn	0.849964439	5.28E-45	GO:0005515,GO:0016021	AT1G17520.1	2IFL1	carbohydrate transporter, putative
Sapur.002G0769600.1	2629.632667	1.439255143	0.070836741	20.31792	8.93E-92	9.18E-91	cpsn	0.851362511	2.81E-45	GO:0005544,GO:0005509	AT5G15720.1	ANNAT1,ATCRYS,CRYS	annexin
Sapur.003G0255900.1	51.75381161	1.178361762	0.077926808	20.25439	1.32E-90	1.29E-89	cpsn	0.801269003	2.06E-36		AT3G22120.1		O-fucosyltransferase family protein
Sapur.001G1954600.1	55.6343691	2.027604974	0.100136431	20.24842	3.67E-91	3.76E-90	cpsn	0.799813868	3.49E-36	GO:0016021,GO:0015116,GO:0008272,GO:0055085,GO:0016020,GO:0008271	AT5G15990.1	SULTR3;4	sulfate transporter 3;4
Sapur.011G0730300.1	117.7603914	0.984607998	0.048602388	20.22016	3.88E-91	3.95E-90	cpsn	0.840268483	2.00E-44	GO:0004683,GO:0005516,GO:0004672	AT2G18600.1		calmodulin-binding protein
Sapur.011G1117000.1	416.3878407	0.823831885	0.040707928	20.21322	7.48E-91	7.59E-90	cpsn	0.843270207	1.83E-43	GO:0016491,GO:0008152	AT4G20760.1		NADP(+)-binding Rossmann-fold superfamily protein
Sapur.010G0394800.1	196.9472272	1.189266456	0.045755137	20.17906	1.51E-90	1.52E-89	cpsn	0.832368014	6.08E-40		AT4G26710.1		Iron-sulphur cluster biosynthesis family protein
Sapur.001G1195300.1	83.27578843	1.431085502	0.070929455	20.17618	1.58E-90	1.60E-89	cpsn	0.809737181	1.03E-37	GO:0052726,GO:0052775,GO:0047325,GO:0003957,GO:0005522,GO:0005524,GO:0000028	AT5G16760.1		Inositol 1,3,4-trisphosphate 5/6-kinase family protein
Sapur.006G0862300.1	535.3000787	0.590539499	0.029303362	20.15331	2.52E-90	2.53E-89	cpsn	0.846047012	3.43E-44		AT4G27690.1	VPS26B	vacuolar protein sorting 26B
Sapur.004G0842800.1	6.7317663	1.807922588	0.093060154	20.15176	2.60E-89	2.60E-88	cpsn	0.661543951	4.06E-21		AT5G08150.1		GRAM domain/coronavirus protein / ABA-responsive protein-related
Sapur.016G2258300.1	380.9134660	-0.908295369	0.045195502	-20.0953	8.12E-90	8.09E-89	cpsn	-0.854735993	2.00E-46	GO:0070569,GO:0008152,GO:0006364	AT5G46430.1		16S rRNA processing protein RimM family
Sapur.005G1447000.1	108.9801537	-1.158.484	0.058239487	-20.0039	4.18E-89	3.91E-88	cpsn	-0.858620957	7.61E-47	GO:0008270,GO:0005178,GO:0005615,GO:0003713,GO:0003677	AT4G20580.1		zinc knuckle (CCHC-type) family protein
Sapur.010G1370800.1	12.77206634	1.797151115	0.289669714	20.01297	4.52E-89	4.19E-88	cpsn	0.654536148	1.45E-20		AT3G21820.1		
Sapur.016G2300300.1	216.8404053	1.818686619	0.090915141	19.99501	6.09E-89	5.96E-88	cpsn	0.823002306	1.81E-41		AT3G69920.1		transmembrane proteins, putative
Sapur.T046900.1	1159.176971	0.457232734	0.022934709	19.94454	1.67E-88	1.64E-87	cpsn	0.845408847	4.52E-44	GO:0008152,GO:0003824	AT5G65940.1	CHY1	beta-hydroxyisobutyryl-CoA hydrolase 1
Sapur.001G1808000.1	153.1473494	0.950622763	0.047663169	19.93475	3.03E-88	2.96E-87	cpsn	0.844362601	7.77E-44		AT5G49550.1		alpha/beta-hydrolase domain protein
Sapur.005G2000100.1	790.2876701	0.545202261	0.027309127	19.9037	3.78E-88	3.68E-87	cpsn	0.845892569	3.51E-44		AT3G20540.1		Transducin/WD40 repeat-like superfamily protein
Sapur.008G1143600.1	2612.901919	0.595476893	0.029973464	19.86678	7.89E-88	7.65E-87	cpsn	0.844105889	8.34E-44	GO:0005515	AT3G30050.1		transducin family protein / WD-40 repeat family protein
Sapur.006G0860600.1	1222.660211	0.741017889	0.037388866	19.86225	8.64E-88	8.36E-87	cpsn	0.840438872	2.46E-43	GO:0047262	AT4G38650.1	GALUT7,LGT7	galactosyltransferase family 8 protein
Sapur.019W0095000.1	290.6316044	0.719367157	0.036313025	19.75558	7.18E-87	6.89E-86	cpsn	0.833695579	8.15E-42		AT2G04840.1		scramblase-related
Sapur.011G0263000.1	63.12828293	1.867966156	0.146828291	19.7606	1.04E-86	9.93E-86	cpsn	0.628032068	1.10E-18	GO:0005634	AT4G22370.1	CYCD6;1	Cyclin D6;1
Sapur.010G1359000.1	7.271329154	5.401282957	0.273817635	19.75584	1.29E-86	1.24E-85	cpsn	0.723037409	1.77E-26	GO:0055114,GO:0020037,GO:0004879,GO:0004601	AT5G30870.1		Peroxidase superfamily protein
Sapur.005G1360200.1	1734.024014	0.718189211	0.035233427	19.69771	2.26E-86	2.16E-85	cpsn	0.820463641	1.42E-36	GO:0008152,GO:0005506,GO:0070008,GO:0005622	AT5G16140.1		Prolyl oligopeptidase family protein
Sapur.006G0240400.1	2252.003909	0.722747182	0.036829255	19.62427	9.58E-86	9.07E-85	cpsn	0.81092517	1.68E-41	GO:0008299	AT5G47730.1	FPS1	farnesyl diphosphate synthase 1
Sapur.011G0462300.1	301.2150534	0.874688325	0.044628281	19.59503	1.70E-85	1.61E-84	cpsn	0.798423663	1.48E-34		AT5G44661.1		
Sapur.016G0705500.1	204.9024661	1.142741021	0.058513493	19.52953	6.16E-85	5.75E-84	cpsn	0.794076526	2.45E-35		AT3G15040.1		Protein of unknown function, DUF584
Sapur.005G0126600.1	25.75805518	1.937331537	0.100139438	19.40744	1.15E-83	1.07E-82	cpsn	0.643720164	5.19E-19	GO:0004574,GO:0048544,GO:0006468,GO:0004672	AT5G61680.1	B120	S-locus lectin protein kinase family protein
Sapur.010G0494900.1	23.52092887	5.218042706	0.268338691	19.44573	3.17E-84	2.93E-83	cpsn	0.466430643	7.42E-10	GO:0005515	AT2G22670.1	ATGSTU7,GSTZ5,GSTU7	glutathione S-transferase tau 7
Sapur.002G0310300.1	4.843002957	3.231858923	0.169215615	19.39657	8.25E-84	7.59E-83	cpsn	0.74822113	2.96E-29		AT3G26570.1		Plant protein of unknown function (DUF827)
Sapur.008G0897005.1	124.6841302	-0.419247277	0.07329415	-19.3637	1.51E-83	1.40E-82	cpsn	-0.851418087	1.01E-45	GO:0008168,GO:0008152	AT4G05125.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.006G1532000.1	836.5638276	0.777578842	0.040170882	19.35678	1.79E-83	1.63E-82	cpsn	0.84065251	4.11E-43		AT5G24290.1		Protein of unknown function (DUF3368)
Sapur.013G0753200.1	4.753817752	2.867372265	0.268360697	19.34997	2.04E-83	1.86E-82	cpsn	0.77839304	3.74E-33	GO:0005515	AT3G58410.1		F-box/RNI-like superfamily protein
Sapur.012G0347000.1	663.715863	0.552571299	0.028676716	19.26899	9.78E-83	8.86E-82	cpsn	0.815871091	1.92E-46	GO:0015031,GO:0008565	AT4G35410.2		Clathrin adaptor complex small chain family protein
Sapur.005G0470500.1	224.8183300	0.947009159	0.049173209	19.26009	1.12E-82	1.04E-81	cpsn	0.802463641	1.42E-36	GO:0004857,GO:0045454,GO:0030599,GO:0005618	AT5G05690.1		Plant invertase/pectinesterase inhibitor superfamily
Sapur.010G0505600.1	17.8358859	3.272354349	0.175480331	19.21868	2.51E-82	2.31E-81	cpsn	0.702112064	1.25E-24		AT3G04320.1		DC1 domain-containing protein
Sapur.003G0143400.1	315.4103604	0.748836141	0.038998133	19.1958	4.44E-82	3.88E-81	cpsn	0.825058578	1.68E-41	GO:0005085,GO:0003925,GO:0008824,GO:0006812	AT4G33670.1		Calcium efflux family protein
Sapur.015W0320400.1	268.3897325	0.813206359	0.042400538	19.17779	5.67E-82	5.08E-81	cpsn	0.834973405	4.73E-42	GO0006397,GO0006348,GO0004721	AT5G37820.1		Sm/Lsm family protein
Sapur.005G1384600.1	652.8852885	0.723125142	0.038108498	19.15409	8.95E-82	8.00E-81	cpsn	0.823822264	2.36E-41	GO0016020,GO0004679,GO0004672	AT4G31860.1		Protein phosphatase 2C family protein
Sapur.008G1623000.1	910.2870208	0.923955623	0.049263423	19.13354	1.33E-81	1.18E-80	cpsn	0.810749846	7.06E-38	GO0016757,GO0016021	AT5G02580.1	ATXT2,XT2,XDT2	UDP-xylosyltransferase 2
Sapur.005G1857600.1	6.710517866	1.382655907	0.281984079	19.09824	2.61E-81	2.32E-80	cpsn	0.671132171	6.74E-22	GO0002246,GO0005975,GO0004553	AT4G36360.1	BGAL3	beta-galactosidase 3
Sapur.006G1210000.1	231.6567944	0.777205924	0.045577191	19.04027	4.74E-81	4.09E-80	cpsn	0.819377216	2.34E-39	GO0016192,GO0016020	AT1G11530.1	AT1MVAP7,1;VAMP713	vesicle-associated membrane protein 713
Sapur.014G1358000.1	7.584362045	4.165349695	0.220008823	18.9527	6.68E-80	5.83E-79	cpsn	0.731615259	9.61E-28		AT3G57730.1	SAP	Transducin/WD40 repeat-like superfamily protein
Sapur.008G1434900.1	4.953870324	2.968966969	0.157664866	18.92597	8.67E-80	6.88E-79	cpsn	0.807799461	2.28E-37		AT5G44190.1		Meiliase family protein
Sapur.004G0452300.1	484.5615744	0.896091857	0.047574346	18.89607	1.16E-79	1.01E-78	cpsn	0.829495164	4.75E-41		AT5G46230.1		Protein of unknown function, DUF538
Sapur.010G1414500.1	1305.617703	0.7	0.037188523	18.87289	1.63E-79	1.41E-78	cpsn	0.817329976	1.41E-38	GO:0008886	AT3G56190.1	ALPHA-SNAP2,ASNAP	Alpha-soluble NSF attachment protein
Sapur.002G1828000.1	725.8517933	0.777870164	0.041218411	18.8791	1.94E-79	1.68E-78	cpsn	0.792106237	8.83E-36	GO:0003677	AT3G19186.1		Phosphoglycerate mutase family protein
Sapur.006G0700300.1	153.9766639	0.253464469	0.018018578	18.6507	7.66E-73	5.54E-72	cpsn	0.812292615	4.00E-38	GO0006123,GO0005739	AT5G27520.1		Major facilitator superfamily protein
Sapur.006G1607000.1	179.150704	1.060117049	0.058727749	18.05138	7.68E-73	6.03E-72	cpsn	0.813002501	3.07E-38	GO0005515	AT5G12300.1		Calcium-dependent lipid-binding (CaB domain) family protein
Sapur.011G1232000.1	9.161175421	1.245456349	0.289445317	18.01615	1.46E-72	1.14E-71	cpsn	0.61854118	2.26E-17				
Sapur.008G0904000.1	1763.158664	0.64795349	0.035967817	18.01481	1.49E-72	1.17E-71	cpsn	0.813587527	2.47E-38	GO0016020,GO0005509,GO0046171	AT5G15190.1	MANRB,MNS1	mannosyl-oligosaccharide 1,2-α-mannosidase, putative
Sapur.016G1388800.1	310.4808019	0.787832869	0.043790605	17.9969	2.30E-72	1.79E-71	cpsn	0.808020385	1.92E-37	GO0016192,GO0016021,GO0008810	AT4G26550.1		Golt1/SFK2-like vesicle transport protein family
Sapur.008G0918500.1	72.46809995	0.861835142	0.047416849	17.95586	4.32E-72	3.36E-71	cpsn	0.782610043	6.61E-41	GO0016740,GO0006508,GO0005622	AT5G22200.1	LTA3	2Hydroxyglutarate dehydrogenase, long form protein
Sapur.010G1018000.1	1839.173934	0.782274864	0.044605469	17.53674	7.38E-69	5.46E-68	cpsn	0.82934835	1.30E-40		AT5G20190.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.008G0410600.1	1255.501329	0.6329792	0.033275627	17.53623	7.58E-69	5.59E-68	cpsn	0.779826129	4.01E-34	GO0016746,GO0008152,GO0006644	AT3G05530.1	AAC2	mitochondrial carrier protein family protein
Sapur.017G0627600.1	873.4248984	0.452057256	0.025867054	17.47618	2.18E-68	1.59E-67	cpsn	0.80034734	3.16E-36	GO0051082,GO0006457,GO0005783,GO0005509	AT5G17580.1	ATCNX1,CNX1	calnexin 1
Sapur.010G0468800.1	278.1624471	0.501303394	0.026009475	17.61044	3.94E-71	2.81E-70	cpsn	0.81245149	1.98E-41	GO0005515	AT5G05710	ATSIGE5,ATSIF31,SIE5,SIF5	sensitivity of plants 31
Sapur.010G0493000.1	1061.905264	0.896847414	0.050408914	17.79144	8.23E-71	6.28E-70	cpsn	0.795808728	1.37E-35		AT5G01170.1		Protein of unknown function (DUF1138)
Sapur.007G0250700.1	162.2181475	0.574497423	0.041129664	17.72522	2.67E-70	2.02E-69	cpsn	0.820357256	2.11E-39		AT5G58190.1		
Sapur.008G1587500.1	3.865615657	0.929143187	0.276328142	17.70983	3.52E-70	2.65E-69	cpsn	0.708602279	3.02E-25				
Sapur.006G0300300.1	791.5200254	0.665374169	0.038775628	17.68796	5.18E-70	3.91E-69	cpsn	0.810434116	2.70E-38	GO0016557,GO0006463,GO0005515	AT3G20030.1		ARM-repeat superfamily protein
Sapur.016G2307200.1	10.39753033	2.291363188	0.126622846	17.67717	6.28E-70	4.72E-69	cpsn	0.735523174	5.35E-28				
Sapur.018G0222000.1	808.8294802	0.931785643	0.052079479	17.58439	3.24E-69	2.41E-68	cpsn	0.724539884	7.77E-27	GO0016192,GO0016021	AT1G11510.1	ATVAMP713,VAMP713	vesicle-associated membrane protein 713
Sapur.006G1843000.1	65.54769162	0.811691555	0.057622188	17.54625	6.34E-69	4.68E-68	cpsn	0.782610043	1.28E-34	GO0016491	AT4G34410.1	BHLH3M	basic helix-loop-helix transcription factor
Sapur.010G0787000.1	1838.173934	0.782274864	0.044605469	17.53674	7.38E-69	5.46E-68	cpsn	0.78908876	6.70E-34	GO0008168	AT5G58550.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.010G0468100.1	1255.501329	0.6329792	0.033275627	17.53623	7.58E-69	5.59E-68	cpsn	0.810215496	8.48E-38		AT4G21490.1	AAC2	ADP/ATP carrier protein 2
Sapur.017G0627600.1	873.4248984	0.452057256	0.025867054	17.47618	2.18E-68	1.59E-67	cpsn	0.824936759	1.77E-40	GO0016020,GO0008375	AT5G15050.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
Sapur.010G0462600.1	545.3240569	0.903736645	0.056037734	17.44152	3.98E-68	2.91E-67	cpsn	0.751418407	3.81E-32	GO0016491,GO0005975	AT5G17230.1		Galactose mutarotase-like superfamily protein
Sapur.009G0808300.1	148.4912511	1.478931255	0.078173109	17.36186	1.60E-67	1.16E-66	cpsn	0.74342846	1.20E-28		AT5G45230.1		hydroxyproline-rich glycoprotein family protein
Sapur.T005500.1	120.4126633	1.728121316	0.099617085	17.35618	1.80E-67	1.30E-66	cpsn	0.680767523	2.18E-20	GO0005085,GO0042626,GO0016021,GO0008810,GO0005524,GO0016887	AT3G08920.1	ATMRP3,MRP3	multidrug resistance protein ABC transporter family protein
Sapur.014G0741000.1	5.927015664	3.150071352	0.202499932	17.33665	2.49E-67	1.79E-66	cpsn	0.790838045	7.17E-35	GO0080123,GO0006464,GO0006394,GO0009611	AT4G36730.4	PIN2\19;AR1	Auxin-responsive GH3 family protein
Sapur.006G0467500.1	166.3232788	1.779967849	0.102796805	17.33181	2.57E-67	1.85E-66	cpsn	0.744334177	1.06E-29	GO0005208,GO0005185	AT4G24370.1	scp40	serine carboxypeptidase-like 40
Sapur.018G0890900.1	71.75442656	1.623854413	0.152074432	17.31293	3.76E-67	2.70E-66	cpsn	0.821261774	1.31E-39		AT5G25240.1		stress induced protein, putative
Sapur.010G0231100.1	2917.453552	0.515727785	0.029788857	17.30028	4.68E-67	3.37E-66	cpsn	0.815440272	1.22E-38	GO0016624,GO0008152	AT5G09660.1	AT-E2 ALPHA,E1 ALPHA	pyruvate dehydrogenase complex E1 alpha subunit
Sapur.010G0165000.1	3695.665691	1.505456734	0.087102743	17.28671	6.13E-67	4.40E-66	cpsn	0.818952538	6.51E-43	GO0016020,GO0008302	AT1G05215	ATTPR1,2,GAMMA-TPR,TIP	tonoplast intrinsic protein 1,2
Sapur.006G0984300.1	4.092749866	4.911270688	0.284656427	17.26683	8.38E-67	5.88E-66	cpsn	0.673931663	3.93E-22	GO0006468,GO0005136,GO0046872,GO0030246	AT5G08370.1		Concanavalin A-like lectin protein kinase family protein
Sapur.005G0730900.1	207.8665493	0.871208169	0.062211599	17.24521	1.22E-66	8.88E-66	cpsn	0.77736901	1.56E-29	GO0008897,GO0006542,GO0004356	AT1G14160.1	AT1GLN1;1,ATGSR1,GLN1;1	glutamine synthetase 1;1
Sapur.016G0219000.1	6.538755461	5.548966643	0.364645254	17.18902	3.21E-66	2.28E-65	cpsn	0.706663603	1.71E-24		AT4G10550.1		PQ-loop repeat family protein / transmembrane family protein
Sapur.010G1244000.1	128.6862624	0.578897343	0.033488926	-17.165	4.85E-66	3.44E-65	cpsn	-0.820574151	1.71E-39		AT4G14390.1		alpha/beta-hydrolase superfamily protein
Sapur.003G0808200.1	275.9686677	0.498656459	0.028862583	17.13527	5.94E-66	4.20E-65	cpsn	0.82773065	9.80E-41		AT5G58130.2		Basic-leucine zipper (bZIP) transcription factor family protein
Sapur.015G0194400.1	575.4624764	0.667363131	0.038906957	17.14855	5.46E-66	3.86E-65	cpsn	0.794239815	1.23E-35	GO0016020	AT5G15170.1	SPIN1(Based DNA domain-containing membrane-associated protein family	hypersensitive-induced reaction protein
Sapur.003G0932300.1	774.4312463	1.582999546	0.092673382	17.08075	2.06E-65	1.45E-64	cpsn	0.683382152	6.15E-23	GO0055114,GO0020037,GO0016705,GO0005506	AT2G45970.1	CYP86A8,LCR	cytochrome P450, family 86, subfamily A, polypeptide 8
Sapur.012G1398800.1	1505.154874	1.240382171	0.072751719	17.04925	3.54E-65	2.48E-64	cpsn	0.75837609	1.80E-30	GO0008152	AT5G57520.1	ACO3	aconitase 3
Sapur.005G0421050.1	19.11559943	4.527581386	0.267048813	16.95427	1.79E-64	1.24E-63	cpsn	0.517896622	1.11E-15		AT2G05580.1	DRH20	DEAD/A-interacting protein 2
Sapur.010G0465500.1	12.58301751	4.089258223	0.24200381	16.8947	4.92E-64	3.38E-63	cpsn	0.643895647	9.35E-20				
Sapur.016G1446000.1	74.19821462	0.627374175	0.029488779	-16.8854	5.76E-64	3.95E-63	cpsn	-0.815327628	1.10E-38		AT3G01870.1		
Sapur.002G0790600.1	730.6336213	0.360631143	0.02858154	16.86569	8.05E-64	5.51E-63	cpsn	0.78168658	1.35E-32		AT3G76280.1		transferases, transferring glycosyl groups
Sapur.008G0843000.1	2.264616458	1.663302077	0.276648582	16.8467	1.38E-64	9.74E-64	cpsn	0.82445542	2.42E-41		AT5G47540.2		
Sapur.012G0932300.1	659.3362674	1.016423464	0.060330567	16.8505	1.04E-63	7.11E-63	cpsn	0.779542349	2.62E-33		AT3G55130.1		Single hybrid motif superfamily protein
Sapur.018G0271000.1	15.43223669	1.750802194	0.104000192	16.84021	1.19E-63	7.08E-63	cpsn	0.652278346	1.69E-20		AT5G61160.1		Choline-phosphate cytidylyltransferase family protein
Sapur.009G0914000.1	1221.003011	0.814282475	0.048429398	16.82398	1.68E-63	1.15E-62	cpsn	0.767961753	8.49E-32	GO0070102,GO0003779	AT4G34490.1	ATCAP,CAP,CAP1	cyclase-associated protein 1
Sapur.010G0429000.1	2123.508964	0.821385156	0.049122739	16.73157	3.26E-62	2.08E-61	cpsn	0.805913136	2.08E-37	GO0016021,GO0006810	AT5G07080.1		cytochrome b5 family/Cytochrome b5 family protein
Sapur.016G1030300.1	76.6834972	1.555906225	0.092838634	16.75025	4.85E-63	3.28E-62	cpsn	0.75527539	3.06E-30		AT5G01650.1		Tautomerase/MIF superfamily protein
Sapur.013G0050900.1	860.278214	0.534883183	0.032103316	16.66516	2.35E-62	1.57E-61	cpsn	0.781190607	1.57E-33	GO0016021	AT5G09330.1		FAMILIA-like protein, putative
Sapur.015G0895900.1	2181.687636	0.587307645	0.035243571	16.65857	2.42E-62	1.75E-61	cpsn	0.809147665	1.04E-37		AT2G38040.2	CAC3	acetyl Co-enzyme a carboxylase carboxyltransferase/alpha subunit
Sapur.003G1423000.1	87.78269327	1.227008198	0.127653582	16.65391	2.93E-62	1.96E-61	cpsn	0.776603865	3.91E-32		AT3G46600.1		calcium-binding EF-hand family protein
Sapur.006G0888200.1	30.86823838	1.377147976	0.083166645	16.61924	5.06E-62	3.37E-61	cpsn	0.774025776	1.41E-32	GO0005634	AT2G22520.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Sapur.010G0271000.1	18.94789866	1.958017142	0.118643102	16.53656	2.00E-61	1.32E-60	cpsn	0.67576647	7.77E-22		AT5G17580.1		
Sapur.T000500.1	162.1984823	0.873184242	0.053057369	16.4387	1.01E-60	6.60E-60	cpsn	0.7773356	4.87E-32		AT5G22920.1		hypothetical protein
Sapur.006G1122000.1	1259.408864	0.422967396	0.025751336	16.42428	1.28E-60	8.36E-60	cpsn	0.806730431	3.05E-37	GO0040379,GO0006499	AT5G57020.1	ATNMT1,NMT1	myristoyl-CoA:protein N-myristoyltransferase
Sapur.006G1317000.1	186.8677456	0.602160008	0.040602379	16.41432	1.47E-60	9.60E-60	cpsn	0.767924716	6.82E-32	GO0005515	AT5G66630.1		F-box family protein
Sapur.004G0750500.1	840.2533271	-1.121261399	0.068606795	-16.3433	4.88E-60	3.14E-59	cpsn	-0.864179245	4.33E-48		AT3G30300.1		O-fucosyltransferase family protein
Sapur.007G1155500.1	1319.225239	0.770428059	0.047199975	16.32364	6.81E-60	4.39E-59	cpsn	0.799581588	1.30E-35		AT5G59480.1		pfkB-like carbohydrate kinase family protein
Sapur.010G1261000.1	7.389417793	4.000502281	0.245936456	16.26706	1.09E-59	7.06E-59	cpsn	0.709896955	2.48E-25				
Sapur.013G1122000.1	590.5739641	0.633867255	0.039005581	16.24943	2.25E-59	1.44E-58	cpsn	0.80189188	1.08E-36	GO0005525	AT4G08680.1	AKRABAT,RABA5f	Rab-related GTPase family protein
Sapur.018G1177500.1	1389.408804	0.867889026	0.053364688	16.22064	3.62E-59	2.32E-58	cpsn	0.763092823	1.53E-31	GO0003824	CAS1	CRI6	cycloartenol synthase
Sapur.014G1409000.1	3.070694443	4.235301853	0.261228033	16.21304	4.08E-59	2.60E-58	cpsn	0.758140969	1.39E-30		AT5G42140.1		NA
Sapur.010G1261000.1	525.9124773	0.516186969	0.037742667	16.13689	4.39E-59	2.73E-58	cpsn	0.80021810	3.01E-36		AT3G25120.1		Domain of unknown function (DUF543)
Sapur.015G1391800.1	549.1298592	0.680536404	0.042140164	16.13986	1.34E-58	8.45E-58	cpsn	0.748079296	1.22E-29	GO0055114,GO0045300,GO0006631	AT3G26320.1		Plant steanoyl-acyl-carrier-protein desaturase family protein
Sapur.018G1177500.1	1389.408804	0.867889026	0.053364688	16.22064	3.62E-59	2.32E-58	cpsn	0.762092182	1.52E-31	GO0003824	AT2G07050.1	CRI6	cycloartenol synthase 2 (ARGENIUS-like protein)
Sapur.003G1161000.1	591.1512117	0.503026893	0.031323362	16.06542	4.46E-58	2.79E-57	cpsn	0.778329806	3.17E-33	GO0019211	AT4G08960.1		phosphotyrosyl phosphatase activator (PTPA) family protein
Sapur.010G0394300.1	1008.342031	0.703027614	0.044136856	15.99391	1.61E-57	9.75E-57	cpsn	0.746986942	3.70E-29	GO0016020,GO0015992,GO0006783,GO0004427	AT4G39240.1	ATAVP2,AVNAP1;1,AVP-3,AV	tonoplasts-engraded vacuolar membrane proton pump protein
Sapur.002G0690000.1	41.19236241	1.515706621	0.094791024	15.98992	1.50E-57	9.32E-57	cpsn	0.787606706	2.44E-34		AT5G24320.1		hypothetical protein
Sapur.018G0470800.1	231.8651284	0.528879399	0.033151512	15.9534	2.70E-57	1.67E-56	cpsn	0.79132272	1.62E-35	GO0003676,GO0006260,GO0005634,GO0003677	AT4G35310.1	ATRPA1A,ATRPA70A,RPA1A	replication protein A 70 kDa DNA-binding subunit A
Sapur.010G0461000.1	693.8514521	0.468466168	0.031394755	15.93396	4.23E-57	2.66E-56	cpsn	0.780817757	1.77E-33	GO0055114,GO0016491,GO0016616,GO0016615,GO0006108	AT4G33030.1		Lactate/malate dehydrogenase family protein
Sapur.008G1383000.1	1528.401424	0.673344706	0.042338832	15.92304	4.84E-57	2.75E-56	cpsn	0.753791947	2.65E-30		AT5G43830.1		Aluminium induced protein with YGL and LRDR motifs
Sapur.005G0341200.1	31.97843777	1.163936454	0.101786143	15.9134	5.12E-57	2.91E-56	cpsn	0.731882647	1.26E-27		AT5G62960.1	WIF3	WIP domain protein 3
Sapur.007G0821000.1	55.08233306	2.373637979	0.149154091	15.89819	6.52E-

Sapur.009G105800.1	2567.543365	0.25249802	0.02047612	12.33391	5.95E-35	2.48E-34	open	0.67539158	2.97E-22	GO:0008540;GO:0006511	ATMCB1;MBP1;MCB1;RPN1	regulatory particle non-ATPase 10	26S proteasome non-ATPase regulatory subunit, putative
Sapur.009G031400.1	8574.634435	0.68734958	0.05605384	12.26636	1.37E-34	5.68E-34	open	0.68421567	5.20E-23	GO:0016788	ATG10370.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-esterase/lipase
Sapur.009G230400.1	557.288892	0.61969462	0.05053189	12.26446	1.47E-34	6.12E-34	open	0.76091939	1.67E-24	GO:0003924;GO:0007017;GO:0005874	ATG20010.1	TUBS	tubulin beta-5 chain
Sapur.014G048500.1	186.9561816	0.52443464	0.04337055	12.10402	1.01E-33	4.10E-33	open	0.67914506	1.43E-22	GO:0016021;GO:0006888;GO:0005801;GO:0000139	ATG45200.1	ATG5G12;GO512	golgi snare 12
Sapur.017G138800.1	646.0016634	0.56333164	0.04670541	12.06237	1.36E-33	5.47E-33	open	0.67758715	1.94E-22	GO:0120043;GO:0016651;GO:0005740	ATG52840.1	NADH ubiquinone oxidoreductase-related	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 5, putative
Sapur.002G109200.1	3.46210572	2.20058893	0.18674172	11.91138	1.03E-32	4.13E-32	open	0.65689791	9.50E-21	GO:0019205;GO:0006139;GO:0005524	ATG26667.3	PYR6	P-loop containing nucleoside triphosphate hydrolases superfamily protein	adenylate kinase
Sapur.006G179400.1	1833.363558	0.30079188	0.02777221	11.9105	1.04E-32	4.17E-32	open	0.68529884	4.19E-23	GO:0055114;GO:0016491	ATG20880.1	FAD/NAD(P)-binding oxidoreductase	NADH-cytochrome b5 reductase, putative
Sapur.016G204500.1	30.68064079	1.40065541	0.12602785	11.85805	1.95E-32	7.77E-32	open	0.63389324	1.60E-20		ATG20570.1	RGA;RGA1	GRAS family transcription factor family protein	NA
Sapur.016G133800.1	702.3801757	0.68661361	0.05790648	11.84851	2.19E-32	8.69E-32	open	0.67305183	4.67E-22		ATG07540.1	TRF1;2	TRF-like 2	double-strand telomere-binding protein, putative
Sapur.016G092200.1	144.2363033	0.38896269	0.03284242	11.8392	2.24E-32	8.91E-32	open	0.65351709	1.20E-20	GO:0005085;GO:0016021;GO:0016020;GO:0006810;GO:0005215	ATG37900.1	Rab27a	Rab27a/Rab27b family protein	peptide transporter, putative
Sapur.010G076000.1	199.6144883	0.47756573	0.04038956	11.69355	1.38E-31	5.36E-31	open	0.67520738	3.04E-22	GO:0008270;GO:0005515	RHF1A	RHF1A	RING-H2 zinc finger protein	RING-H2 zinc finger protein
Sapur.009G234600.1	862.8587769	0.55417844	0.03116263	11.67184	1.78E-31	6.90E-31	open	0.66209391	2.94E-21	GO:0016887;GO:0005524	ATG10910.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	ATPase ASNA1-like protein
Sapur.003G413200.1	240.8009142	-0.66695944	0.05751117	-11.6428	2.52E-31	9.67E-31	open	-0.71181502	1.05E-25		ATG60950.1	MEE47	Protein of unknown function (DUF688)	DUF688 family protein
Sapur.009G103700.1	2.20097023	1.23177407	0.27862409	11.62622	2.98E-31	1.48E-30	open	0.65438611	9.80E-20		ATG68800.1	BRC1;TCP12	TCP transcription factor	TCP transcription factor, putative
Sapur.017G063300.1	2084.646333	0.46211853	0.03825773	11.55088	7.31E-31	2.80E-30	open	0.65706296	9.11E-21	GO:0008152;GO:0003824	ATG34590.1		Transketolase family protein	pyruvate dehydrogenase E1 component subunit beta
Sapur.016G201700.1	99.39356819	0.61231017	0.04929933	11.54624	7.78E-31	2.95E-30	open	0.67648889	2.56E-22		ATG27010.1			transmembrane protein, putative
Sapur.15WG004900.1	259.1224881	0.69930488	0.06069237	11.52311	1.02E-30	3.90E-30	open	0.63458029	4.52E-19		ATG53650.1			transmembrane protein, putative
Sapur.016G058800.1	835.4532663	0.39511754	0.03430756	11.48679	1.54E-30	5.85E-30	open	0.65427812	2.51E-20	GO:0016020	ATG06660.1		Protein of unknown function DUF106, transmembrane	transmembrane and coiled-coil protein
Sapur.006G194700.1	758.4002861	0.45611605	0.03959587	11.52467	2.16E-30	8.18E-30	open	0.64621149	6.27E-20	GO:0003145;GO:0006007;GO:0005737;GO:0004619;GO:0004872;GO:0003824	ATG30780.1	2-hydroxyethylphosphonate dioxygenase-independent	2%2C3-bisphosphoglycerate-independent phosphoglycerate mutase
Sapur.008G149500.1	1649.103058	0.56730816	0.04884946	11.21584	3.41E-29	1.26E-28	open	0.65048867	2.12E-21		ATG24360.1		NADP(H)-binding Rossmann-fold superfamily protein	3-ketoacyl-(acyl-carrier) reductase
Sapur.011G058100.1	2540.941109	0.38896269	0.03473222	11.1001	4.37E-29	1.61E-28	open	0.66953724	7.7E-22		ATG46290.1	KAS I;KAS1	3-ketoacyl carrier protein synthase I	3-oxoacyl-(acyl-carrier) synthase I
Sapur.002G059000.1	60.76219283	0.93693284	0.08411749	11.13859	8.14E-29	2.99E-28	open	0.61909303	5.52E-18		ATG77010.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein, putative
Sapur.006G149100.1	1271.952214	0.28393618	0.02558642	11.07719	1.62E-28	5.90E-28	open	0.62289368	3.66E-21		ATG23570.1		O-fucosyltransferase family protein	auxin-independent growth promoter-like protein
Sapur.012G110000.1	340.0524987	1.01128163	0.09159885	11.00021	3.81E-28	1.38E-27	open	0.60923608	2.53E-17		ATG52420.1			plant/KZM2-17 protein, putative
Sapur.009G134300.1	1.38618752	0.75908828	0.07214346	10.97146	3.96E-28	1.43E-27	open	0.57402764	3.13E-15					NA
Sapur.15WG022900.1	317.4964252	0.34186851	0.03120821	10.95638	6.19E-28	2.23E-27	open	0.67350285	4.7E-22	GO:0016021	ATG27750.1	ISI1	binding	impaired surcose induction-like protein
Sapur.006G115700.1	820.9714967	0.51280469	0.04725691	10.84689	2.06E-27	7.35E-27	open	0.61527319	1.02E-17		ATG22730.1		copper ion binding	FUT0-ATPase inhibitor protein, putative
Sapur.016G266800.1	425.5995666	0.52631006	0.04851889	10.85399	3.35E-27	1.17E-26	open	0.62479825	2.28E-18	GO:0006950	ATG44630.1	ATPHOS2;PHOS32	Adenosine triphosphate alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.016G170200.1	1222.191638	0.37118428	0.03445811	10.77309	4.63E-27	1.63E-26	open	0.64117778	1.50E-19		ATG41220.1	PIP	proline iminopeptidase	proline iminopeptidase
Sapur.009G122500.1	419.1854473	0.29109116	0.02688879	10.71307	8.33E-27	3.1E-26	open	0.60718715	1.46E-17	GO:0005515	ATG07410.1	ATBPM;BPM4	BTB POZ and MATH domain protein	BTB POZ and MATH domain protein
Sapur.15WG052400.1	11.00852512	2.03110713	0.18973847	10.70469	9.64E-27	3.38E-26	open	0.49143314	6.35E-11	GO:0006412;GO:0005840;GO:0005622;GO:0003735	ATG16780.1		Ribosomal protein L18e family protein	NA
Sapur.014G065100.1	17.88485204	0.95934163	0.08976248	10.6202	1.24E-26	4.32E-26	open	0.6491312	1.68E-20		ATG19160.1	ATPRD1;PRD3	putative recombination initiation defects 1	recombination initiation defects protein, putative
Sapur.007G047900.1	538.6196836	0.46368679	0.04344761	10.67208	1.36E-26	4.75E-26	open	0.59523268	2.01E-16	GO:0005515;GO:0016021	ATG31340.1	ATRAMP1;NRAMP3	natural resistance-associated macrophage protein 3	metal transporter NRAMP2
Sapur.009G161200.1	130.2295467	0.97017643	0.09121186	10.64029	1.94E-26	6.75E-26	open	0.56158256	1.25E-14		ATG44300.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/lipid transfer family protein
Sapur.016G060600.1	1.06733249	2.88805916	0.27278264	10.59152	3.26E-26	1.13E-25	open	0.60420033	5.40E-17	GO:0006511	ATG75950.1	AS61;ATSP61;SP61;SKP1A.1	S phase kinase-associated protein 1	Skp1 family, tetratricopeptide repeat domain protein
Sapur.014G084600.1	85.95563884	0.85016389	0.08027077	10.55884	4.57E-26	1.57E-25	open	0.56619646	1.01E-14	GO:0006796;GO:0005737;GO:0004427;GO:0000287	ATG00550.1	APPH;1;PPa5	pyrophosphorylase 1	soluble inorganic pyrophosphatase
Sapur.T111700.1	2.08580523	2.39159283	0.22122942	10.51665	4.68E-26	1.60E-25	open	0.53110059	8.52E-13					NA
Sapur.018G284200.1	174.6756612	0.35210336	0.03322581	10.53702	5.83E-26	2.00E-25	open	0.63774918	2.66E-19	GO:0016887;GO:0005524	ATG22270.1	ATNAP10;NAP10	non-intrinsic ABC protein 10	ATP-binding ABC transport
Sapur.016G268800.1	11.67696933	1.28257144	0.17223361	10.52071	6.56E-26	2.24E-25	open	0.58883003	1.32E-14	GO:0004653;GO:0006488;GO:0004672	ATG47300.1		5-lox-lac lectin carbohydrate family protein	Serine/Threonine kinase domain protein
Sapur.003G139800.1	41.70182287	0.76905838	0.07384168	-10.5026	8.41E-26	2.88E-25	open	-0.64892745	5.54E-20		ATG01180.1		5-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase, putative
Sapur.008G127400.1	4736.1514	0.35100161	0.03353889	10.47268	1.24E-25	4.26E-25	open	0.63973837	1.91E-19	GO:0005789	ATG16595.1		Translocon-associated protein (TRAP), alpha subunit	translocon-associated protein subunit alpha
Sapur.T064600.1	994.5765849	0.39105663	0.03767723	10.44553	1.54E-25	5.23E-25	open	0.62409913	2.92E-18		ATG41560.2		Per1-like family protein	psn-GPI attachment to protein factor
Sapur.15WG119800.1	15452.10517	5.42170828	0.54031426	10.44499	1.56E-25	5.28E-25	open	0.64334226	1.68E-20	GO:0006396;GO:0006434;GO:0000287;GO:0000015	ATG36520.1	ENO2;LOS2	Enolase	phosphopyruvate hydratase
Sapur.003G033400.1	300.9366628	0.43006253	0.04133188	10.40414	2.37E-25	8.04E-25	open	0.62531818	2.05E-18	GO:0004872	ATG30580.1	DRIP2	DRIB2A-interacting protein 2	E3 ubiquitin protein ligase DRIP2
Sapur.009G139700.1	541.9773328	-0.31195269	0.03015617	-10.3425	3.16E-25	1.07E-24	open	-0.64504768	7.68E-20		ATG23910.1			reverse transcriptase-like protein
Sapur.013G042500.1	5.08401854	1.96615323	0.19019773	10.34166	4.57E-25	1.54E-24	open	0.53307017	5.86E-14					NA
Sapur.009G105300.1	162.7340866	0.28187149	0.02727429	10.33351	6.12E-25	2.06E-24	open	0.68276928	9.80E-23		ATG15240.1		Transmembrane amino acid transporter family protein	amino acid transporter, putative
Sapur.013G098100.1	4.6403626	2.25720070	0.22031065	10.24542	1.24E-24	4.13E-24	open	0.52970523	9.80E-13	GO:0055114;GO:0016491;GO:0018131	ATG37690.1	ATOPR2;OPR2	12-oxophytodienoate reductase 2	NA
Sapur.017G033600.1	7.94283976	1.40435763	0.13789048	10.18691	2.27E-24	7.51E-24	open	0.57329268	6.21E-15					NA
Sapur.006G203600.1	10.86685842	0.76488056	0.07509637	-10.1837	2.34E-24	7.76E-24	open	-0.61790188	8.86E-18					NA
Sapur.016G136600.1	3.26178707	1.76905838	0.17384845	10.17593	2.54E-24	8.39E-24	open	0.62602126	1.08E-18		ATG29150.1		NADP(H)-binding Rossmann-fold superfamily protein	3-ketoacyl-(acyl-carrier) reductase
Sapur.015G083300.1	1738.71352	0.47705801	0.04691656	10.16663	2.73E-24	8.90E-24	open	0.62564894	4.37E-18	GO:0055114;GO:0016616;GO:0006694;GO:0003854;GO:0019752	ATG47520.1	MDH	malate dehydrogenase	NAD-malate dehydrogenase
Sapur.006G175400.1	140.2150046	0.52612446	0.05176635	10.16344	2.89E-24	9.51E-24	open	0.60907025	2.35E-17		ATG15040.1		Protein of unknown function, DUF584	senescence regulator
Sapur.015G087100.1	447.3853865	0.27104116	0.02667143	-10.1	3.27E-24	1.81E-24	open	-0.62677928	2.18E-18	GO:0006355;GO:0003700	ATG30810.1	ATZIP;-6;ATZIP3;ZIP9	zinc finger (B-box) family protein	AP2/EREBP domain transcription factor
Sapur.016G145600.1	512.10474	0.00732704	0.00204362	10.04892	9.28E-24	3.02E-23	open	0.61372944	2.17E-17	GO:0019149;GO:0010264;GO:0005524	ATG18730.1		pfkB-like carbohydrate kinase family protein	pfkB-like carbohydrate kinase
Sapur.005G105800.1	171.5108885	0.48408168	0.04822025	10.03625	1.05E-23	3.41E-23	open	0.61609372	2.04E-17	GO:0006355;GO:0005739;GO:0003690	ATG07900.1		Mitochondrial transcription termination factor family protein	NA
Sapur.15ZG053800.1	113.7899716	0.56539147	0.05663059	9.987425	1.73E-23	5.59E-23	open	0.58350458	1.06E-15		ATG18845.1		Pentatricopeptide repeat (PPR) superfamily protein	pentatricopeptide (PPR) repeat protein, putative
Sapur.017G208600.1	655.5293729	0.69968729	0.07017824	-9.96689	2.13E-23	6.86E-23	open	-0.64128928	1.66E-19		ATG29120.1	AGPL4;TAGP1	arabinogalactan protein 1	transmembrane protein, putative
Sapur.015W0018300.1	416.7995114	0.58462674	0.05908879	9.907579	2.9E-23	9.33E-23	open	0.60051567	1.00E-16	GO:0016020;GO:0008378;GO:0006486	ATG32440.1		Galactosyltransferase family protein	beta-1%2C3-galactosyltransferase sgx-2, putative
Sapur.007G100700.1	238.0675904	-0.65707782	0.06637149	-9.89824	4.24E-23	1.36E-22	open	-0.61335645	1.35E-17	GO:0055115;GO:0016567	ATG64330.1	JK218;NPH;LRPT1	Phototropic-responsive NPH3 family protein	root phototropism protein
Sapur.016G060800.1	627.0176368	0.28001107	0.02831221	9.889302	4.76E-23	1.52E-22	open	0.62983737	1.97E-19	GO:0055114;GO:0046872;GO:0006801;GO:0004784	ATG30520.1	ATMSD1;MER18;MSD1	Manganese superoxide dismutase family protein	superoxide dismutase [Mn] protein
Sapur.T148900.1	118.0409627	1.18902588	0.12085139	9.842588	7.38E-23	2.35E-22	open	0.57237416	8.32E-15	GO:0016020;GO:0006810;GO:0005215	ATG15960.1	ATRAMP8;NRAMP6	NRAMP metal ion transporter 6	NRAMP metal ion transporter 6
Sapur.009G110100.1	2688.894817	0.53635125	0.05338265	9.834388	8.06E-23	2.51E-22	open	0.58337114	1.18E-15	GO:0055114;GO:0016491;GO:0016614;GO:0005840	ATG12570.1		Glucose-methanol-choline (GMC) oxidoreductase family protein	glucose-methanol-choline (GMC) oxidoreductase, putative
Sapur.019G036100.1	31.75562238	0.80632927	0.08229965	9.805628	1.06E-22	3.37E-22	open	0.53393208	5.26E-14	GO:0043531	ATG50950.2	ZAR1	HORC-ATZVATED RESISTANCE 1	NBS-LRR disease resistance protein, putative
Sapur.004G178700.1	1.12.79436	0.62502149	0.06849451	9.75036	1.44E-22	4.55E-22	open	0.51158187	1.37E-13		ATG51580.1			transmembrane protein, putative
Sapur.018G073000.1	19.80626772	0.30437928	0.03187736	9.761888	1.64E-22	5.19E-22	open	0.5503371	8.24E-14	GO:0016020;GO:0006970	ATG29100.1	ATGLR2.9;GLR2.9	glutamate receptor 2.9	glutamate receptor 2
Sapur.006G273000.1	95.34413386	0.34124286	0.03583865	9.518408	2.56E-22	8.47E-22	open	-0.54230473	4.19E-14	GO:0055114;GO:0010309	ATG40850.1	RHC;Rhc-like-1	Rhc/Rhc-like family protein	1%2C2-dihydroxy-3-keto-5-methylthiopentene dioxygenase
Sapur.016G240600.1	3538.027508	0.31739105	0.03287792	9.653604	4.75E-22	1.48E-21	open	0.60347288	8.61E-17	GO:0055114;GO:0016616;GO:0006694;GO:0003854;GO:0019752	ATG53240.1	mMDH1	Lactate/malate dehydrogenase family protein	malate dehydrogenase
Sapur.011G079900.1	2072.431252	0.18387831	0.03100425	9.602034	7.84E-22	2.46E-21	open	0.61534702	9.91E-18	GO:0016020;GO:0010103	ATG34720.1		Sec1 protein transport family protein	preprotein translocase, Sec1 subunit
Sapur.003G361300.1	541.6403273	0.52138195	0.05360891	9.561884	8.63E-22	2.68E-21	open	0.61504184	9.60E-18	GO:0052726;GO:0052725;GO:0047335;GO:0052007;GO:0005522;GO:0005524;GO:0000028	ATG51760.1		Inositol 1,3,4-trisphosphate 5/6-kinase family protein	inositol-tetrakisphosphate 1-kinase
Sapur.009G103800.1	7.87245935	1.37638367	0.14423625	9.542546	1.19E-21	4.30E-21	open	0.5663866	1.08E-14		ATG06100.2	ATMYB33;MYB33	myb domain protein 33	transcription factor MybS, putative
Sapur.018G051500.1	7.06382213	1.62059684	0.17029368	9.516467	1.79E-21	5.12E-21	open	0.57487068	5.45E-15	GO:0007165;GO:0006468;GO:0005524;GO:0004672	ATG50930.1	CIPK5;SnRK2.24	CBL-interacting protein kinase 5	calcium/calmodulin-dependent protein kinase
Sapur.010G070600.1	329.8587611	0.27718809	0.02953028	9.400921	5.41E-21	1.65E-20	open	0.59605298	1.80E-16		ATG27660.1			transmembrane anterior posterior transformation-like protein
Sapur.003G390600.1	254.2126612	0.30008735	0.03201723	9.37021	6.99E-21	2.12E-20	open	0.58183026	2.16E-16	GO:0006413;GO:0003743	ATG11900.1			translation initiation factor 5G11
Sapur.002G013100.1	1.71525625	2.47372663	0.26384613	9.321823	1.14E-20	3.45E-20	open	0.58228779	7.25E-16	GO:0006511	ATG42190.1	ASK2;SKP1B	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 family protein	SKP1-like protein
Sapur.002G022100.1	252.9893423	0.42488329	0.04784878	-9.2821	1.60E-20	4.80E-20	open	-0.61292088	4.46E-17	GO:0016020	ATG38570.1	ATGIGC;CYSAR1;EMB2269	GTP/CDAG-binding	NA
Sapur.004G106500.1	1549.018707	0.60099857	0.06566124	9.229168	2.73E-20	8.14E-20	open	0.55623846	3.92E-14	GO:0008184;GO:0005975	ATG29320.1		Glycosyl transferase, family 29	alpha-2%2C6 glucan phosphorylase 1, isozyme/amylopectin protein
Sapur.017G110700.1	167.390224	0.44738755	0.04869588	-9.23222	2.88E-20	8.60E-20	open	-0.57958719	1.82E-15	GO:0043531	ATG14470.1		NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.T100100.1	-0.68550813	0.24174181	0.02635821	9.174589	7.92E-20	2.33E-19	open	0.57473329	7.76E-15					NA
Sapur.008G059400.1	121.9384043	0.44845356	0.04907687	9.059952	1.31E-19	3.82E-19	open	0.53893734	2.80E-14		ATG38450.1			Sel1 repeat protein
Sapur.009G098600.1	27.19651943	0.57940385	0.06404812	9.04652	1.48E-19	4.33E-19	open	0.56613702	1.42E-15		ATG38980.1			hypothetical protein
Sapur.009G131500.1	390.7752253	0.35811782	0.03984342	8.987978	2.52E-19	7.33E-19	open	0.57866708	2.06E-15	GO:0005085;GO:0016021	ATG44370.1	PHT4;6	phosphate transporter 4;6	anion transporter, putative
Sapur.006G194200.1	576.1160644	0.75908828	0.03260305	8.363057	2.66E-19	7.75E-19	open	0.55892944	4.5E-14		ATG21070.1			plant/TIFY10-10b protein
Sapur.002G079000.1	878.3502162	0.86368689	0.09400751	-8.96566	3.08E-19	8.96E-19	open	-0.57054764	6.12E-15		ATG68950.1	EKO	Phosphate-responsive 1 family protein	phosphate-induced protein 1 motif protein
Sapur.016G182500.1	615.3922564	0.67249144	0.03877149	8.957467	3.12E-19	9.64E-19	open	0.5482315	1.7E-14		ATG68800.1			transmembrane protein, putative
Sapur.002G045500.1	162.2692452	0.43911267	0.04910783	8.94236	3.81E-19	1.10E-18	open	0.55974802	2.52E-14		ATG39235.1			hypothetical protein
Sapur.003G049400.1	1.45660692	2.42488329	0.27108043	8.898104	5.74E-19	1.64E-18	open	0.51403037	4.37E-15		ATG38530.1			NA
Sapur.008G066700.1	5345.321732	0.36465243	0.03900269	8.853806	8.31E-19	2.38E-18	open	0.54154284	2.41E-13	GO:0006396;GO:0004618	ATG79550.1	PGK	phosphoglycerate kinase	phosphoglycerate kinase
Sapur.005G045500.1	11.27936613	0.85976284	0.09761106	8.848811	8.85E-19	2.54E-18	open	0.54970576	8.91E-14		ATG48880.1	TBL7	TRICHOME BIREFRINGENCE-LIKE 7	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.016G248100.1	1119.318869	0.21082542	0.02403568	-8.77461	1.71E-18	4.87E-18	open	-0.53255106	2.06E-13	GO:0016787;GO:0006541;GO:0008242;GO:0003824	ATG39610.1	ATGGH2;GGH2	gamma-glutamyl hydrolase 2	gamma-glutamyl hydrolase
Sapur.010G141300.1	109.5351882	-0.82680645	0.09483009	-8.76412	1.88E-18	5.35E-18	open	-0.55408192	5.16E-13	GO:0003333	ATG56200.1		Transmembrane amino acid transporter family protein	sodium-coupled neutral amino acid transporter
Sapur.006G193000.1	229.3147513	0.3829161	0.04387724	8.73025	1.98E-18	5.64E-18	open	0.54891793	9.83E-14		ATG29190.1			DUF868 domain protein
Sapur.016G092100.1	552.5854991	0.46209936	0.05276842	8.724721	2.67E-18	7.56E-18	open	0.53743742	4.09E-13		ATG31950.1		glycosyl oxidase-related protein	glycosyl oxidase
Sapur.015G281000.1	2047.435527	0.33483872	0.0383822	8.731065	2.94E-18	8.3E-18	open	0.54164443	8.61E-14	GO:0016021;GO:0006886;GO:0005783	ATG48440.1		8-cell receptor protein-like	arginine induced protein
Sapur.001G121800.1	663.3413651	0.28704591	0.03196922	8.646121	5.33E-18	1.50E-17	open	0.58319814	1.64E-15	GO:0016868;GO:0005975;GO:0017704	ATG18870.1	DRT101	phosphoglucomutase mutase-related	phosphoacetylglucosamine mutase
Sapur.006G120100.1	47.06069756	0.70112447	0.08132219	8.620925	6.67E-18	1.87E-17	open	0.57489637	3.44E-15	GO:0055114;GO:0016491;GO:0016705;GO:0005506	ATG49610.1	CYP94D2	cytochrome P450, family 94, subfamily D, polypeptide 2	NA
Sapur.004G169600.1	347.5423052	0.27832488	0.03237019	-8.59818	8.10E-18	2.27E-17	open	-0.55342923	5.60E-14		ATG01850.1		Protein kinase superfamily protein	kinase domain protein
Sapur.016G137900.1	157.8026969	0.49399403	0.06175321	8.503968	1.05E-17	2.94E-17	open	0.54230763	1.41E-14		ATG42870.1			transferring glycosyl group transferase, putative
Sapur.009G051600.1	7.85327681	1.05207546	0.12653115	8.523371	1.43E-17	3.98E-17	open	0.51253137	6.28E-14		ATG16480.1			hypothetical protein
Sapur.T180400.1	0.58369945	2.57630324	0.3025145	8.515624	1.68E-17	4.59E-17	open	0.57563181	3.11E-15					NA
Sapur.009G120600.1	597.3500039	-0.48780686	0.05798855	-8.41997	3.77E-17	1.03E-16	open	-0.57838421	2.14E-15		ATG11590.1			plant/F24H9-26 protein, putative
Sapur.007G091900.1	96.58041884	0.49495314	0.05900143	8.33862	7.52E-17	2.04E-16	open	0.53305681	6.12E-13		ATG43470.1	ATHDA14;hda14	histone deacetylase 14	histone deacetylase 14
Sapur.006G089500.1	288.1281798	0.61682618	0.08275169	8.33433	7.76E-17	2.11E-16	open	-0.57246841	4.47E-15	GO:0055114;GO:0016491	ATG39000.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein
Sapur.003G020800.1	6456.199838	0.27802671	0.03375514	8.24369	1.67E-16	4.49E-16	open	0.52734634	1.29E-12	GO:0016787;GO:0005524;GO:0003677	ATG54270.1	EIF4A-2	eIF4a-2	eukaryotic initiation factor 4A-2
Sapur.016G125400.2	19.98847468	0.97329982	0.06129886	8.1938	1.81E-16	4.87E-16	open	0.54192165	8.1E-13		ATG60570.1		Major facilitator superfamily protein	plant/T7D19-50 protein
Sapur.003G164000.1	173.4851578	0.29362623	0.03567895	8.231316	1.85E-16	4.97E-16	open	0.52750918	2.68E-12		ATG19010.1		Nuclear transport factor 2 (NTF2) family protein	F-box protein SKIP8
Sapur.016G010900.1	1.98463094	2.23364158	0.27596784	8.09019	5.47E-16	1.40E-15	open	0.52851678	5.01E-12		ATG34150.1		PQ-loop repeat family protein / transmembrane family protein	PQ loop protein
Sapur.008G117200.1	9.72549031	1.17879126	0.14615128	-8.17704	2.93E-16	7.76E-16	open	-0.55864116	2.90E-14	GO:0055114;GO:0016491	ATG42030.1;GA2OX8	gibberellin 2-oxidase 8	gibberellin 2-beta-dioxygenase	gibberellin 2-beta-dioxygenase
Sapur.009G195400.1	37.6779677	0.92938813	0.11804264	8.072945	3.46E-15	8.97E-15	open	0.53189969	1.90E-11		ATG38950.1		Major facilitator superfamily protein	nodulin family protein
Sapur.016G277000.1	695.3023217	0.31670776	0.04620954	8.737029	4.9E-15	9.01E-15	open	0.5187623	4.01E-12	GO:0055114;GO:0005506	ATG39120.1;ATPDL5-3;PDL12	PDI-like 5-3	protein disulfide isomerase	protein disulfide isomerase
Sapur.008G095800.1	140.9263139	-0.45069139	0.05769228	-7.86281	3.76E-15	9.72E-15	open	-0.53157431	7.54E-12	GO:0005515;GO:0003700	AtSRF48;DRE82C	Integrase-type DNA-binding superfamily protein	dehydration responsive element-binding protein	dehydration responsive element-binding protein
Sapur.002G004300.1	751.3664627	0.11804508	0.04232773	2.789647	4.88E-15	1.26E-14	open	0.49994019	2.01E-11	GO:0016021;GO:0006486;GO:0005783;GO:0004579		Ribophorin I	Ribophorin I	dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 1
Sapur.001G121900.1	8.58143823	0.32910274	0.04172364	7.813438	5.56E-15	1.43E-14	open	0.50507033	1.38E-11		ATG45420.1		Duplicated homeodomain-like superfamily protein	MybS DNA-binding domain protein, putative
Sapur.005G200600.1	435.9475068	0.28633337	0.03667668	7.808239	5.86E-15	1.46E-14	open	0.52267228	1.29E-12	GO:0008270;GO:0005198;GO:0046811	ATG29290.1		2n-dependent nucleotide superfamily protein	zinc carbopeptidase
Sapur.15WG117900.1	672.2227211	0.99692995	0.12782858	7.752035	9.04E-15	2.31E-14	open	0.5193449	3.19E-12	GO:0016021	ATG50790.1		Nodulin MtN3 family protein	sugar efflux transporter for intercellular exchange protein
Sapur.014G113300.1	252.9687531	0.56148164	0.07266176	7.688201	1.49E-14	3.76E-14	open	0.52720728	1.29E-12		ATG47920.1			plant/MAC/U-34 protein, putative
Sapur.010G124500.1	601.4914031	-0.46256458	0.06094455	-7.58969	3.21E-14	8.06E-14	open	-0.51029693	8.67E-12		ATG03420.1			NA
Sapur.005G037300.1	35.40378802	0.61413686	0.07913137	7.761103	3.23E-14	8.11E-14	open	0.50603014	1.79E-10		ATG60810.1			root determined nodulation protein
Sapur.T068300.1	1.15700532	1.92870649	0.25709207	7.502007	6.28

Sapur.01G0132700.1	217.3206613	6.79073443	0.118296226	57.40449	0	0	cpm	0.89348707	9.49E-56		ATG5:ATG4B.1	Ms25 family protein	NA
Sapur.01G0032700.1	1095.402063	9.71263543	0.232753687	41.72722	0	0	cpm	0.7899512146	9.59E-35	GO:0004488;GO:0016307	ATG:SI6960.1	PIP5K6	phosphatidylinositol-4-phosphate 5-kinase
Sapur.01G0261100.1	4344.428253	41.19273974	0.07844862	52.51031	0	0	cpm	0.855466164	3.76E-46		ATG:I2119.1	ACT11	actin-11
Sapur.01G0061100.1	399.773243	0.051929866	0.08475564	47.8072	0	0	cpm	0.858007517	1.66E-40	GO:0004648;GO:0004672	ATG:SI8930.1	CPK20	calcium-dependent protein kinase 20
Sapur.01G0265300.1	208.3593037	5.711657843	0.109533364	52.14541	0	0	cpm	0.86366654	5.68E-48	GO:0008872;GO:0000145	ATG:SI2340.1	exoxylt subunit exo70 family protein A2	exoxylt subunit EXO70
Sapur.01G0294800.1	860.6501828	6.825764653	0.109309942	62.39659	0	0	cpm	0.829154776	5.46E-41	GO:0003924;GO:0007017;GO:0005874	ATG:SI3860.1	TUB8	tubulin beta 8
Sapur.01G0151800.1	2254.853463	3.888788566	0.077902194	49.91886	0	0	cpm	0.868387022	5.27E-49	GO:0008168;GO:0008152;GO:0006694	ATG:SI3710.1	CYP51MT1	sterol methyltransferase 1	S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase, putative
Sapur.01G0166900.1	386.4238155	10.71167543	0.276065512	38.79685	0	0	cpm	0.76105615	6.14E-31	GO:0005385;GO:0016020;GO:0015296;GO:0006812	ATG:SI7060.1	ATCHX24;CHX24	cation/H+ exchanger 24	cation/H+ antiporter
Sapur.01G0194200.1	221.3840957	3.348619466	0.108502222	58.48555	0	0	cpm	0.892752285	1.53E-55	GO:0016021;GO:0015609;GO:0015095	ATG:SI3800.1		Protein of unknown function (DUF803)	NA
Sapur.01G0266100.1	126.0705611	1.56464688	0.107742365	47.0052	0	0	cpm	0.879938232	8.16E-52	GO:0016020	ATG:SI7945.0.1	ALISS	cell division control protein	cell division control protein
Sapur.01G0251900.1	1299.227115	9.451802888	0.245268645	38.56833	0	0	cpm	0.72145651	1.12E-27		ATG:SI2914B.1		Pollen Ole e 1 allergen and extension family protein	anther-specific protein LAT52, putative
Sapur.01G0224200.1	1174.901135	5.904885882	0.098849667	59.13758	0	0	cpm	0.844002342	3.46E-44	GO:0006355;GO:0003677	ATG:SI5120.1	ANAC056;ATNAC2;NAC2;NAC	NAC domain containing protein 2	NAC transcription factor
Sapur.01G0365800.1	1923.019634	5.598236454	0.177761226	53.99511	0	0	cpm	0.832631382	1.27E-41	GO:0006508;GO:0004252	ATG:SI5833.1	ATSBT5.4;SBT5.4	Subtilase family protein	subtilisin-like serine protease
Sapur.01G0462600.1	1386.363839	11.11764007	0.229275111	48.63023	0	0	cpm	0.829532	2.87E-33	GO:0016157;GO:0005886	ATG:SI4920.1	SUCRP;SPL9F	sucrose phosphorylase 3F	sucrose-phosphate synthase
Sapur.01G0521000.1	99.47601331	5.442829175	0.112544197	40.33869	0	0	cpm	0.832989023	1.10E-41		ATG:SI5490.1	ATGCX1;GEX1	gamete expressed protein 1	NA
Sapur.01G0782500.1	285.1123561	4.361857517	0.08284876	48.394	0	0	cpm	0.854575544	9.25E-38	GO:0005085;GO:0016020;GO:0006811;GO:0005216	ATG:SI8050.1	ATCNGC16;CNGC16	cyclic nucleotide-gated ion channel 16	cyclic nucleotide-gated ion channel protein, putative
Sapur.01G0221800.1	696.4966275	6.984320151	0.139611975	50.02666	0	0	cpm	0.84135576	2.96E-43	GO:0016597;GO:0008152	ATG:SI5320.1		ACT-like superfamily protein	ACT domain protein
Sapur.01G0071400.1	527.7759454	9.814666763	0.202032271	48.57967	0	0	cpm	0.817329221	5.96E-39	GO:0016758;GO:0008152	ATG:I7592.1	UGT78D2	UDP-glucosyl transferase 78D2	UDP-glucose:flavonoid 3-O-glucosyltransferase
Sapur.01G0275000.1	139.2435068	6.290203317	0.150049545	40.66025	0	0	cpm	0.84603421	3.44E-44	GO:0003333	ATG:SI8960.1		Transmembrane amino acid transporter family protein	amino acid transporter
Sapur.01G0289300.1	180.3765476	6.012473954	0.131002286	45.89595	0	0	cpm	0.81262564	3.54E-38		ATG:SI5090.1			hypothetical protein
Sapur.01G0290800.1	151.1419635	5.401885263	0.127136178	42.51388	0	0	cpm	0.79217733	4.31E-35	GO:0005509	ATG:SI2060.1		calcium-binding EF hand family protein	NA
Sapur.01G0167600.1	161.7227131	4.900881921	0.127856649	38.33107	0	0	cpm	0.834838914	5.01E-42	GO:0004648;GO:0004672	ATG:SI7650.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.01G0280800.1	527.9699014	4.783142589	0.120661848	39.57545	0	0	cpm	0.82068095	1.77E-38	GO:0004648;GO:0004672	ATG:SI6570.1	ATCPK4;CPK4	calcium-dependent protein kinase 4	calcium-dependent kinase
Sapur.01G0097900.1	657.018266	5.596537637	0.172859353	55.51645	0	0	cpm	0.863329433	2.26E-47	GO:0003132;GO:0030138;GO:0016192;GO:0006886;GO:0051198	ATG:SI2760.1		Clathrin light chain protein	clathrin light chain
Sapur.01G0186300.1	186.9126093	11.11764007	0.329275111	42.27557	0	0	cpm	0.863329433	2.26E-47	GO:0005385;GO:0016020;GO:0015299;GO:0008121;GO:0006814;GO:0006813;GO:0005451	ATG:SI4135.1	CHX15;CHX15	cation/hydrogen exchanger 15	cation proton exchanger
Sapur.01G0052100.1	494.6452327	4.763490038	0.095752328	49.74803	0	0	cpm	0.848167242	1.27E-44	GO:0008234;GO:0005508	ATG:SI2160.1		Cysteine proteinases superfamily protein	KDEL-tailed cysteine endopeptidase CEP2
Sapur.01G0612600.1	682.3149663	6.839238855	0.113345588	60.3397	0	0	cpm	0.855258905	4.74E-45		ATG:SI1030.1		NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase family protein
Sapur.01G0155200.1	1169.121881	9.307709238	0.167113163	54.45746	0	0	cpm	0.841260642	1.02E-43	GO:0005622;GO:0003779;GO:0030042;GO:0015629	ATG:SI5180.1	ADF7	actin depolymerizing factor	actin depolymerizing factor
Sapur.01G0150700.1	64.20881606	5.018516436	0.126180357	39.77042	0	0	cpm	0.840501473	4.23E-44	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATG:SI2400.1	CYP71S41	cytochrome P450, family 71S, subfamily A, polypeptide 1	cytochrome P450 family protein
Sapur.01G0267100.1	789.4567792	1.58640386	0.060473449	62.7684	0	0	cpm	0.89392627	1.24E-55		ATG:SI2910.2		Calcium-binding EF-hand family protein	calcium-binding protein CML27, putative
Sapur.01G0247600.1	838.5699077	7.078053872	0.12186388	58.09113	0	0	cpm	0.826551881	1.58E-40	GO:0008017;GO:0007100;GO:0005524;GO:0003777;GO:0005871	ATG:SI6340.2		F-loop nucleotide triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain	NA
Sapur.01G0300600.1	110.4113687	5.683762364	0.136887137	41.54983	0	0	cpm	0.82693976	1.36E-40		ATG:I2060.1			NA
Sapur.01G0086600.1	82.32296784	3.320292726	0.159919666	39.5253	0	0	cpm	0.828413719	7.41E-41		ATG:I2060.2			NA
Sapur.01G0106600.1	113.3107151	5.764895321	0.136618898	42.19688	0	0	cpm	0.831664546	1.96E-41		ATG:I2060.3			NA
Sapur.01G0108000.1	118.5747079	6.884293691	0.170032556	40.48809	0	0	cpm	0.777720191	4.60E-33		ATG:I2060.4			NA
Sapur.01G0211600.1	68.37703864	4.567485725	0.122025533	37.4575	3.15E-206	1.82E-304	cpm	0.832957656	6.66E-40		ATG:SI5490.1	ATGCX1;GEX1	gamete expressed protein 1	NA
Sapur.01G0227300.1	166.6692771	9.861915672	0.263800374	37.37083	1.16E-305	6.69E-304	cpm	0.828673123	6.66E-41		ATG:SI6556.1	RIC7	PAX-box/PD1-Rho-binding family protein	P21-Rho-binding domain protein
Sapur.01G0138800.1	522.9679814	9.960862259	0.180239266	37.28953	2.41E-304	1.39E-302	cpm	0.791818605	1.35E-33		ATG:SI6670.1		Calexcoin-related family protein	calcium ion-binding protein, putative
Sapur.01G0420600.1	130.5895459	4.880880651	0.13138268	37.21864	3.41E-303	1.94E-301	cpm	0.816822211	7.28E-39					NA
Sapur.01G0076000.1	65.06384205	4.637391863	0.125405885	36.97903	2.49E-299	1.39E-297	cpm	0.829995431	3.86E-41					NA
Sapur.01G0269700.1	48.80028973	3.294364472	0.159822759	36.88075	9.40E-298	5.20E-296	cpm	0.87566566	4.10E-50	GO:0008168;GO:0008152	ATG:I4480.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase
Sapur.01G0419700.1	2538.072545	3.664472356	0.099615147	36.78814	2.86E-296	1.57E-294	cpm	0.786325171	1.07E-34	GO:0016887;GO:0005524;GO:0016020	ATG:SI5590.1		ABC-2 type transporter family protein	white-brown-complex ABC transporter family protein
Sapur.01G0126600.1	122.7164468	2.387759	0.200824139	36.78719	2.96E-296	1.61E-294	cpm	0.771375495	1.61E-32	GO:0055114;GO:0020037;GO:0009570;GO:0004601	ATG:SI2180.1		Peroxidase superfamily protein	peroxidase
Sapur.01G0122200.1	295.4856639	8.54342384	0.232694071	36.78238	3.53E-296	1.93E-294	cpm	0.649665755	3.43E-20	GO:0016597;GO:0008152	ATG:SI5320.1		ACT-like superfamily protein	ACT domain protein
Sapur.01G0190100.1	149.5794684	3.555856269	0.097415834	36.62035	9.74E-292	5.26E-290	cpm	0.744323305	1.68E-29		ATG:SI2175.1			transmembrane protein, putative
Sapur.01G0141900.1	309.2229852	6.027918832	0.110404682	36.48322	2.05E-291	1.10E-289	cpm	0.749802516	1.34E-29		ATG:SI0800.1			transmembrane protein, putative
Sapur.01G0188700.1	164.5766611	3.765867389	0.112505634	36.28047	1.29E-288	1.74E-286	cpm	0.731263612	5.12E-27	GO:0016758;GO:0008152	ATG:SI4250.1		UDP-Glycosyltransferase superfamily protein	NA
Sapur.01G0154000.1	191.2524871	4.363443701	0.113636433	35.21664	9.36E-288	4.94E-286	cpm	0.759576898	9.30E-31	GO:0008234;GO:0005508	ATG:SI2160.1		Cysteine proteinases superfamily protein	KDEL-tailed cysteine endopeptidase CEP2
Sapur.01G0161300.1	930.0719607	-2.489023301	0.068969847	-36.0885	3.42E-285	1.77E-283	cpm	-0.837402834	1.66E-42		ATG:SI6690.1		NAD(P)-linked oxidoreductase superfluorly protein	alditol/keto reductase family protein
Sapur.01G0062900.1	358.6646204	4.070087026	0.113014603	36.07487	2.28E-283	1.18E-281	cpm	0.818313311	1.01E-39	GO:0005975;GO:0004553	ATG:SI2450.1	BGLU40	beta glucosidase 40	NA
Sapur.01G0244100.1	354.1911294	8.893942679	0.135488447	35.99353	1.06E-283	5.40E-282	cpm	0.838182596	1.08E-42	GO:0008017;GO:0007100;GO:0005524;GO:0003777;GO:0005871	ATG:SI6340.1		F-loop nucleotide triphosphate hydrolases superfluorly protein with CH (Calponin Homology) domain	NA
Sapur.01G0260600.1	365.0020868	7.267209154	0.116729259	35.54408	1.26E-276	5.00E-275	cpm	0.78991952	7.91E-35					transmembrane protein, putative
Sapur.01G0249400.1	362.1908767	2.821607043	0.079459983	35.51256	3.15E-276	1.53E-274	cpm	0.849698374	6.18E-45	GO:0008270;GO:0005515	ATG:SI5830.1	ATL43	RING/U-box superfamily protein	RING-H2 zinc finger protein, putative
Sapur.01G0230600.1	471.1432037	5.807159	0.088575521	35.41809	9.96E-275	4.36E-273	cpm	0.831609775	1.97E-41	GO:0005886;GO:0008411;GO:0005216	ATG:SI5180.1	AHT6;PIPK	Shaker potassium channel family protein	NA
Sapur.01G0181200.1	88.32962415	3.189686844	0.090095889	35.40526	1.42E-274	6.84E-273	cpm	0.81872028	3.51E-39		ATG:I2430.1		Protein of unknown function (DUF679)	transmembrane protein, putative
Sapur.01G0300900.1	131.3456432	5.183978885	0.147378667	35.23176	5.30E-273	2.54E-271	cpm	0.834591844	1.07E-42	GO:0004648;GO:0004672	ATG:SI7650.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.01G0130900.1	978.0862247	1.593347031	0.04538803	35.10501	5.65E-270	2.66E-268	cpm	0.897637386	1.01E-57	GO:0005525	ATG:SI4663.1	ATRABA4B;ATRAB11B;RA66;	Ras-related small GTP-binding family protein	Ras-related protein Rab-6
Sapur.01G0625400.1	451.8079902	2.556071077	0.07125287	34.89371	9.26E-247	4.27E-245	cpm	0.85201757	3.91E-45	GO:0005515;GO:0035556;GO:0007165;GO:0006629;GO:0004435	ATG:SI2120.1	ATPAC2;PLC2	phosphoglycerol 2 C	phosphoinositide-specific phospholipase C
Sapur.01G0156700.1	60.18065863	2.238227277	0.088439152	34.87604	2.04E-246	9.37E-245	cpm	0.831763142	8.82E-41		ATG:SI5320.1		D-fucosylmethionine family protein	GDP-Fucose protein O-Fucosyltransferase
Sapur.01G0250800.1	534.2658006	2.527232204	0.072918833	34.66006	3.15E-243	1.41E-241	cpm	0.85024755	4.71E-46	GO:0016192;GO:0006904	ATG:SI2010.1	SEC13A	secretory 13A	NA
Sapur.01G0628700.1	574.4219276	2.556873889	0.112494734	34.52986	2.84E-241	1.26E-239	cpm	0.79132632	1.52E-27		ATG:SI6230.1		Regulator of Vps4 activity in the MVB pathway protein	regulator of Vps4 activity in the MVB pathway protein
Sapur.01G0155300.1	69.07623364	1.556887389	0.153017128	34.33019	2.78E-238	1.20E-236	cpm	0.788854186	1.37E-34	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATG:SI8820.1	SRF2	STRUBBELIG-receptor family 2	strubbelig-receptor family protein
Sapur.01G0091100.1	42.58505007	3.318515835	0.155586849	34.15625	3.65E-236	1.56E-234	cpm	0.822231585	6.91E-41	GO:0005515;GO:0005525;GO:0004672	ATG:SI8120.1		Protein kinase superfamily protein	NA
Sapur.01G0061000.1	115.8496158	2.824328969	0.082645582	34.17523	5.64E-236	2.40E-234	cpm	0.860751326	2.60E-47	GO:0008168;GO:0008152	ATG:SI4480.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase domain protein
Sapur.01G0152800.1	1700.452563	4.371629744	0.088141654	34.14929	6.78E-234	2.89E-232	cpm	0.81399437	2.12E-38		ATG:SI2600.1	APK3	adenosine-5'-phosphosulfate (APS) kinase 3	adenylylsulfate kinase
Sapur.01G0113700.1	27.80512737	6.473362727	0.248517122	34.0877	1.12E-224	4.72E-253	cpm	0.880692228	2.56E-62	GO:0006468;GO:0004672	ATG:SI7650.2		Leucine-rich repeat transmembrane protein kinase	tyrosine kinase domain protein
Sapur.01G0074200.1	1087.713828	3.152611888	0.103645834	33.90704	2.46E-253	1.05E-251	cpm	0.777684695	6.02E-33	GO:0005515	ATG:SI7360.1	YSL7	YELLOW STRIPE like 7	OPT superfamily oligopeptide transporter
Sapur.01G0132400.1	4661.193327	4.243978215	0.125444779	33.83145	6.80E-251	2.80E-249	cpm	0.790639468	7.65E-35	GO:0015977;GO:0008964;GO:0006399	ATG:SI8750.1	ATPPC4;PPC4	phosphoenolpyruvate carboxylase 4	phosphoenolpyruvate carboxylase
Sapur.01G0244000.1	107.6765868	4.960884078	0.145306121	33.71407	3.60E-249	1.47E-247	cpm	0.85102597	2.60E-45					NA
Sapur.01G0269600.1	191.8787927	-2.947947284	0.121668023	33.67777	1.22E-248	4.97E-247	cpm	-0.77392852	2.60E-32	GO:0055114;GO:0009916	ATG:SI2X10	AOX1D	alternative oxidase 1D	ubiquinol oxidase
Sapur.01G0421600.1	163.5210083	8.976079205	0.266278238	33.66289	2.02E-248	8.19E-247	cpm	0.683386663	6.15E-23	GO:0008270;GO:0005622	ATG:SI2710.1		B-box type zinc finger family protein	B-box zinc finger protein
Sapur.01G0281700.1	5078.82432	4.000163163	0.118835007	33.64013	4.15E-248	1.68E-246	cpm	0.76429915	7.80E-25		ATG:SI2510.1		Pectin lyase-like superfamily protein	glycoside hydrolase family 28 protein
Sapur.01G0102400.1	1247.581824	4.181808628	0.102199663	33.45323	2.31E-245	9.22E-244	cpm	0.80257861	1.36E-36		ATG:I2710.1		Protein of unknown function (DUF679)	transmembrane protein, putative
Sapur.01G0275100.1	424.0210122	3.334691151	0.099733883	33.4359	1.44E-245	5.64E-244	cpm	0.758834874	1.05E-30	GO:0055114;GO:0050660;GO:0016491;GO:0019139;GO:0009690	ATG:SI6440.1	ATCOX6;ATCOX7;CX6S	cytokinin oxidase/dehydrogenase 6	cytokinin oxidase/dehydrogenase
Sapur.01G0139800.1	600.1955759	1.175064052	0.125056766	33.38535	2.24E-244	8.88E-243	cpm	0.727103601	4.21E-27		ATG:SI7620.1		Arabidopsis protein of unknown function (DUF241)	DUF241 domain protein
Sapur.01G0280200.1	224.0492171	4.780741323	0.116475822	33.26569	1.21E-242	4.76E-241	cpm	0.81328061	1.05E-40		ATG:I2600.1			hypothetical protein
Sapur.01G0270400.1	100.0563217	5.551403277	0.16696411	33.24912	2.10E-242	8.25E-241	cpm	0.816612947	7.88E-39	GO:0003151;GO:0003677	ATG:SI2380.1	anac090;NAC090	NAC domain containing protein 90	NAC transcription factor
Sapur.01G0218800.1	915.1319001	5.393211679	0.162583069	33.17204	2.73E-241	1.06E-239	cpm	0.879378791	6.32E-52		ATG:SI8420.1		alpha/beta-Hydrolases superfamily protein	alpha/beta hydrolase family protein
Sapur.01G0161800.1	509.2536535	4.277906858	0.129751146	33.14207	7.37E-241	2.86E-239	cpm	0.851383601	2.62E-45	GO:0016020	ATG:SI8480.1		Lineage-specific protein family (UPF0497)	CAAP-like protein
Sapur.01G0116200.1	545.7740211	3.347144429	0.102635235	32.94901	4.37E-238	1.67E-236	cpm	0.786470359	2.96E-34	GO:0016790;GO:0006633	ATG:SI8510.1	FATB	fatty acyl-ACP thioesterases B	acyl acyl-carrier thioesterase, putative
Sapur.01G0285200.1	395.4671372	2.200201983	0.067780571	32.94361	5.48E-238	2.08E-236	cpm	0.88251005	1.00E-55	GO:0004648;GO:0004672	ATG:SI4040.1		Leucine-rich repeat protein kinase family protein	leucine-rich receptor-like kinase
Sapur.01G0138300.1	72.39143033	3.370201027	0.284658504	32.94161	5.58E-238	2.13E-236	cpm	0.746010089	6.16E-29	GO:0005385;GO:0016020;GO:0015299;GO:0008121	ATG:SI6970.1	ATCHX14;CHX14	cation/hydrogen exchanger 14	cation proton exchanger
Sapur.01G0192700.1	138.9988664	3.929437385	0.089087185	32.90522	1.85E-237	7.06E-236	cpm	0.843917358	8.95E-44		ATG:SI6320.1	DCPS1	decapping 1-like	Scd6-like Sm domain protein
Sapur.01G0014000.1	14888.29871	2.336629125	0.070187248	32.84174	1.49E-236	5.67E-235	cpm	0.832237799	1.49E-41	GO:0006556;GO:0004798;GO:0005524	ATG:SI6880.2	MAT3	methionine adenosyltransferase 3	S-adenosylmethionine synthase
Sapur.01G0122700.1	2166.118825	2.296344102	0.069040809	32.82824	2.04E-236	7.64E-235	cpm	0.838157104	1.61E-42	GO:0016887;GO:0000166;GO:0005524	ATG:SI1070.1	CLS;AATPase	Clp ATPase	ATP-dependent Clp protease ATP-binding subunit
Sapur.01G0250000.1	4794.206423	3.114369531	0.09501206	32.77847	1.19E-235	4.50E-234	cpm	0.813954239	2.15E-38	GO:0016740	ATG:SI3930.1	SHM4	serine hydroxymethyltransferase 4	serine hydroxymethyltransferase
Sapur.01G0164500.1	1169.817065	2.967204504	0.091337553	32.75842	2.20E-235	8.67E-234	cpm	0.85642635	1.51E-45		ATG:SI6000.1		Ribonuclease MRP/MRP protein	T-box protein SKIP14
Sapur.01G0247900.1	40.25345726	5.973050862	0.182507833	32.72764	6.32E-235	2.37E-233	cpm	0.838762109	9.13E-43		ATG:I1090.1		serine-rich protein related	hypothetical protein
Sapur.01G0280400.1	546.3254275	2.88603044	0.088245261	32.70465	1.34E-234	5.03E-233	cpm	0.864057085	6.62E-48	GO:0016787	ATG:SI9400.1	PP1-AT;TOPP1	type one protein phosphatase 1	serine/threonine-protein phosphatase
Sapur.01G0308900.1	201.5898799	3.674691984	0.112188563	32.68476	2.57E-234	9.42E-233	cpm	0.84461612	4.14E-44	GO:0016788	ATG:SI5180.1	NPC4	non-specific phospholipase C3	Non-specific phospholipase C3
Sapur.01G0108400.1	103.1328668	3.790273908	0.116202917	32.61772	2.30E-233	8.54E-232	cpm	0.775962628	2.96E-34	GO:0055085;GO:0016021;GO:0008324;GO:0006812	ATG:SI8580.1	FATA8	Cation efflux family protein	metal tolerance protein
Sapur.01G0152100.1	385.5064472	2.183164227	0.067303861	32.54361	8.22E-231	2.98E-229	cpm	0.837876051	1.02E-42	GO:0005886;GO:0005515	ATG:SI9060.1	ATMBAC2;BAC2	Mitochondrial distribution and morphology protein	carnitine/acylcarnitine carrier protein, putative
Sapur.01G0413400.1	324.7234887	3.348853786	0.103658542	32.30659	5.65E-229	2.03E-227	cpm	0.768227935	7.85E-32		ATG:SI8200.1		C2H2-type zinc finger family protein	C2H2-type zinc-finger protein
Sapur.01G0143900.1	184.1842531	2.163451328	0.097029475	32.3299	1.15E-229	2.28E-227	cpm	0.775238317	7.5E-32		ATG:SI5410.1	DCPS2	Decapping 1-like	plant DFF180-2D protein
Sapur.01G0131300.1	151.3450368	3.378164466	0.104999199	32.17466	3.99E-227	1.42E-225	cpm	0.790815677	7.23E-35	GO:0016021;GO:0016020;GO:0021857	ATG:SI6340.1	nodulin MtN21 /EamA-like transporter family protein	nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4
Sapur.01G0088600.1	180.3477113	3.262656629	0.101424627	32.10458	1.81E-226	1.34E-224	cpm	0.78184	6.78E-34		ATG:SI4120.1		Protein of unknown function (DUF677)	transmembrane protein, putative
Sapur.01G0260400.1	726.3049826	1.998584161	0.062155329	32.05154	2.09E-225	7.32E-224	cpm	0.883849743	1.31E-52	GO:0016021	ATG:SI7680.2	HHP4	heptahelical protein 4	adiponectin receptor protein
Sapur.01G0188500.1	202.1268889	3.402484623	0.107097611	32.04665	2.16E-225	7.36E-224	cpm	0.734089174	4.68E-28		ATG:SI4645.1			transmembrane protein, putative
Sapur.01G0269500.1	38.43640964	6.282208805	0.196731653	31.93457	8.85E-224	3.05E-222	cpm	0.847622245	1.64E-46		ATG:SI1570.1	TBL8	TRICHOME BIREFRINGENCE-LIKE 8	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.01G0115600.1	234.9202074	3.417039225	0.107054724	31.91862	1.47E-223	5.07E-222	cpm	0.764378806	2.99E-31	GO:0003824;GO:0006470;GO:0004722	ATG:SI7430.1	HA12	highly ABA-induced PP2C gene 2	protein phosphatase 2C
Sapur.01G0245900.1	58.63915722	5.811127887	0.185585252	31.88977	1.24E-223	4.48E-221	cpm	0.763875957	7.16E-31	GO:0015112;GO:0008270;GO:0005622	ATG:SI6640.1	AT-HSFA5;HSFA5	Matrin family protein	matrin metalloproteinase
Sapur.01T0050300.1	565.9667229	1.103727239	0.034021981	31.62578	1.61E-219	5.44E-218	cpm	0.914305121	2.01E-62	GO:0003565;GO:0006355;GO:0003700	ATG:SI3980.1		winged-helix DNA-binding transcription factor family protein	heat stress transcription factor A-5
Sapur.01G0071500.1	15.12500003	5.267664851	0.226895604	31.6137	2.40E-219	7.97E-218	cpm	0.82061396	1.94E-41		ATG:SI6700.1		RNA-binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.01G0209900.1	2119.610933	1.542363876	0.048941216	31.52688	1.72E-218	1.23E-216	cpm	0.88271878	1.05E-52	GO:0006470;GO:0004722	ATG:SI7510.1	WIN2	HOPW1-1-interacting 2	protein phosphatase 2C
Sapur.01G0284600.1	884.0807737	1.703300522	0.054032103	31.51015	4.60E-218	3.52E-216	cpm	0.864024907	4.65E-48		ATG:SI2160.1	TBL18	TRICHOME BIREFRINGENCE-LIKE 18	leaf senescence-like protein
Sapur.01G0131800.1	2197.869421	2.208673269	0.070091143	31.51144	6.05E-218	1.99E-216	cpm	0.837811294	1.39E-42	GO:0005385;GO:0016021	ATG:SI7120.1	TMT2	tonoplast monosaccharide transporter2	hexose transporter, putative
Sapur.01G0154300.1	44.14487218	4.170561396	0.210804042	31.44429	5.02E-217	1.64E-215	cpm	0.823378547	6.68E-41		ATG:SI5280.1		C2H2-like zinc finger family protein	zinc finger protein
Sapur.01G0889300.1	83.25710331	6.058807301	0.193476113	31.31553	2.87E-215	9.31E-214	cpm	0.720864404	1.85E-26	GO:0005385;GO:0016020;GO:0015297;GO:0015138;GO:0006855	ATG:SI1540.1		MATE efflux family protein	MATE efflux family protein
Sapur.01G0285500.1	435.7936905	3.810436777	0.121888148	31.29036	6.31E-215	2.04E-213	cpm	0.730237313	1.97E-27		ATG:SI5625.2			hypothetical protein
Sapur.01G0138300.1	124.3516335	2.274802127	0.105061189	31.15569	1.24E-212	3.87E-211	cpm	0.828847043	1.60E-41	GO:0016021;GO:0015020;GO:0004629	ATG:SI4500.1		glycosyltransferase family protein 47	glycosyltransferase family protein
Sapur.01G0068700.1	90.7014854	3.800468807	0.122970533	31.14931	5.18E-212	1.65E-211	cpm	0.767668842	3.72E-25		ATG:SI6880.1		NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase reductase
Sapur.01G0287200.1	2131.616043	2.149224429	0.069378825	31.11087	1.24E-212	4.08E-211	cpm	0.841124134	2.01E-43		ATG:SI2820.1		Phosphoglycerate mutase-like family protein	phosphoglycerate mutase-like protein
Sapur.01G0081100.1	2916.375079	1.371123207	0.044535209	30.7874	3.86E-208	1.21E-206	cpm	0.870645256	2.98E-49	GO:0055114;GO:0016491	ATG:SI0400.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.01G0139500.1	52.97545573	3.960697534	0.281646202	30.7465	1.24E-207	3.86E-206	cpm	0.719054387	2.82E-25		ATG:SI7190.1	RTL19	ROTUNDIFOLIA like	NA
Sapur.01G0091300.1	2037.146519	2.662257916	0.086819473	30.66429	1.70E-206	5.25E-205	cpm	0.80564685	3.11E-36	GO:0006622;GO:0008234;GO:0080019	ATG:SI3790.1	CERA;FARA;LG7	isopina acyl CoA reductase-related male sterility protein	fatty acyl CoA reductase
Sapur.01G0127100.1	2902.142843	1.488602167	0.047806451	30.47643	5.48E-206	1.66E-205	cpm	0.888692629	1.96E-57	GO:0005525	ATG:SI2130.1	ARA-L;ARA5;ATRAB11B;ATRA	RAS-like prot

Sapur.0006200800.1	201.0176445	-1.13925588	0.04497014	-25.334	1.35E-141	2.45E-140	cpm	-0.908818391	9.98E-61	GO:0009055		ATG2G3180.1	UCC1	urlacyamin 1	NA
Sapur.0006054700.1	80.25432884	-0.962944025	0.156795514	-25.2804	5.25E-141	9.51E-140	cpm	-0.822626947	7.63E-40						hypothetical protein
Sapur.0006142600.1	877.3351795	-1.462245793	0.057679705	-25.2386	1.94E-140	3.50E-139	cpm	0.845124792	5.66E-42			ATG4G10810.1			hypothetical protein
Sapur.0006059400.1	70.9538533	-0.842041309	0.120751351	-25.1926	4.83E-140	8.68E-139	cpm	-0.822802004	7.12E-40			ATG5G7123.1			NA
Sapur.0006127900.1	1009.346021	1.519364011	0.060362647	25.1706	8.41E-140	1.51E-138	cpm	0.849897037	1.38E-45	GO:0016747,GO:0008610,GO:0016020,GO:0006633	KCS12	ATG2B6301.1		3-ketoacyl-CoA synthase 12	3-ketoacyl-CoA synthase
Sapur.0006200900.1	1233.701157	0.741985637	0.029500096	25.15197	1.34E-139	2.40E-138	cpm	0.865168449	2.91E-49	GO:0005525		ATG4G17130.1	AT-RAB2,ATRAB-B18,ATRA1	RAB GTPase homolog B1C	small GTPase family Rab protein
Sapur.0013128100.1	226.904524	1.461838312	0.058198479	25.11815	3.15E-139	5.61E-138	cpm	0.849896498	8.25E-45						NA
Sapur.0006077700.1	20.12644009	4.701894989	0.188422227	25.109	3.97E-139	7.05E-138	cpm	0.772816855	2.57E-32			ATG4G6120.1	CDCP1,LE11	Cytotrichrome beta-synthase (CBS) family protein	CBS-pair ACT-assoc protein, putative
Sapur.0105012700.1	171.6870718	-1.912883364	0.116016868	-25.10487	4.40E-139	7.81E-138	cpm	0.681119559	9.66E-23			ATG1B9980.1		ARM-repeat superfamily protein	armadillo/beta-catenin-like repeat protein
Sapur.0006076000.1	304.1852537	1.347188729	0.054126488	25.06128	5.37E-139	9.53E-138	cpm	0.9129266	1.05E-55			ATG2G6130.1			hypothetical protein
Sapur.0013146900.1	415.9481147	1.471009905	0.058732962	25.04573	1.94E-138	3.42E-137	cpm	0.8305384	6.41E-43			ATG2G6920.1		Ubiquitin-associated/translation elongation factor EF1B protein	UBA/TS-N domain protein
Sapur.0006208300.1	81.56012221	-0.962964654	0.152995654	-25.02397	1.16E-138	1.96E-137	cpm	0.821330331	1.29E-39	GO:0006355,GO:0003677	BLH6,PNF	ATG2T9960.1	BLH6,PNF	BELL-like homeodomain 8	BELL homeobox protein, putative
Sapur.0006059800.1	557.8833625	1.485180213	0.059383246	25.01009	4.75E-138	8.34E-137	cpm	0.822795873	7.13E-40	GO:0005515,GO:0006468,GO:0004672		ATG2J7530.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.0005269400.1	101.8193074	1.450661246	0.058284	25.00062	9.44E-138	8.47E-137	cpm	0.845643116	5.43E-44			ATG4G1840.1	GU/T1	Exostosin family protein 2	beta-1%2C4-xylosyltransferase IRX10, putative
Sapur.0105001700.1	160.1288232	3.327054346	0.133124753	24.992	7.47E-138	1.31E-136	cpm	0.762133646	4.53E-31			ATG4G1290.1		ChaC-like family protein	cation transporter ChaC
Sapur.0006200900.1	33.54554842	2.481435563	0.099497152	24.94182	1.32E-137	2.32E-136	cpm	0.823182927	6.57E-40						NA
Sapur.0010680300.1	40.3922266	1.426037328	0.137406551	24.93385	3.20E-137	5.57E-136	cpm	0.73064162	1.92E-25			ATG5G6005.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant hydroxyproline-rich glycoprotein, putative
Sapur.0006116300.1	744.9375797	1.404275792	0.056654155	24.78681	1.24E-135	2.14E-134	cpm	0.84891117	8.97E-45			ATG6G8370.1		NC domain-containing protein/ankyrin	lecithin retinol acyltransferase
Sapur.0105057800.1	20.08024131	2.750186522	0.112217351	24.76258	1.25E-135	2.17E-134	cpm	0.772816855	2.57E-32	GO:0046881,GO:0003677	AGL62	ATG6H6451.1	AGL62	AGAMOUS-like 62	MADS-box protein AGL75, putative
Sapur.0005189400.1	620.2725018	1.017867222	0.04109299	24.76065	1.89E-135	3.25E-134	cpm	0.887109834	6.49E-54			ATG7G2150.1		Sec14p-like phosphatidylinositol transfer family protein	Sec.4-like phosphatidylinositol transfer protein
Sapur.0006200300.1	1896.907561	2.042164688	0.082494188	-24.7648	2.15E-135	3.67E-134	cpm	-0.851391192	1.75E-49	GO:0006334,GO:0005634,GO:0003677,GO:0000786		ATG7G6620.1		winged-helix DNA-binding transcription factor family protein	histone H1 subtype 5
Sapur.0013121200.1	4533.823197	1.057591015	0.044731782	24.75083	4.99E-135	8.51E-134	cpm	0.880648846	7.51E-52	GO:0055114,GO:0016627,GO:0003995,GO:0006635,GO:0005777,GO:0003997		ATG8G2360.1	ACX3,ACTACX3	acyl-CoA oxidase 3	acyl-coenzyme A oxidase
Sapur.0006200100.1	1110.617602	1.557488954	0.093036569	24.72888	5.10E-135	8.71E-134	cpm	0.867945552	5.90E-49	GO:0005515		ATG9G2440.1		Ubiquitin system component Cue protein	ubiquitin system component CUE protein, putative
Sapur.0107700.1	429.1345105	1.103806669	0.085152476	24.70635	9.14E-135	1.56E-133	cpm	0.836827801	2.13E-42	GO:0005515,GO:0006468,GO:0004672		ATG9G4840.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.0006200600.1	28.39719436	2.058855932	0.083421302	24.70504	9.44E-135	1.61E-133	cpm	0.824053616	1.14E-40	GO:0005515		ATG9G5630.1	BAL,BAP2	BON association protein 2	C2 domain protein
Sapur.0002417500.1	26.33882835	-2.287200167	0.177668285	-24.68614	1.51E-134	2.58E-133	cpm	-0.74800158	1.78E-28	GO:0006396,GO:0006325,GO:0003723		ATG4G15417.1	ATRT1,ILRT1L1	RNAse III-like 1	endoribonuclease dicer-like protein
Sapur.0006208800.1	20.37864985	3.432302382	0.139088517	24.67567	1.95E-134	3.33E-133	cpm	0.74624276	3.44E-29	GO:0004857		ATG4G6220.1	ATC,YVH2,CYVH2	cell wall / vacuolar inhibitor of fructosidase 2	plant invertase/pectin methylesterase inhibitor protein
Sapur.0105118300.1	1829.291915	1.655806106	0.067231366	24.63413	5.45E-134	9.23E-133	cpm	0.831850027	1.77E-41	GO:0016491,GO:0005686,GO:0016491		ATG4G7820.1	EDA28,MER23	FAD binding domain-containing protein	reticuline oxidase, putative
Sapur.0106220400.1	447.9840082	1.701193668	0.069427753	24.62371	5.64E-134	9.54E-133	cpm	0.847032671	2.17E-44	GO:0008270		ATG5E6930.1		DHHC-type zinc finger family protein	zinc finger protein, putative
Sapur.0105178300.1	340.3038166	1.23899999	0.0945383	24.61078	7.57E-134	1.28E-132	cpm	0.77182073	2.70E-32						NA
Sapur.0156005400.1	266.5016253	1.125642426	0.045796266	24.57935	2.10E-133	3.53E-132	cpm	0.85279272	1.41E-45			ATG4G7940.1		DNA heat shock family protein	heat-shock protein, putative
Sapur.0130351300.1	8.38018404	2.375287681	0.25577565	-24.5344	2.19E-133	3.68E-132	cpm	-0.81139191	1.75E-39	GO:0009733		ATG4G7120.1		SAUR-like responsive protein family	NA
Sapur.0156007700.1	21.93968863	-2.461702161	0.08756565	-24.5093	1.18E-132	1.97E-131	cpm	-0.85891541	6.59E-47			ATG6G6190.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	NA
Sapur.0105402000.1	448.9170269	2.939481611	0.120001957	24.49527	1.66E-132	2.78E-131	cpm	0.711880661	1.88E-25			ATG6G6620.1		Protein of unknown function (DUF607)	transcription factor, putative
Sapur.0108260300.1	70.15598184	0.598343535	0.192135467	24.47711	2.59E-132	4.32E-131	cpm	0.621888808	3.55E-18	GO:0005509		ATG6G5060.1		calcium-binding EF hand family protein	NA
Sapur.0106284800.1	1153.068679	1.151166067	0.046533395	24.47487	2.96E-132	4.93E-131	cpm	0.851391192	1.75E-49	GO:0043191,GO:0016020		ATG6G4180.1		Synaptotagmin C2 domain family protein	synaptotagmin family protein
Sapur.0105043900.1	9.962617653	6.253801764	0.255614957	24.46583	3.41E-132	5.68E-131	cpm	0.82642885	1.67E-40			ATG7G2180.1		Zinc finger protein CAF1 family protein	zinc finger protein CAF1, putative
Sapur.0105239800.1	626.7904233	0.807083522	0.033099686	24.39913	1.75E-131	2.89E-130	cpm	0.86639369	1.32E-48	GO:0055114,GO:0016491		ATG7G6650.2		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase
Sapur.0105084300.1	509.7601014	1.362756168	0.080435519	24.38614	1.88E-131	3.10E-130	cpm	0.827634188	6.48E-40			ATG4G5130.1		Terpene synthase family, metal binding domain protein	O-linked N-acetylglucosamine transferase, ugt protein%2C putative
Sapur.0105132600.1	1895.367231	-1.1228373	0.046055338	-24.3704	3.52E-131	5.81E-130	cpm	-0.891492317	1.75E-55	GO:0006206,GO:0006168	PGK1	ATG2T8B0.1	PGK1	phosphoglycerate kinase 1	phosphoglycerate kinase
Sapur.0105000900.1	422.6176156	1.168802164	0.05411639	24.35606	4.45E-131	7.68E-130	cpm	0.83201791	1.66E-41			ATG3G1520.1		Erythronate-4-phosphate dehydrogenase family protein	2-hydroxycid dehydrogenase, putative
Sapur.0108208800.1	275.7595165	1.689001141	0.069434825	24.33795	7.78E-131	1.28E-129	cpm	0.833856442	1.24E-42	GO:0016020,GO:0006970		ATG3G9130.1	ATGLR2,B,GLR2.B	glutamate receptor 2.8	glutamate receptor
Sapur.0105278700.1	201.9648314	-2.258238423	0.091662473	-24.3176	1.28E-130	2.20E-129	cpm	-0.872532624	7.05E-42	GO:0006414,GO:0005525,GO:0048530,GO:0008312		ATG3G9340.1	SAC1C,PSR14,FIC,SRP54C7	phosphoinositide conversion particle 54 kDa subunit	NA
Sapur.0146131100.1	574.21958	0.977597501	0.040152418	24.28668	2.71E-130	4.44E-129	cpm	0.853882423	1.24E-42			ATG4G9660.1		Protein of unknown function (DUF3664)	B2/B7-interaction factor 63-e04, putative
Sapur.0105000200.1	202.8218744	-1.442287104	0.059582663	-24.2065	1.90E-129	3.08E-128	cpm	-0.886322745	1.08E-53	GO:0005089	HCT	ATG4G9220.1	ATROPGEF14,ROPGEF14	RHO guanyl nucleotide exchange factor family protein	Rop guanine nucleotide exchange factor, putative
Sapur.0010276100.1	206.7768088	-0.996698825	0.041179387	-24.2038	2.03E-129	3.29E-128	cpm	-0.90063187	1.64E-58			ATG4G8150.1		alpha/beta-Hydrolases superfamily protein	alpha/beta hydrolase family protein
Sapur.0006200200.1	45.74909029	2.138148326	0.090143273	24.19402	2.57E-129	4.16E-128	cpm	0.83836475	8.00E-43	GO:0005515		ATG4G6510.1		F-box family protein	F-box protein
Sapur.0013113300.1	78.05208153	2.455005663	0.105190048	24.16581	5.09E-129	8.23E-128	cpm	0.783657124	1.36E-33						hypothetical protein
Sapur.0005102200.1	1008.931095	1.208148889	0.050048959	24.1389	9.77E-129	1.57E-127	cpm	0.879273753	8.61E-52	GO:0008121,GO:0006122		ATG3S1520.1		Ubiquinol-cytochrome C reductase hinge protein	cytochrome B-c1 complex subunit 6
Sapur.0196028800.1	115.24719	1.085464849	0.086402088	-24.1366	1.03E-128	1.68E-127	cpm	-0.88787799	9.04E-54						transmembrane protein, putative
Sapur.0146204800.1	1283.677693	0.977771561	0.040552058	24.11152	1.89E-128	3.03E-127	cpm	0.845169614	2.44E-44	GO:0008138,GO:0004708		ATG3S6680.1		Phosphotyrosine protein phosphatases superfamily protein	tyrosine phosphatase, putative
Sapur.0105090000.1	717.5006916	1.167316468	0.043728834	24.09475	2.84E-128	4.52E-127	cpm	0.81200705	4.61E-38	GO:0005515,GO:0005515	RHA2A	ATG3S1020.1	RHA2A	RING-H2 finger A2A	RING finger protein
Sapur.0105196100.1	18.80599004	2.907317244	0.120688832	24.09003	3.17E-128	5.06E-127	cpm	0.802950898	1.17E-36	GO:0008270,GO:0005515	NIP2	ATG1T7300.1	NIP2	NLP interacting protein 2	NA
Sapur.0006205100.1	581.1086473	1.275287344	0.056605556	24.07641	4.42E-128	7.03E-127	cpm	0.84853546	5.92E-44			ATG7H5000.1		NC domain-containing protein-related	lecithin retinol acyltransferase
Sapur.0105056800.1	1056.467979	1.307165643	0.058004303	24.07357	4.73E-128	7.53E-127	cpm	0.831732026	1.88E-41			ATG7J7020.1		Ribonuclease inhibitor	F-box protein
Sapur.0005138600.1	920.4473021	1.150618227	0.051336139	24.06147	1.12E-127	1.64E-126	cpm	0.873262622	1.26E-50	GO:0005085,GO:0005741	ATVDACK1,VDAC4	ATG7M8610.1	ATVDACK1,VDAC4	voltage-dependent anion channel 4	voltage-dependent anion-selective channel protein, putative
Sapur.0042037700.1	1895.967907	1.473026412	0.061274304	24.03995	1.06E-127	1.69E-126	cpm	0.826450913	1.65E-40	GO:0016788		ATG4G9510.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.0106240800.1	1316.747544	0.968165011	0.040315761	24.00594	2.41E-127	3.81E-126	cpm	0.84094846	3.47E-43			ATG7G1100.1		Tubulin binding cofactor C domain-containing protein	tubulin-binding cofactor C
Sapur.0105026100.1	2545.248816	0.985461946	0.070785814	-24.0051	2.46E-127	3.88E-126	cpm	-0.875656263	1.36E-51	GO:0016747	HCT	ATG7G6920.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	NA
Sapur.0106208800.1	28.22403924	1.830402154	0.076295466	23.99209	3.36E-127	5.30E-126	cpm	0.863512216	6.16E-48	GO:0005515		ATG7G8480.2		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.0005139600.1	19.95084115	2.320202209	0.097107488	23.99103	3.45E-127	5.43E-126	cpm	0.610500319	2.06E-17	GO:0055114		ATG7G9150.1		Ferredoxin-nitrite reductase family protein	peroxidase, putative
Sapur.0002649800.1	348.8807514	0.940375429	0.039339251	23.9729	5.31E-127	8.38E-126	cpm	0.857619026	2.18E-46	GO:0005525	ATRABG3A,RABG3A	ATG8G2730.1	ATRABG3A,RABG3A	RAB GTPase homologs G3A	Rab-related GTPase family protein
Sapur.0105000300.1	468.3260993	1.116549322	0.046416868	23.97276	5.66E-127	8.92E-126	cpm	0.877467671	1.57E-53	GO:0005789		ATG8G7120.1		Plant VAMP family protein	vesicle-associated membrane protein, putative
Sapur.0096121300.1	39.8428812	5.119079821	0.214960569	23.82007	2.07E-125	3.21E-124	cpm	0.687919657	2.46E-23	GO:0016021,GO:0006476,GO:0030247,GO:0006468,GO:0005524,GO:0004672	WAK2	ATG2J7170.1	WAK2	wall-associated kinase 2	tyrosine kinase domain protein
Sapur.0016288800.1	15.77870264	3.302802303	0.139267489	23.80241	3.15E-125	4.87E-124	cpm	0.799419565	4.80E-36	GO:0006813,GO:0005515	AGAMOUS-like 6	ATG4H4630.1	AGAMOUS-like 6	AGAMOUS-like 6	NA
Sapur.0105065400.1	835.9316857	0.674897097	0.070134162	23.80021	3.32E-125	5.13E-124	cpm	0.823792791	1.82E-40	GO:0055114,GO:0020037,GO:0016705,GO:0005506	CYP714A1	ATG4H2310.1	CYP714A1	cytochrome P450, family 714, subfamily A, polypeptide 1	cytochrome P450 family protein
Sapur.0105145300.1	275.0274693	1.104899949	0.046557788	23.71384	1.61E-124	2.47E-123	cpm	0.84603834	4.46E-44			ATG4G6690.1			ubiquitin and WLM domain protein
Sapur.0106135100.1	45.62692838	1.867563057	0.163034472	23.72236	2.12E-124	3.24E-123	cpm	0.645725541	1.77E-19	GO:0015743		ATG4G8440.1		Aluminum activated malate transporter family protein	aluminum activated malate transporter
Sapur.0006090600.1	379.7714154	0.771688816	0.032602066	23.66987	7.37E-124	1.12E-122	cpm	0.873841162	1.98E-50			ATG4G8480.1			NA
Sapur.0106257900.1	248.5583337	1.363184688	0.057869609	23.66355	8.56E-124	1.30E-122	cpm	0.814719141	4.13E-38			ATG5G4040.1		Protein of unknown function (DUF616)	DUF616 family protein
Sapur.0105103400.1	33.03730119	0.017604586	0.35425721	23.66354	8.56E-124	1.30E-122	cpm	0.559287764	2.06E-16	GO:0005515		ATG5H430.1	ATGGTU7,GGT25,GGTU7	glutathione S-transferase tau 7	tau class glutathione transferase GGTU27
Sapur.0106204100.1	10.4522864	3.781882529	0.158356254	23.64958	1.11E-123	1.81E-122	cpm	0.67413956	1.78E-22	GO:0016844,GO:0009058	SI3	ATG7H5000.1	SI3	strictosidine synthase 3	NA
Sapur.0105091500.1	180.413933	2.471592715	0.104564174	23.64216	1.42E-123	2.15E-122	cpm	0.782135942	1.17E-32			ATG7G5030.1		Copper transport protein family	hypothetical protein
Sapur.0105000400.1	988.7645368	0.996361898	0.042157418	23.62602	1.71E-123	2.58E-122	cpm	0.838377738	7.55E-42	GO:0016021,GO:0004252,GO:0006508		ATG7R9250.1		Rhomboid family protein	rhomboid family protein
Sapur.0002619200.1	1797.490119	1.062209661	0.044989121	23.61037	3.02E-123	4.54E-122	cpm	0.86061869	2.78E-47			ATG7G3130.1	ATCSLC06,ATCSLC5,CSLC06	Cellulose-synthase-like C6	cellulose synthase-like C2, glycosyltransferase family 2 protein
Sapur.0106208800.1	287.0887115	1.095422969	0.046415629	23.60463	3.29E-123	4.96E-122	cpm	0.85265149	2.05E-45			ATG7G4180.1		RD domain containing protein	RD domain protein, putative
Sapur.0106266700.1	4275.321878	1.283611439	0.054762222	23.60612	3.34E-123	5.02E-122	cpm	0.855223236	4.81E-45	GO:0006872,GO:0000166		ATG8H9680.1	AHA1,HA1,OST2,PMA	H(+)-ATPase 1	plasma membrane H+-ATPase
Sapur.0105037200.1	30.28849515	6.153302635	0.176188259	23.57314	7.27E-123	1.09E-121	cpm	0.68223476	7.75E-23			ATG9G2490.1		Seed maturation protein	NA
Sapur.0105042400.1	56.39045276	-2.042929486	0.086896536	-23.5149	1.16E-122	1.75E-121	cpm	-0.82416847	1.40E-41			ATG9G4610.2		Staphylococcal nuclease homologue	Ca(2+)-dependent nuclease
Sapur.0108295100.1	70.77988714	9.903635457	0.408615129	23.50389	7.79E-122	5.68E-121	cpm	0.6868153	3.65E-17	GO:0005509		ATG9G2060.1		calcium-binding EF hand family protein	NA
Sapur.0106237400.1	27.90691617	-2.405288914	0.102634135	-23.4356	1.85E-121	2.75E-120	cpm	-0.80917077	1.37E-37			ATG4G6220.1			hypothetical protein
Sapur.0106208300.1	1586.496717	1.212760753	0.051793553	23.41586	2.95E-121	4.36E-120	cpm	0.833743414	8.00E-42	GO:0005524		ATG4G9510.1	NSF	AAA-type ATPase family protein	vesicle-fusing ATPase
Sapur.0105135700.1	18.50716004	2.320156661	0.099217365	23.40877	3.48E-121	5.15E-120	cpm	0.814936997	1.61E-38			ATG7T7710.1			NA
Sapur.0002602700.1	347.6276944	-0.055986703	0.041481912	-23.4047	3.82E-121	5.65E-120	cpm	-0.862922048	8.40E-48	GO:0005515		ATG4G7730.1		Calcium-dependent lipid-binding (CaLB domain) family protein	Arf GTPase activator, putative
Sapur.0105000100.1	7779.449779	1.091892883	0.046678187	23.36055	1.16E-119	1.87E-118	cpm	0.852284021	1.94E-45	GO:0016491,GO:0003824	AW101,VEP1	ATG4G2620.1	AW101,VEP1	NADPH-dependent farnesal reductase family protein	progesterone 5 beta-reductase, putative
Sapur.0156017800.1	531.6113342	1.755427936	0.075158879	23.35623	1.19E-119	1.76E-118	cpm	0.826219933	1.81E-40			ATG4G7940.1	ATMTM1,MTM1	manganese tracking factor for mitochondrial SOD2	carrier CGI protein
Sapur.0106202300.1	355.3328893	1.152180667	0.052885217	-23.3206	2.22E-119	3.27E-118	cpm	-0.873654551	4.04E-50	GO:0006457		ATG4G8170.1		PEBP-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase
Sapur.0105094500.1	118.2819615	2.359264987	0.101219933	23.30992	3.52E-120	5.16E-119	cpm	0.765628898	1.67E-31			ATG4G8480.1			transmembrane protein, putative
Sapur.0096011400.1	33.73215561	5.235484518	0.224828994	23.28652	6.07E-120	8.88E-119	cpm	0.675278085	3.04E-22	GO:0017261		ATG4G8440.1		Aluminum activated malate transporter family protein	aluminum activated malate transporter
Sapur.0106400.1	29.47668801	4.159341288	0.179120853	-23.2149	1.22E-119	4.68E-118	cpm	-0.816851123	2.00E-37	GO:0005975		ATG4G9200.1		Galactose mutarotase-like superfamily protein	NA
Sapur.0106170600.1	1397.816191	0.781799144	0.033707627	23.19216	5.46E-119	7.92E-118	cpm	0.84837758	9.26E-44			ATG4G5120.1		CBS domain-containing protein with a domain of unknown function (DUF21)	metal transporter CNNM4
Sapur.0105180600.1	1337.723262	-1.08588663	0.04682971	-23.1866	6.22E-119	9.01E-118	cpm	-0.86565461	4.88E-48	GO:0009941,GO:0009523,GO:0005509	PSBQ,PSBQ-2,PSII-Q	ATG5G1180.1	PSBQ,PSBQ-2,PSII-Q	photosystem II subunit Q-2	oxygen-evolving enhancer protein
Sapur.0106192500.1	731.0822882	0.964914547	0.040754752	23.18538	6.39E-119	9.26E-118	cpm	0.848556677	1.06E-44	GO:0006032,GO:0016021,GO:0006621		ATG4G8790.1		ER lumen protein retaining receptor family protein	ER lumen protein retaining receptor, putative
Sapur.0105128800.1	23.88925016	7.539121254	0.325318828	23.17458	7.22E-119	1.04E-117	cpm	0.8009169	1.46E-19	GO:0005509	ARA22,RR22	ATG4G2860.1	ARA22,RR22	response regulator protein	response regulator protein
Sapur.0105301300.1	288.8890739	-3.334667378	0.157469818	-23.1548	1.30E-118	1.88E-117	cpm	-0.89037908	7.80E-55			ATG4G2630.1	CCB3	cofactor for assembly of complex C	transmembrane protein, putative
Sapur.0105082000.1	22.88076437	2.782682266	0.136225929	23.14526	1.62E-118	2.32E-117	cpm	0.66847635	2.22E-22	GO:0055114,GO:0020037,GO:0016705,GO:0005506		ATG4G7370.1	CYP81D8	cytochrome P450, family 81, subfamily D, polypeptide 8	cytochrome P450 family protein
Sapur.0105058200.1	2932.409444	1.450843032	0.061906855	23.1128	3.44E-118	4.92E-117	cpm	0.76697838	1.13E-31			ATG4G1250.1	NYC1	NADP(+)-binding Rossmann-fold superfamily protein	chlorophyll(ide) 8 reductase
Sapur.0105205500.1	438.5152628	1.506208416	0.065185154	23.1088	3.62E-118	5.45E-117	cpm	0.864704628	3.64E-48	GO:0016779,GO:0009058	APL2	ATG4G7680.1	APL2	ADP/ATP-dependent phosphofructokinase family protein	glucose 1-phosphate adenylyltransferase large protein
Sapur.0105205100.1	456.6648344	-1.274754861	0.055185122	-23.1012	4.50E-118	6.42E-117	cpm	-0.876609159	1.28E-51	GO:0009886,GO:0009709,GO:0009654,GO:0005923,GO:0005509		ATG7E4550.1		Photosystem II reaction center PsbP family protein	PsbP domain protein
Sapur.0102100.1	37.22040057	4.30654124	0.186322734	23.07784	7.73E-118	1.10E-116	cpm	0.529272384	1.01E-12	GO:0055114,GO:0020037,GO:0006979,GO:0004601		ATG4G6070.1		Peroxidase superfamily protein	NA
Sapur.0130520800.1	87.93480177	1.750806274	0.076119942	23.06815	9.67E-118	1.37E-116	cpm	0.80760173	3.54E-41	GO:0005509,GO:0005506,GO:0004672	RLK1	ATG4G8060.1	RLK1	receptor-like kinase 1	Serine/Threonine kinase domain protein
Sapur.0105134600.1	371.0879984	1.031771929	0.044704389	23.06104	1.14E-117	1.61E-116	cpm	0.843806434	9.57E-44			ATG4G8460.2		Protein of unknown function (DUF1644)	DUF1644 family protein
Sapur.0002594100.1	581.7943291	1.070092621	0.046438818	23.0403	1.21E-117	2.41E-116	cpm	0.853181515	1.66E-42	GO:0016887,GO:0006355,GO:0003677,GO:0003677	SIG1,SIGC	ATG3J3520.1	SIG1,SIGC	RNA polymerase sigma factor	RNA polymerase sigma factor
Sapur.0106131200.1	50.14302163	1.664515503	0.072278888	23.029	2.39E-117	3.36E-116	cpm	0.862308866	1.16E-47	GO:0006872	DRIP2	ATG3G5580.1	DRIP2	DRB2EA-interacting protein 2	E3 ubiquitin protein ligase DRIP2, putative
Sapur.0105284800.1	657.6442217	-1.11829872	0.048475852	-23.029	2.39E-117	3.36E-116	cpm	-0.890072009	5.50E-55	GO:0004554,GO:0015035,GO:0006662	ATHM2	ATG3G3120.1	ATHM2	Thioredoxin superfamily protein	thioredoxin M-type protein
Sapur.0106216200.1	406.264078	1.065558656	0.045482918	23.0103	3.68E-117	5.16E-116	cpm	0.83815414	1.39E-42	GO:0007034	VPS24.1	ATG3G2950.1	VPS24.1	SNF7 family protein	charged multivesicular body protein
Sapur.0106178800.1	1138.91539	1.173005554	0.051008554	22.96637	5.07E-117	7.09E-116	cpm	0.870634298	1.01E-50	GO:0006631,GO:0016020,GO:0003700	FDH,ICS10	ATG3G2620.1	FDH,ICS10	3-ketoacyl-CoA synthase 10	3-ketoacyl-CoA synthase
Sapur.0106149200.1	41.21510068	-0.075361635	0.090289143	-22.9857	6.48E-117	9.06E-116	cpm	-0.718512028	1.30E-26	GO:0005515,GO:0006468,GO:0004672		ATG2J7060.1		Leucine-rich repeat protein kinase family protein	receptor kinase, putative
Sapur.0106190900.1	451.3517924	-0.938982185	0.040576588	-22.9724	8.80E-117	1.23E-115	cpm	-0.858992218	3.83E-47	GO:0006415,GO:0003747,GO:0016149,GO:0005737	APG3	ATG2G9310.1	APG3	Peptide chain release factor 1	peptide chain release factor 1
Sapur.0105150500.1	59.71606577	-2.252888886	0.098098969	-22.9604	9.16E-117	1.28E-115	cpm	-0.850464034	4.47E-45	GO:0016853,GO:0005737		ATG2B7720.1		Cyclophilin like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase, putative
Sapur.0006097300.1	2768.351188	0.911330651	0.039703257	22.95156	1.42E-116	1.98E-115	cpm	0.84345197	1.12E-43			ATG3D0510.1	OMR1	L-O-methylthreonine resistant 1	threonine dehydratase biosynthetic protein
Sapur.0006102500.1	848.0397917	1.284773384	0.056152575	22.9033	2.14E-116	2.98E-115	cpm	-0.842547564	2.60E-43	GO:0016887,GO:0003001		ATG3E6950.1		Heavy metal transporter/detoxifier superfamily protein	heavy metal-associated domain protein
Sapur.0105209400.1	125.4248115	-1.496461759	0.065305277	-22.9153	2.27E-116	4.54E-115	cpm	-0.885939316	1.27E-54	GO:0019898,GO:0015979,GO:0009654,GO:0005923,GO:0005509		ATG2B6050.1		Photosystem II reaction center PsbP family protein	PsbP domain protein
Sapur.0105130200.1	236.7319316	1.675176279	0.073363314	22.8547	2.96E-115	1.78E-114	cpm	0.77008404	4.52E-32			ATG2B7780.1	

Sapur.0562346500.1	9.71559726	2.775857969	0.1308563	21.24549	3.63E-100	4.54E-99	cpm	0.823161893	7.66E-40	GO:0008270;GO:0005515	MSTG35490.1	RING/U-box superfamily protein	HE1ID
Sapur.001G155400.1	11.55476252	2.921858322	0.137550005	21.24215	3.90E-100	4.44E-99	cpm	0.796926804	1.26E-35	GO:0005515	MSTG15670.1	Galactose oxidase/kelch repeat superfamily protein	kelch repeat F-box protein
Sapur.0132G074400.1	277.8842215	5.468970555	-0.126897055	-21.2349	4.55E-100	5.18E-99	cpm	0.888706262	5.26E-40	GO:0005515	MSTG46960.1	purple acid phosphatase 24	NA
Sapur.0061G163000.1	393.5141765	1.102638228	0.051938047	21.22987	5.06E-100	5.76E-99	cpm	0.80079032	2.48E-36	GO:0035434;GO:0016021;GO:0005375	MSTG20650.1	copper transporter 5	copper transporter
Sapur.0162G209300.1	37.54734428	3.703155634	0.080237872	21.2263	5.46E-100	6.21E-99	cpm	0.84850236	1.31E-44		MSTG47580.1	Pentatricopeptide repeat (PPR) superfamily protein	NA
Sapur.001G419000.1	19.25235025	2.759711201	0.130415871	21.16085	2.19E-99	2.48E-98	cpm	0.724615111	4.73E-27	GO:0055114;GO:0016491	MSTG15532.1	AT3G03K1;GA3OX1;GA4	gibberellin 3-oxidase 1
Sapur.0061G185100.1	630.517684	0.871787588	0.04139931	-21.1602	2.23E-99	2.52E-98	cpm	-0.868675016	3.82E-49	GO:0003676	MSTG23380.1	chloroplast RNA-binding protein 43	RNA recognition motif (RRM) superfamily protein
Sapur.0110G127001.1	264.8293019	0.761189766	0.036022609	-21.15749	2.35E-99	2.67E-98	cpm	0.844892146	5.72E-44		MSTG22320.2		hypothetical protein
Sapur.0064G127000.1	1264.49641	0.599373072	0.028322282	-21.1555	2.45E-99	2.78E-98	cpm	-0.18230831	1.16E-47	GO:0008152;GO:0004807	MSTG21170.1	TOTR,TIM	triosephosphate isomerase
Sapur.0036G141500.1	3120.013906	0.359966359	0.017179737	-21.1463	2.86E-99	3.24E-98	cpm	0.835737088	1.68E-42	GO:0016020	MSTG16180.2	Serine- domain containing serine and sphingolipid biosynthesis protein	TMS membrane protein/tumor differentially protein
Sapur.0061G152100.1	1672.424673	1.405595232	0.066329081	21.12753	4.44E-99	5.01E-98	cpm	0.843854547	9.34E-44	GO:0005975;GO:0004553	MSTG27500.2	Glycosyl hydrolase superfamily protein	glucan endo-1%2C3-beta-glucosidase
Sapur.0110G207300.1	1490.682754	0.705145144	0.033425565	-21.1346	4.84E-99	5.46E-98	cpm	0.841102566	1.15E-43		MSTG27000.1	Protein of unknown function (DUF1664)	B2IP transcription factor
Sapur.0072G090900.1	139.8338672	1.108255583	0.052481121	-21.1168	5.57E-99	6.27E-98	cpm	-0.85817036	9.70E-47	GO:0005635;GO:0003713;GO:0003677	MSTG09250.1	KIWI	nuclear-localizing transcriptional regulator
Sapur.0072G296600.1	877.4417023	2.183238662	0.103396124	21.05302	1.24E-98	1.39E-97	cpm	0.742736235	5.11E-29		MSTG27630.1	CMU41	calmodulin-like 41
Sapur.0072G090000.1	409.9250605	0.855607453	0.040588435	-21.0784	1.25E-98	1.40E-97	cpm	-0.871227673	9.25E-50		MSTG34480.1		
Sapur.0061G173000.1	735.8336811	0.855819375	0.040618371	-21.0532	1.87E-98	2.10E-97	cpm	0.856809679	2.98E-46		MSTG37440.2	Heat shock protein Dnaj 4h, terminal with domain of unknown function (DUF3977)	chaperone protein Dnaj 4h
Sapur.0062G076100.1	68.9257661	1.680416316	0.079784476	21.06195	1.78E-98	1.99E-97	cpm	0.801276668	2.10E-36	GO:0008650	MSTG33990.1	Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.0161G138500.1	262.1538147	1.364965054	0.064650704	-21.0581	1.93E-98	2.15E-97	cpm	-0.785379477	3.77E-34	GO:0008270;GO:0005515	MSTG06240.1	XERICO	RING/U-box superfamily protein
Sapur.0035G035000.1	170.7782376	1.150625001	0.077245557	21.05756	1.95E-98	2.18E-97	cpm	0.763909087	1.46E-31	GO:0008274;GO:0006628	MSTG16645.1	AYPOX1,PDAT,PDAT1	phospholipid diacylglycerol acyltransferase
Sapur.0105G098100.1	534.5140123	1.331455877	0.062233139	21.0563	2.00E-98	2.24E-97	cpm	-0.796113294	1.24E-35		MSTG68630.1	alpha/beta-Hydrolases superfamily protein	carboxylesterase
Sapur.0075D042001.1	504.3375374	1.369884019	0.066317096	21.03889	2.85E-98	3.22E-97	cpm	-0.816978854	2.62E-38	GO:0006468;GO:0005634;GO:0004672	MSTG42630.1	Protein kinase superfamily protein	brassinosteroid insensitive 1-associated receptor kinase, putative
Sapur.0032G179600.1	1446.064606	0.896842803	0.042558947	21.02503	3.87E-98	4.31E-97	cpm	0.81372875	2.34E-38	GO:0016021;GO:0004190	MSTG43070.1	ATSPP5,SPP5,3	SIGNAL PEPTIDE PEPTIDASE-LIKE 3
Sapur.0162G209400.1	608.2119366	0.842924827	0.033617277	-21.0215	4.17E-98	4.64E-97	cpm	-0.863482731	3.46E-48	GO:0015031;GO:0005686	MSTG22440.1	HCF106	Sec-independent protein translocase tatA/E-like protein, putative
Sapur.0061G211000.1	16.27827362	4.285334976	0.203889194	21.01768	4.52E-98	5.03E-97	cpm	0.728737227	2.84E-27	GO:0002247;GO:0006468;GO:0005524;GO:0004672	MSTG21270.1	WAK2	wall-associated kinase 2
Sapur.0062G176000.1	42.01022756	3.656897227	0.174000149	20.95762	8.16E-97	8.56E-96	cpm	0.82406012	2.98E-40	GO:0016758;GO:0008152	MSTG49630.1	Cellulose synthase/transferase superfamily protein	UDP-glucosyltransferase family protein
Sapur.0082G171700.1	354.4240601	1.172061604	0.055840718	20.98901	8.26E-98	9.16E-97	cpm	-0.799939399	1.27E-36	GO:0006468;GO:0004672	MSTG14000.1	VIK	Vir1-interacting kinase
Sapur.0152G056400.1	123.0730185	1.055309536	0.050502487	20.97421	1.13E-97	1.25E-96	cpm	0.86447968	1.32E-48	GO:0016020;GO:0005509;GO:0004571	MSTG27520.1		Glycosyl hydrolase family 47 protein
Sapur.0132G087000.1	278.4944114	1.156367319	0.055605511	20.7349	1.68E-97	1.86E-96	cpm	0.765646091	1.66E-31		MSTG26320.1	Choline-phosphotransferase family protein	Choline-phosphotransferase family protein
Sapur.0106G091000.1	2541.039997	1.198857795	0.057264726	20.93526	2.55E-97	2.81E-96	cpm	0.80602334	3.94E-37	GO:0016020;GO:0015171;GO:0003333	MSTG38330.1	CAT2	cationic amino acid transporter 2
Sapur.0061G490001.1	154.6168942	1.152966001	0.055090455	20.93007	5.13E-97	5.85E-96	cpm	0.782176099	1.16E-33		MSTG36361.1		hypothetical protein
Sapur.0162G212000.1	127.3201008	1.510526689	0.072275629	20.90011	5.34E-97	5.86E-96	cpm	0.80666064	3.13E-37		MSTG40730.1	Domain of unknown function (DUF23)	NA
Sapur.0175D051900.1	271.8849158	1.553904794	0.051155666	20.88708	7.02E-97	7.68E-96	cpm	0.81377538	2.30E-38		MSTG25600.1		hypothetical protein
Sapur.0032G098800.1	57.13787621	-0.65372631	0.079251597	-20.8882	7.14E-97	7.82E-96	cpm	-0.84929181	3.20E-44		MSTG22530.1		hypothetical protein
Sapur.0061G184000.1	344.1680609	-0.676720858	0.032406475	-20.8823	7.56E-97	8.49E-96	cpm	-0.877618273	1.96E-51	GO:0004237	MSTG16881.1	Eukaryotic translation initiation factor 2B (eIF-2B) family protein	translation initiation factor eif-2B subunit alpha
Sapur.0032G033500.1	180.4555004	1.173029669	0.056407429	20.88075	8.01E-97	8.76E-96	cpm	0.773087476	5.58E-33		MSTG15180.1	PRAL1,F2,PRA7	PRA1 family protein
Sapur.0106G090600.1	11.53122047	3.139386006	0.160025151	20.88266	1.26E-96	1.38E-95	cpm	0.763805605	5.01E-34	GO:0005515	MSTG40462.2	XERICO	ZU-alpha protein ligase
Sapur.0081G274000.1	1776.164691	0.818862615	0.042469659	20.84378	1.74E-96	1.89E-95	cpm	0.81007968	9.30E-38	GO:0055114;GO:0010309	MSTG14710.2	ATARD2	RmlC-like cupins superfamily protein
Sapur.0064G205100.1	1213.199554	1.080257121	0.051835499	20.8401	1.87E-96	2.06E-95	cpm	0.796887874	9.54E-36		MSTG61100.1		disease resistance protein (TIR class), putative
Sapur.0061H484001.1	546.8611098	-1.3793076	0.066205807	-20.81684	2.12E-96	2.31E-95	cpm	0.81930608	1.14E-39	GO:0005975;GO:0004553	MSTG13130.1	Cellulase (glycosyl hydrolase family 5) protein	glycosyl hydrolase family 5 protein
Sapur.0041G122001.1	1406.361679	1.331182271	0.063941632	-20.8275	2.44E-96	2.65E-95	cpm	-0.809071069	2.80E-37	GO:0055114;GO:0051287;GO:0016616;GO:0008152	MSTG68010.1	ATHPRL1,HPR	hydroxypyruvate reductase
Sapur.0036H400001.1	24.5245682	4.275486566	0.209276424	20.80805	3.68E-96	3.97E-95	cpm	0.6227215	1.34E-20		MSTG20040.1		pectagalacturonase GH28
Sapur.0021G163000.1	114.0552772	-1.13455069	0.054524245	-20.8013	4.21E-96	4.56E-95	cpm	-0.84681297	2.40E-44	GO:0043565;GO:0006355;GO:0003700	MSTG34830.1	AtWRKY15,WEE24,WRKY35	WRKY DNA-binding protein 35
Sapur.0132G087200.1	11.46473723	3.580464591	0.175206758	20.78825	5.51E-96	5.98E-95	cpm	0.83545025	1.66E-39				NA
Sapur.0080G045700.1	235.1592078	0.250829119	0.2045838	20.76255	6.23E-96	6.73E-95	cpm	-0.73913257	1.95E-28	GO:0016746;GO:0008152	MSTG43120.1	ATGPAT5,GPAT5	glycerol-3-phosphate acyltransferase 5
Sapur.0032G140001.1	188.5742312	0.923830208	0.044475185	-20.7633	8.74E-96	9.45E-95	cpm	-0.824661164	1.7E-40		MSTG75240.1	HEMB1,HEM12	hemeobox protein 12
Sapur.0082G053000.1	2251.128118	1.132783311	0.054589719	-20.7661	8.77E-96	9.47E-95	cpm	0.86015914	1.51E-47	GO:0016020;GO:0009765	MSTG40100.1	LHCB4.3	light harvesting complex photosystem II
Sapur.0105G097700.1	130.3875831	1.190266109	0.058395286	-20.7639	9.32E-96	1.00E-94	cpm	0.876273408	1.98E-52	GO:0005515	MSTG29630.1		F-box protein
Sapur.0082G093600.1	38.01858648	2.110645521	0.101653037	-20.7613	9.68E-96	1.04E-94	cpm	0.819942956	2.19E-39		MSTG13245.1	DVL4,RTL17	RotD ribosyltransferase 17	DVL5
Sapur.0105G100000.1	1562.877657	0.647007523	0.031168019	-20.7587	1.02E-95	1.10E-94	cpm	0.851492504	2.52E-45	GO:0007264;GO:0005525	MSTG02680.1	AGAP1,ATSAR2,ATSAR4,ATSAR3,C.5	secretion-associated RAS super family 2	GTP-binding protein SAR1, putative
Sapur.0146G029900.1	26.68400885	-1.528541688	0.07361887	-20.7517	1.18E-95	1.27E-94	cpm	0.84607776	6.63E-44		MSTG17950.1			hypothetical protein
Sapur.0122G082000.1	632.801606	1.007632221	0.048562431	20.74667	1.37E-95	1.47E-94	cpm	0.811100408	6.22E-38	GO:0016887;GO:0005524;GO:0019138	MSTG10570.1	CLPD,ERD1,SAG15	Clp ATPase
Sapur.0071G028500.1	224.2287593	1.246066466	0.061050384	20.7385	1.56E-95	1.68E-94	cpm	0.831376285	2.88E-38		MSTG20461.1		hydroxyproline-rich glycoprotein family protein
Sapur.0050G077700.1	1309.610121	0.927059836	0.044706631	20.73745	1.58E-95	1.71E-94	cpm	0.831718355	1.88E-41		MSTG52290.1	PNC1	peroxisomal adenine nucleotide carrier 1
Sapur.0161G146000.1	1946.114924	0.931177168	0.058605511	-20.7349	1.68E-95	1.81E-94	cpm	0.835450357	1.68E-42		MSTG27090.1	rbuBase bisphosphate carboxylase small chain 1A	rbuBase bisphosphate carboxylase small chain
Sapur.0162G164800.1	842.7678258	0.750336447	0.036203554	-20.7255	2.04E-95	2.19E-94	cpm	-0.863626246	1.65E-47	GO:0003676	MSTG50520.1	CP31B	chloroplast RNA-binding protein 31B
Sapur.0062H086300.1	9.205806969	3.727308205	0.181313369	20.67525	3.67E-95	3.97E-94	cpm	-0.824661164	4.18E-37		MSTG49140.1	TBL4	TBD/CHOKE BINDING/CNCS-LIKE 4
Sapur.0051G191000.4	15.13614336	-2.928413356	0.141771128	-20.6559	8.64E-95	9.23E-94	cpm	-0.816665366	7.73E-39		MSTG25482.2	LOL1	lol one like 1
Sapur.0064G167000.1	194.0402745	-1.267184865	0.061307387	-20.6493	9.91E-95	1.06E-93	cpm	-0.574129628	1.81E-15	GO:0051085;GO:0016020;GO:0008810;GO:0005215	MSTG27810.1	ATNAT12,NAT12	nucleobase-ascorbate transporter 12
Sapur.0086G185305.1	545.4651244	0.918027405	0.042634744	-20.6123	1.44E-94	1.53E-93	cpm	0.835435063	3.90E-42	GO:0016020;GO:0008152;GO:0005102	MSTG31460.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.0032G097900.1	80.01051974	2.904681297	0.134838595	20.62088	1.78E-94	1.90E-93	cpm	0.623030171	4.08E-18	GO:0005509;GO:0030247;GO:0006468;GO:0005524;GO:0004672	MSTG12170.1	WAK2	wall-associated kinase 2
Sapur.0061G145001.1	473.8818873	0.752000215	0.036929544	-20.6029	1.92E-94	2.04E-93	cpm	-0.768929544	1.08E-31	GO:0005515;GO:0016020	MSTG20550.1	SFH7	sugar transporter protein 7
Sapur.0141G137500.1	88.4878875	0.960606048	0.047007232	20.61514	2.01E-94	2.13E-93	cpm	0.82231044	8.92E-40		MSTG35850.3	NO1	RPW8-interacting protein
Sapur.0086G000400.1	1165.841879	-0.564924206	0.027463938	-20.6149	2.02E-94	2.14E-93	cpm	-0.859546469	4.83E-47	GO:0055114;GO:0016491;GO:0016616;GO:0019752	MSTG27821.1	PMDH1	peroxisomal NAD-malate dehydrogenase 1
Sapur.0031G147300.1	2220.894304	1.044327741	0.050677479	20.60822	2.32E-94	2.46E-93	cpm	0.818637792	3.61E-39	GO:0055114;GO:0016491;GO:0045454	MSTG24170.2	ATGR1,GR1	glutathione-disulfide reductase
Sapur.0075D026001.1	171.8817844	0.872024162	0.042372154	20.6058	2.85E-94	3.02E-93	cpm	-0.812018184	2.80E-38		MSTG78965.1		glutathione transferase
Sapur.0125G145001.1	274.8195864	-2.240534267	0.060215769	-20.5881	2.96E-94	3.03E-93	cpm	-0.85559	5.54E-46	GO:0043565;GO:0006355;GO:0003700;GO:0003677	MSTG04470.1	ATHB-1,ATHB1,HAT5,HB-1,I	homeobox transfer factor gene 1
Sapur.0056G000100.1	78.31852168	1.139110376	0.05 5876	3.554	3.76E-94	3.84E-93	cpm	-0.835281474	4.86E-43		MSTG36170.2	ATHAP3B,HAP3B,NF-YC2	nuclear factor Y, subunit C2	nuclear transcription factor Y subunit C4
Sapur.0105G105100.1	98.81157995	-1.478600059	0.071832632	-20.584	3.82E-94	4.05E-93	cpm	-0.849802242	5.88E-45	GO:0016021	MSTG36100.1		Cytochrome b561/ferric reductase transmembrane protein family
Sapur.0105G197900.1	323.9512052	0.887338985	0.043133287	20.56735	5.18E-94	5.49E-93	cpm	0.822330227	8.92E-40		MSTG27320.2		alpha/beta-Hydrolases superfamily protein
Sapur.0075D052400.1	2005.132508	-0.883895056	0.05050871	-20.5439	8.73E-94	9.20E-93	cpm	-0.867836919	9.21E-49	GO:0055114;GO:0016491	MSTG00520.1	ATLPNR2,PNR2	ferredoxin-NADP reductase
Sapur.0105G190900.1	154.7601657	-1.344635751	0.065325538	-20.5308	1.40E-93	1.48E-92	cpm	-0.876123179	1.59E-51	GO:0003676	MSTG39950.3		RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.0161G146000.1	1946.114924	0.931177168	0.058605511	-20.7349	1.68E-93	1.81E-92	cpm	0.837665931	1.68E-39		MSTG04680.1		helicase 6 dehalogenase-like hydrolase
Sapur.0140G073300.1	90.79038417	1.840806336	0.089714139	20.51055	1.73E-93	1.82E-92	cpm	0.763665329	2.90E-31		MSTG16070.2	PDV2	plastid division2
Sapur.0086G000300.1	2321.239869	0.722708205	0.035265	-20.5126	1.75E-93	1.84E-92	cpm	0.863315663	7.41E-48	GO:0007264;GO:0005525	MSTG26080.1	AGAP1,ATSAR2,ATSAR4,ATSAR3,C.5	secretion-associated RAS super family 2	GTP-binding protein Sar1, putative
Sapur.0082H073000.1	183.3849961	-0.980261113	0.04780207	-20.5067	1.88E-93	1.97E-92	cpm	-0.845190934	5.08E-44		MSTG13380.1		Protein of unknown function (DUF1218)	fiber protein Fb34
Sapur.0032G000100.1	30.42544645	-2.357790264	0.116836277	-20.4949	2.36E-93	2.51E-92	cpm	-0.761378896	2.57E-31	GO:0005524;GO:0007165;GO:0005515	MSTG36930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.0082G089100.1	17.16066443	2.006060505	0.097041385	20.49145	2.57E-93	2.69E-92	cpm	-0.713038855	1.12E-25		MSTG25597.1		hypothetical protein
Sapur.0161G235200.1	387.2559861	-0.658751354	0.032156022	-20.4884	2.73E-93	2.86E-92	cpm	-0.853048855	1.23E-45		MSTG08970.1		SNARE-like superfamily protein
Sapur.0075D030800.1	809.9731746	-0.813502051	0.03977667	-20.454	5.38E-93	5.62E-92	cpm	-0.854964011	4.82E-46		MSTG49410.1		sequence-specific DNA binding transcription factors;transcription regulators	transcription factor, putative
Sapur.0020H084001.1	8.582343865	5.938579644	0.290407695	20.44931	6.12E-93	6.39E-92	cpm	0.647841895	4.72E-20	GO:0055114;GO:0020037;GO:0016705;GO:0005506	MSTG37340.1	CYP81D3	cytochrome P450, family 81, subfamily D, polypeptide 3	cytochrome P450 family protein
Sapur.0062G200001.1	851.3989984	-0.843029125	0.041380851	-20.4425	7.08E-93	7.39E-92	cpm	-0.855218128	4.27E-46	GO:0007017;GO:0005875	MSTG27810.1		Dynein light chain family protein	dynein light chain protein
Sapur.0126G105100.1	100.8362585	-1.23419839	0.060387266	-20.4381	7.67E-93	8.00E-92	cpm	-0.856281655	2.91E-46	GO:0006351;GO:0003899;GO:0003677	MSTG51940.1	NRPB6A,NRPD6A,NRPE6A	RNA polymerase Rpb6	NA
Sapur.0162H080001.1	45.56105928	2.178018137	0.102569226	-20.4053	1.16E-92	1.14E-91	cpm	0.545890466	1.44E-13	GO:0004648;GO:0006672	MSTG12600.1	B120	5-lysine protein kinase family protein	serine/Threonine-kinase
Sapur.0182H012001.1	24.25355644	0.858005539	0.394718388	20.41691	1.18E-92	1.23E-91	cpm	0.617798856	8.61E-18		MSTG10560.1		calcium-binding EF-hand family protein	NA
Sapur.0075D049400.1	312.2795419	1.321812154	0.059455564	20.38518	2.24E-92	2.35E-91	cpm	0.815498401	1.20E-38		MSTG22461.1		DNA heat shock C-terminal domain-containing protein	Dnaj heat shock amino-terminal domain protein, putative
Sapur.0032G072300.1	6.048061044	5.328703262	0.271216491	20.38493	2.28E-92	2.36E-91	cpm	0.696882055	3.85E-24					transmembrane protein, putative
Sapur.0061G111000.1	60.95916668	0.916006169	0.044678804	20.3363	2.34E-92	2.41E-91	cpm	0.623368671	8.46E-18	GO:0005085;GO:0016021;GO:0015299;GO:0006812	MSTG16680.1	ATCHX20,CHX20	cation/H+ exchanger 20	NA
Sapur.0031H185300.1	1601.133739	-1.283310876	0.062905528	-20.3812	2.48E-92	2.56E-91	cpm	0.873864085	1.80E-51	GO:0015979;GO:0009538;GO:0009522	MSTG42800.1	PSAL	photosystem I subunit l	photosystem I reaction center subunit XI
Sapur.0102H149000.1	689.018879	1.38091891	0.06777085	20.37665	2.69E-92	2.76E-91	cpm	0.779369758	3.77E-33	GO:0016772;GO:0016310;GO:0016301;GO:0005524;GO:0050342;GO:0006090	MSTG15330.5	PFK6	pyruvate orthophosphate dikinase	pyruvate orthophosphate dikinase
Sapur.0105G160001.1	642.3042948	1.374597594	0.067418388	20.37583	2.88E-92	2.95E-91	cpm	0.560818043	3.76E-16	GO:0005975;GO:0004553	MSTG48160.1	ATBXL1,BXL1	beta-xylosidase 1	alpha-L-arabinofuranosidase/beta-D-xylosidase
Sapur.7157700.1	20.80481223	2.863014325	0.139138709	20.3522	4.44E-92	4.58E-91	cpm	0.817523856	5.56E-39		MSTG08110.1		nucleic acid binding,ATP-dependent helicases;ATP-binding helicases;ATP-dependent helicases	NA
Sapur.0062G200001.1	481.8379701	-0.153730495	0.05678637	-20.3467	5.07E-92	5.22E-91	cpm	-0.829609802	1.40E-44		MSTG27810.1		Dynein light chain family protein	transmembrane protein, putative
Sapur.0162H052000.1	19.1004891	3.263945694	0.160431133	20.34484	5.16E-92	5.32E-91	cpm	0.658920354	2.99E-24		MSTG52251.1			DUF4535 domain protein
Sapur.0050H080001.1	1457.910674	-0.921832207	0.044331526	-20.3406	5.56E-92	5.72E-91	cpm	0.854281514	2.36E-50	GO:0055114;GO:0016491	MSTG16190.1	ATLPNR1,PNR1	ferredoxin-NADP(+)-oxidoreductase 1	ferredoxin-NADP reductase
Sapur.0131G152001.1	13.1435855	4.603669162	0.236349055	20.33894	5.82E-92	5.99E-91	cpm	0.719672663	2.44E-26		MSTG79960.1	ATOPF04,OPF04	ovate family protein 14	ovate transcriptional repressor
Sapur.0105G000100.1	30002.84609	-0.025401821	0.012047817	-20.3347	6.34E-92	6.52E-91	cpm	-0.818350348	3.74E-39	GO:0016020;GO:0009765	MSTG19930.1	AB140,CAB1,CAB140.1,HCB1	chlorophyll a/b binding protein 140	photosystem I light harvesting chlorophyll A/B-binding protein
Sapur.0162H047000.1	199.2188174	1.902205732	0.070903978	20.32645	7.52E-92	7.72E-91	cpm	0.7919683	1.35E-35	GO:0005515;GO:0043531	MSTG27220.1		Ras-ABC domain-containing disease resistance protein	NA
Sapur.0175G123900.1	13.30895007	3.230645855	0.158966865	20.32482	7.76E-92	7.98E-91	cpm	-0.738530307	2.02E-28	GO:0005515	MSTG28410.1		F-Box/kelch-like superfamily protein	F-Box/URP protein, putative
Sapur.0132G045900.1	159.5385738	0.951054384	0.046822672	20.31183	1.01E-91	1.04E-90	cpm	0.833974636	7.25E-42		MSTG24735.1		Haem oxygenase-like, multi-helical	heme oxygenase-like, multi-helical protein
Sapur.0156G225600.1	677.2609852	-1.679478299	0.082658866	-20.3061	1.14E-91	1.17E-90	cpm	-0.783994792	6.62E-34		MSTG10310.1		Rubredoxin-like superfamily protein	electron transporter
Sapur.0134G082300.1	292.8525761	-1.204614179	0.059323615	-20.3058	1.14E-91	1.18E-90	cpm	-0.855092527	2.03E-46		MSTG18450.1	ARPA,ATARP4	actin-related protein 4	actin-related protein 4
Sapur.0162G161000.1	1063.704828	3.312879209	0.164676295	20.29923	1.31E-91	1.34E-90	cpm	0.777896636	4.36E-33	GO:0005515	MSTG15470.1		Transducin/WD40 repeat-like superfamily protein	WD40 domain protein
Sapur.0140G029700.1	229.1200005	-0.018895453	0.00935889	-20.2985	1.33E-91	1.36E-90	cpm	-0.86487891	4.08E-47	GO:0004412;GO:0005840;GO:0003735	MSTG76970.1	RPS8,TWN3	ribosomal protein S8	30S ribosomal protein S9
Sapur.0152H080001.1	1765.469138	1.026125716	0.050585891	-20.2958	1.40E-91	1.46E-90	cpm	-0.838493269	1.03E-42		MSTG25050.1	ACP4	acyl carrier protein 4	acyl carrier protein
Sapur.0075D085400.1	216.5427898	0.799685225	0.038681328	20.2912	1.54E-91	1.57E-90	cpm	0.807546185	2.28E-37		MSTG43570.1	STOP1	C2H2 and C2HC zinc fingers superfamily protein	transparent TEST16 protein, putative
Sapur.0072G030400.1	105.1947283	1.941485861	0.095704896	20.28617	1.73E-91	1.76E-90	cpm	-0.75830867	1.32E-30					transmembrane protein, putative
Sapur.0062G161000.1	7.008165275	5.986685449	0.295461837	20.26186	2.76E-91	2.85E-90	cpm	0.615732035	2.70E-19	GO:0003723;GO:0016576	MSTG36680.1	PAB7	poly(A) binding protein 7	polypeptide-binding protein, animal type 1, 2, 3, 4 family protein
Sapur.0052H015200.1	236.0034682	1.043367339	0.051497235	-20.2568	3.10E-91	3.16E-90	cpm	-0.85205195	1.23E-45	GO:0015031;GO:0008565	MSTG28750.1		Bacterial sec-independent translocation protein mttA/Hcf106	twin arginine-targeting protein translocase
Sapur.0020H001001.1	222.3165623	0.863344551	0.042661381	-20.2405	4.35E-91	4.43E-90	cpm	0.82683571	1.31E-40		MSTG21070.1		Nucleotide-sugar transporter family protein	NA
Sapur.0105G203001.1	231.5267867	0.915376628	0.047651567	-20.2387	4.52E-91	4.60E-90	cpm	0.765914374	1.52E-31		MSTG19010.1		Disease resistance response (dirigent-like protein) family protein	disease resistance response protein, putative
Sapur.0162G193200.1	620.7692249	1.026399755	0.050752772	20.22352	6.08E-91	6.18E-90	cpm	0.831768609	4.88E-38	GO:0055114;GO:0005670;GO:0006559;GO:0004411	MSTG40860.2	HGO	homogentisate 1,2-dioxygenase	homogentisate 1%2C2-dioxygenase
Sapur.0134G000100.1	757.6208997	1.320665875	0.067146229	20.20166	6.52E-91	6.61E-90	cpm	0.81314917	2.58E-38	GO:0008080;GO:0006206;GO:0005634	MSTG42610.1		N-acetyltransferase superfamily protein	NA
Sapur.0050B015000.1	648.2419914	0.733068209	0.036281095	20.2073	6.91E-91	7.00E-90	cpm	0.83801365	1.27E-42		MSTG55510.1			hypothetical protein
Sapur.0105G203100.1	72.96017213	-1.015384286	0.10664115	-20.1788	7.34E-91	7.46E-90	cpm	0.722232223	1.32E-28	GO:0043565;GO:0006355;GO:0003700	MSTG36720.1	AtWRKY47,WRKY47	WRKY family transcription factor	WRKY transcription factor
Sapur.0096G132500.1	104.5232406	1.341363592	0.066495654	20.16776	1.02E-90	1.04E-89	cpm	0.796785839	5.00E-36		MSTG17530.1			hypothetical protein
Sapur.0051G166000.1	1729.248832	1.014452167	0.050311466	20.1668	1.23E-90	1.25E-89	cpm	0.820680652	2.18E-39	GO:0030170	MSTG20580.1		Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	aspartate aminotransferase
Sapur.0026H094000.1	234.4994717	0.253317746	0.012608384	-20.1689	1.28E-90	1.29E-89	cpm	-0.869303893	1.91E-49		MSTG32870.1		Ca2+-dependent phosphotriesterase family protein	calmodulin-binding family protein
Sapur.0036H000001.1	8359.992754	1.083281242	0.053780858	20.1715	1.71E-90	1.72E-89	cpm	-0.832660823	2.34E-41		MSTG76100.1	PETE1	plastocyanin 1	plastocyanin A/A
Sapur.0096G078800.1	172.1356413	1.820554229	0.090334048	-20.158	2.26E-90	2.30E-89	cpm	-0.863616874	5.83E-48	GO:0005515	MSTG14680.1		SWIB/MDM2 domain superfamily protein	SWIB/MDM2 domain protein
Sapur.0126G205001.1	236.9226269	0.796535

Sapur.003G051000.1	9.14406683	5.150509337	2.063332594	19.33864	2.54E-83	2.32E-82	ppm	0.719944941	2.29E-26	GO:0005789	Plant VAMP (vesicle-associated membrane protein) family protein
Sapur.010G151100.1	1575.312454	6.697947969	0.936108837	19.32601	3.06E-83	2.79E-82	ppm	0.864012028	8.71E-44		
Sapur.005G239000.1	5028.192928	6.645272518	0.933108319	19.3235	3.41E-83	3.11E-82	ppm	0.808313446	1.76E-37	GO:0055114,GO:0016630	glyceraldehyde-3-phosphate dehydrogenase B subunit
Sapur.007G111300.1	5.884655946	6.923974272	0.254863133	19.32006	3.64E-83	3.32E-82	ppm	0.796573277	7.57E-35	GO:0006468,GO:0005634,GO:0004672	Protein kinase superfamily protein
Sapur.016G087200.1	4313.363824	6.585393002	0.930300795	-19.3175	3.81E-83	3.46E-82	ppm	0.844509427	6.94E-44	GO:0055114,GO:0051920,GO:0016491	2-Cys Prx B,2CPB
Sapur.005G239600.1	15.84462548	-2.274817661	0.117788628	-19.316	3.94E-83	3.59E-82	ppm	-0.829694802	4.37E-41		
Sapur.005G092600.1	279.4820759	9.936461936	0.948488916	19.31291	4.18E-83	3.81E-82	ppm	0.804519713	6.72E-37		Zinc finger C-x8-C-x5-C-x3-H type family protein
Sapur.017G075100.1	62.33916757	5.333539394	0.360807408	-19.2986	5.51E-83	5.02E-82	ppm	-0.830050012	3.76E-41	GO:0016021	EXS (ERD1/XPR1/SYG1) family protein
Sapur.010G127100.1	935.935896	9.558300311	0.928929567	19.29861	5.52E-83	5.02E-82	ppm	0.84527434	4.66E-44	GO:0006468,GO:0006672	VIK
Sapur.T030500.1	85.25144445	5.812660425	0.175724655	19.29847	5.61E-83	5.10E-82	ppm	0.627880545	4.96E-21		
Sapur.003G149700.1	109.1042963	-1.053671235	0.059826184	-19.2892	6.01E-83	6.01E-82	ppm	-0.85429842	2.03E-46		
Sapur.011G028300.1	14.10973963	2.842075451	0.147284752	19.28817	6.75E-83	6.13E-82	ppm	0.742508875	8.94E-29	GO:0016567,GO:0006842	
Sapur.016G045500.1	603.7429804	-0.767370175	0.039791754	-19.2847	7.23E-83	6.56E-82	ppm	-0.851890037	2.16E-45	GO:0006468,GO:0005634,GO:0004672	
Sapur.002G045800.1	1675.85502	9.956857287	0.946429962	19.27806	8.21E-83	7.46E-82	ppm	0.802813446	1.76E-37	GO:0055114,GO:0016770,GO:0009072,GO:0003868	
Sapur.006G108900.1	330.9764715	2.215474216	0.063059968	19.27499	8.71E-83	7.90E-82	ppm	0.818621769	2.65E-39		
Sapur.016G078000.1	139.0078869	2.168369927	0.045639054	19.2481	9.31E-83	1.18E-81	ppm	-0.85438632	3.46E-46	GO:0007049,GO:0005634	cyclin-dependent kinase-activatine kinase assembly factor-related / CDK-activatine kinase assembly factor-relates
Sapur.010G116800.1	9312.008849	-1.492066176	0.077495612	-19.2533	1.32E-82	1.20E-81	ppm	-0.844977928	2.22E-44		
Sapur.006G058800.1	749.5342711	1.790335416	0.092988822	19.25087	1.39E-82	1.25E-81	ppm	0.779323293	7.66E-33	GO:0006529,GO:0004066	asparagine synthetase [glutamine-hydrolyzing] protein
Sapur.009G110200.1	61.26031127	-1.631511296	0.053195404	-19.2486	1.45E-82	1.31E-81	ppm	-0.831191108	2.91E-41		zinc finger protein, putative
Sapur.010G089900.1	86.5053066	-1.799398417	0.093476862	-19.2479	1.47E-82	1.33E-81	ppm	-0.825817543	2.13E-40	GO:0016787	
Sapur.005G052400.4	18.72702299	-1.904409147	0.179703382	-19.2421	1.66E-82	1.49E-81	ppm	-0.84702435	2.77E-44	GO:0005975,GO:0004553	
Sapur.017G051200.1	82.87608926	1.499009369	0.077661187	19.23819	1.77E-82	1.60E-81	ppm	0.751978186	7.49E-30		
Sapur.011G052800.1	437.8689048	1.881826767	0.104182074	19.23779	1.79E-82	1.61E-81	ppm	0.813818514	2.27E-38		Putative adipose-regulatory protein (Seipin)
Sapur.018G054500.1	421.2166651	6.620737671	0.032269804	19.23556	1.87E-82	1.68E-81	ppm	0.83592831	3.14E-42	GO:0005515	
Sapur.006G131500.1	405.6310125	5.174856446	0.268866746	19.23115	2.46E-82	2.20E-81	ppm	0.830384852	4.26E-42		
Sapur.004G168300.1	134.7936065	1.322492358	0.068807344	19.22022	2.51E-82	2.26E-81	ppm	0.737034954	3.66E-28	GO:0016567,GO:0006842	
Sapur.006G010100.1	548.8632245	8.843481679	0.043888559	19.21893	2.57E-82	2.31E-81	ppm	0.793976905	4.09E-28	GO:0051082,GO:0031072	
Sapur.010G086200.1	1526.051795	9.551461264	0.034217217	19.20881	3.06E-82	2.75E-81	ppm	0.832094851	1.39E-41		
Sapur.010G198300.1	359.539122	1.930813165	0.100978534	19.1925	4.19E-82	3.76E-81	ppm	0.721167014	1.72E-26		
Sapur.013G082500.1	83.67664797	1.910000215	0.052630276	-19.1921	4.31E-82	3.87E-81	ppm	-0.828466222	6.73E-41	GO:0010468,GO:0005777	
Sapur.010G072900.2	5.250487461	-3.997022768	0.208335022	-19.1899	4.50E-82	4.03E-81	ppm	-0.82742629	1.11E-40		
Sapur.006G132600.1	55.77212187	-1.663082079	0.088288966	-19.1764	5.82E-82	5.21E-81	ppm	-0.81835131	3.02E-38		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.001G195800.1	680.4087973	0.582471313	0.030303322	19.16645	7.33E-82	6.56E-81	ppm	0.815117739	1.38E-38		Thioredoxin superfamily protein
Sapur.004G101500.1	51.52449007	-0.911780921	0.048607848	-19.1629	7.55E-82	6.76E-81	ppm	-0.849587217	6.53E-45	GO:0006351,GO:0005739,GO:0003690	Mitochondrial transcription termination factor family protein
Sapur.008G017300.1	119.6713863	1.093458186	0.057076503	-19.1593	8.08E-82	7.23E-81	ppm	-0.83448819	5.80E-42		Duplicated homeodomain-like superfamily protein
Sapur.005G186400.1	527.0130353	1.030240444	0.054000149	-19.1567	8.54E-82	7.64E-81	ppm	0.817549204	4.50E-38	GO:0016787	purple acid phosphatase
Sapur.017G001400.1	289.2276931	-1.910076082	0.099775913	-19.1497	9.74E-82	8.70E-81	ppm	0.797887445	6.76E-36	GO:0055114,GO:0016491,GO:0008270	Zinc-binding dehydrogenase family protein
Sapur.006G097300.1	448.3070795	0.724031946	0.037809782	-19.1494	9.79E-82	8.75E-81	ppm	-0.83811466	1.31E-42	GO:0005515,GO:0016020,GO:0015297,GO:0015238,GO:0006855	MATE efflux family protein
Sapur.010G087800.1	7.78652504	1.574856446	0.291103748	-19.1468	9.79E-82	8.75E-81	ppm	0.657869890	7.90E-21		Root hair defective 3 GTP-binding protein (RHD3)
Sapur.019G108700.1	45.46939432	-1.619860784	0.084619322	-19.1427	1.11E-81	9.93E-81	ppm	-0.851780027	1.41E-45	GO:0055114,GO:0016491,GO:0005507	laccase 3
Sapur.010G088300.1	898.5787742	5.660455128	0.036381882	19.13203	1.69E-81	1.50E-80	ppm	0.82189725	1.02E-39	GO:0005525	Rab-related small GTP-binding protein
Sapur.006G099700.1	296.6228813	0.748544952	0.039154177	-19.1379	1.79E-81	1.59E-80	ppm	-0.836250842	2.25E-42	GO:0005525	Ras small GTPase family Ras protein
Sapur.017G075300.1	60.36660884	1.000241359	0.044692256	-19.1178	1.79E-81	1.59E-80	ppm	0.816861224	2.01E-42		C2H2 type of c-met zinc finger protein
Sapur.004G058800.1	191.0041959	-2.023460613	0.105829906	-19.1143	1.92E-81	1.71E-80	ppm	-0.807196409	2.58E-37	GO:0006872	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain
Sapur.010G094000.1	15.53174231	4.804648427	0.251604138	19.09682	2.68E-81	2.38E-80	ppm	0.634093426	4.90E-19	GO:0016316,GO:0005779	peroxin 11A
Sapur.019G070400.1	3708.594829	1.009315364	0.052851646	19.09366	2.85E-81	2.53E-80	ppm	0.814373416	1.84E-38	GO:0020037,GO:0009055	CYTOCHROME C-1
Sapur.005G138700.1	162.6514619	1.102126704	0.058209886	19.09223	2.93E-81	2.60E-80	ppm	0.762697858	7.69E-32	GO:0003824,GO:0006508	cathepsin B-like cysteine protease
Sapur.005G178800.1	1121.374823	1.183269143	0.061872617	19.07656	3.95E-81	3.50E-80	ppm	0.770580941	3.94E-32	GO:0055085,GO:0016021	phosphate transporter 1;4
Sapur.002G097900.1	1541.329315	1.118335505	0.058628629	19.0749	4.08E-81	3.61E-80	ppm	0.773785604	1.52E-32		NADPH-binding Rossmann-fold superfamily protein
Sapur.011G042000.1	225.6805791	-1.602026296	0.108022448	-19.0728	4.26E-81	3.77E-80	ppm	-0.81016039	8.30E-38		Plant protein of unknown function (DUF642)
Sapur.007G031300.1	7625.397296	0.879985235	0.046139152	-19.07	4.48E-81	3.96E-80	ppm	-0.814422271	2.81E-43	GO:0042549,GO:0016898,GO:0051979,GO:0009654,GO:0009523,GO:0005509	MSP-1.OE23.OE61.OE613.P	PS II oxygen-evolving complex 1
Sapur.010G087400.1	776.4469938	2.000241359	0.105458128	-19.0453	4.61E-81	4.85E-80	ppm	-0.797937038	7.98E-36	GO:0055051	Transducin/WD40 repeat-like superfamily protein
Sapur.014G057700.1	21.9060049	-2.750788844	0.146025582	-19.0431	7.50E-81	6.61E-80	ppm	-0.792747387	3.82E-35		
Sapur.019G028800.1	73.74803671	-1.696208881	0.094469256	-19.0178	7.78E-81	6.86E-80	ppm	-0.817371211	2.54E-42	GO:0005085,GO:0016020,GO:0008811,GO:0005216	ATCNGC20,CNBT1,CNGC20
Sapur.018G093000.1	242.6587248	-0.455430931	0.022868773	-19.0404	7.88E-81	6.95E-80	ppm	-0.817964609	2.58E-37	GO:0006872	RNA-binding KH domain-containing protein
Sapur.015G078300.2	86.77087597	1.238481269	0.106443485	19.01884	8.21E-81	7.16E-80	ppm	0.752278865	8.04E-30	GO:0007165	ABI five binding protein 3
Sapur.001G059000.1	107.6729432	-0.882564126	0.046381832	-19.028	1.00E-80	8.76E-80	ppm	-0.837272136	1.79E-42		
Sapur.001G190300.1	5343.477913	3.328462606	0.069819537	19.0271	1.02E-80	8.96E-80	ppm	0.794030059	6.43E-34	GO:0007481	Pseudouridine synthase/archaeosine transglycosylase-like family protein
Sapur.011G126700.1	771.2608872	-0.750440871	0.039606629	-19.0077	1.45E-80	1.26E-79	ppm	-0.819449012	2.16E-38		alpha/beta-hydrolase domain protein
Sapur.013G062900.1	23.52181999	2.461774808	0.128477112	19.00552	1.54E-80	1.35E-79	ppm	0.717219488	4.31E-26		
Sapur.005G188500.1	768.8253154	-1.785194769	0.0467087	-19.0047	1.95E-80	1.70E-79	ppm	-0.806365351	5.00E-37	GO:0003677,GO:0007275	Integrase-type DNA-binding superfamily protein
Sapur.009G115100.1	183.119402	1.487239147	0.078347274	18.98332	2.34E-80	2.05E-79	ppm	0.799868808	1.80E-36	GO:0005662,GO:0008384,GO:0080019	CERAFAR1,G7
Sapur.009G107000.1	326.3015508	0.767800734	0.042037179	-18.9792	2.54E-80	2.22E-79	ppm	-0.841356163	2.84E-42	GO:0016762,GO:0017004,GO:0000188	UGT{*}
Sapur.010G138800.1	2567.566196	-1.19415943	0.062920403	-18.9789	2.55E-80	2.23E-79	ppm	-0.805326797	4.99E-37	GO:0016597,GO:0008152	VAT1
Sapur.005G146700.1	1107.122026	-0.698398104	0.044729287	-18.9789	2.56E-80	2.24E-79	ppm	-0.808676339	1.05E-37	GO:0055114,GO:0016491,GO:0008152	ALDH3H1,ALDH4
Sapur.016G084900.1	215.6816539	-0.638476368	0.033476114	-18.9754	2.73E-80	2.38E-79	ppm	-0.820650373	4.10E-42		
Sapur.010G186700.1	520.7105564	-0.890321485	0.052668233	-18.9619	3.52E-80	3.08E-79	ppm	-0.828698182	1.26E-43	43708	stress enhanced protein 1
Sapur.013G020600.1	75.05315944	1.197197203	0.116074824	18.92915	6.56E-80	5.72E-79	ppm	0.695839868	4.77E-24	GO:0006468,GO:0005634,GO:0004672	Protein kinase superfamily protein
Sapur.013G198800.1	217.8130005	-0.962008024	0.05088142	-18.922	7.53E-80	6.55E-79	ppm	-0.829325874	5.24E-43		transmembrane protein, putative
Sapur.017G061600.1	14.23810022	2.757160155	0.145588402	18.9144	7.52E-80	6.55E-79	ppm	0.753825256	8.66E-31		hypothetical protein
Sapur.008G163000.1	105.4723571	-0.072066372	0.056705135	-18.9148	8.05E-80	7.01E-79	ppm	-0.84423609	7.87E-44		
Sapur.005G131700.1	608.3826201	1.507963847	0.084476699	18.91522	8.51E-80	7.42E-79	ppm	0.767835616	2.00E-34	GO:0016021,GO:0015116,GO:0008272,GO:0055085,GO:0016020,GO:0008371,GO:0005887	SULTR1;3
Sapur.010G073800.1	908.0952203	0.706664666	0.037157561	18.91511	8.56E-80	7.45E-79	ppm	0.823846939	4.52E-40	GO:0006468,GO:0006672	AFC1,AMSE2,FC1
Sapur.010G083600.1	159.6105542	-0.918845491	0.048617803	-18.9037	1.06E-79	9.23E-79	ppm	-0.817412726	2.96E-38	GO:0005515	
Sapur.005G165600.1	601.4541419	0.596726461	0.03157852	-18.8966	1.22E-79	1.06E-78	ppm	0.837152545	1.85E-42	GO:0005525	GTP-binding family protein
Sapur.011G052500.1	76.35124311	1.154806256	0.114054227	18.88657	1.47E-79	1.27E-78	ppm	0.734208107	3.94E-27		
Sapur.017G022500.1	135.4369836	0.938952369	0.049731376	18.88428	1.54E-79	1.33E-78	ppm	0.808540751	1.59E-37	GO:0016791	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.010G023100.1	23.02120526	-2.335078376	0.123749347	-18.8767	1.77E-79	1.54E-78	ppm	-0.766894587	1.14E-31	GO:0006351,GO:0003677	BEL1-like homeodomain 11
Sapur.010G068400.1	140.0010965	-0.567097147	0.041753661	-18.8743	1.80E-79	1.56E-78	ppm	-0.83589666	1.31E-42		hypothetical protein
Sapur.019G051900.1	4700.365501	0.445075857	0.023586427	18.87144	1.96E-79	1.69E-78	ppm	0.826262177	1.81E-40	GO:0005515	ARM repeat superfamily protein
Sapur.004G085700.1	180.2751383	1.933984391	0.102906048	18.86618	2.21E-79	1.90E-78	ppm	0.825405443	2.10E-40	GO:0016787,GO:0048544,GO:0006468,GO:0004672	receptor kinase 3
Sapur.15WG038200.1	895.9283951	3.314772651	0.069731925	18.86008	2.43E-79	2.09E-78	ppm	0.836009148	3.03E-42	GO:0016301,GO:0008152,GO:0005524	Phosphorthioloxinase / Uridine kinase family
Sapur.006G113300.1	10.20457157	1.529826739	0.240225241	18.85579	2.62E-79	2.27E-78	ppm	0.708910989	8.82E-25	GO:0003247,GO:0006488,GO:0055052,GO:0004672	WAH2
Sapur.006G023500.1	83.18517806	-2.527849949	0.134009715	-18.8515	2.86E-79	2.46E-78	ppm	-0.75561673	2.79E-30	GO:0005681,GO:0008398,GO:0003887	PEBP-type peptidyl-prol cis-trans isomerase family protein
Sapur.006G084200.1	24.42864244	2.119401888	0.112466046	18.84482	2.74E-79	2.36E-78	ppm	0.742709313	1.41E-28		Peptidyl-prolyl cis-trans isomerase family protein
Sapur.002G199700.1	1062.834052	-1.060252585	0.05123197	-18.841	3.48E-79	3.00E-78	ppm	-0.81994796	2.18E-39	GO:0016020,GO:0015979,GO:0009654,GO:0009523	photosystem II reaction center PSB28 protein
Sapur.017G025000.1	176.7705815	2.213171389	0.064503589	18.83946	3.58E-79	3.08E-78	ppm	0.750364505	3.13E-30	GO:0016020,GO:0005515	RING/U-box superfamily family protein
Sapur.003G040700.1	14.81730745	2.768149493	0.147119255	-18.8154	5.65E-79	4.85E-78	ppm	-0.84257782	1.71E-43	GO:0016829,GO:0010333,GO:0008127,GO:0008152	ABC33.ATCPS1,CPS,CPS1,G4
Sapur.010G075100.1	17.53097991	-2.021524774	0.107495383	-18.8149	5.70E-79	4.89E-78	ppm	-0.809543937	1.02E-37		Terpenoid cyclases/Prenyltransferases superfamily protein
Sapur.007G011700.1	456.3237036	-1.664868784	0.088516005	-18.8088	6.28E-79	5.38E-78	ppm	-0.784193131	4.30E-33	GO:0006334,GO:0005634,GO:0003677,GO:0000786	HIS1-3
Sapur.005G162100.1	19.67651828	1.326634916	0.070503228	18.80412	6.99E-79	5.96E-78	ppm	0.796028713	1.27E-35		Homeodomain-like superfamily protein
Sapur.012G080000.1	20.87513282	1.963566194	0.103737684	18.80381	7.03E-79	6.02E-78	ppm	0.76027256	7.64E-31	GO:0005515	SIROS
Sapur.014G097800.1	1345.50848	1.335851421	0.070157819	18.7988	7.73E-79	6.61E-78	ppm	0.786178311	1.71E-34	GO:0005515	Heat shock protein DnaJ with tetratricopeptide repeat
Sapur.006G122600.1	15.24054557	1.327661427	0.183488163	18.79427	8.41E-79	7.20E-78	ppm	0.595803986	1.85E-16		
Sapur.T126600.1	17.96746611	2.251402208	0.119814378	18.7894	9.22E-79	7.88E-78	ppm	0.755613673	2.79E-30	GO:0005681,GO:0008398,GO:0003887	ARM repeat superfamily protein
Sapur.004G045600.1	39.23828869	1.145184249	0.060095451	-18.7885	9.39E-79	8.02E-78	ppm	-0.84032306	5.48E-44		
Sapur.016G093600.1	84.00938017	-0.053778167	0.056185136	-18.7567	1.71E-78	1.46E-77	ppm	-0.84051575	5.25E-43	GO:0008270	RING/FYVE/PHD zinc finger superfamily protein
Sapur.002G018800.1	755.8234079	1.310086612	0.069858711	18.7542	1.82E-78	1.55E-77	ppm	0.727948264	2.68E-29	GO:0016787,GO:0006508	Survival protein kinase 1 / Peptidyl-dipeptidase/tuftsin/substance
Sapur.009G112000.1	503.0954195	-1.629125597	0.086885203	-18.7503	1.92E-78	1.64E-77	ppm	-0.879953159	8.15E-51	GO:0080085,GO:0045038,GO:0009507,GO:0009416	chloroplast signal recognition particle component (CAD)
Sapur.003G169300.2	18.97557934	-1.520507937	0.081101105	-18.7483	2.00E-78	1.70E-77	ppm	-0.834587965	5.58E-42	GO:0006353	antitermination NusB domain-containing protein
Sapur.T050500.1	758.7580224	-1.149181285	0.06139474	18.74714	2.04E-78	1.74E-77	ppm	-0.786028435	2.12E-33		Plant protein of unknown function (DUF946)
Sapur.T089800.1	827.6409418	0.506146831	0.027000781	-18.7456	2.10E-78	1.79E-77	ppm	-0.843331517	4.56E-43	GO:0006457,GO:0003755,GO:0006413	cyclophilin 18
Sapur.005G169200.1	145.1667004	-0.854441383	0.04568932	-18.7449	2.13E-78	1.81E-77	ppm	-0.84921817	7.52E-45		
Sapur.002G091000.1	226.5182536	-1.037165447	0.055340203	-18.7416	2.27E-78	1.93E-77	ppm	-0.82209213	9.41E-40		
Sapur.006G199000.1	889.7387521	1.024852229	0.033882932	18.7376	2.48E-78	2.11E-77	ppm	0.811126776	4.16E-38		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.003G169600.1	2423.883921	0.896696177	0.047879533	18.7287	2.92E-78	2.47E-77	ppm	0.798213137	6.05E-36		
Sapur.009G230300.1	386.7945845	0.610509837	0.033629155	18.7233	3.21E-78	2.72E-77	ppm	0.816214553	4.85E-39		
Sapur.014G084000.1	2196.396618	-0.831671693	0.044441894	-18.7137	3.83E-78	3.24E-77	ppm	-0.823430744	1.39E-41		
Sapur.002G045700.1	330.2816462	0.902445317	0.048234412	18.70957	4.14E-78	3.50E-77	ppm	0.801267865	1.11E-36	GO:0020037	
Sapur.002G090600.1	706.4247812	-0.844978394	0.045212588	-18.7078	4.28E-78	3.62E-77	ppm	-0.827886146	1.48E-40	GO:0016020	plastid-specific 30S ribosomal protein 6
Sapur.007G024600.1	260.2976861	-1.054569715	0.056396876	-18.706	4.42E-78	3.75E-77	ppm	-0.83016734	3.59E-41		
Sapur.009G200400.1	1.030169868	3.817255197	0.204109157	18.7051	4.58E-78	3.81E-77	ppm	0.821885791	1.05E-39	GO:0016787	Exostosin family protein
Sapur.016G100300.1	761.1347889	-1.05427829	0.061759182	-18.6956	5.18E-78	4.54E-77	ppm	-0.82187567	1.93E-39	GO:0016020,GO:0009765	light harvesting complex photosystem II
Sapur.010G100600.1	4.168805253	5.379269155	0.287676919	18.6951	5.41E-78	4.57E-77	ppm	0.688338138	1.12E-22	GO:0016787	P-loop/RNA-binding protein
Sapur.004G018800.1	1691.496783	-0.452615963	0.07772285	-18.6888	5.99E-78	5.06E-77	ppm	-0.762764258	3.79E-31	GO:0006632,GO:0003824	NADPH-binding Rossmann-fold superfamily protein
Sapur.006G146000.1	496.4824166	-0.699588197	0.06139474	18.6856	6.20E-78	5.43E-77	ppm	-0.78023835	1.71E-34	GO:0008270,GO:0005622,GO:0005515	CONSTANS-LIKE 5
Sapur.010G096300.1	29.31942205	-0.456685409	0.079800188	-18.6801	6.78E-78	6.06E-77	ppm	-0.812201666	4.11E-38		Protein of unknown function (DUF962)
Sapur.006G039700.1	30.48461303	-1.61357585	0.086882116	18.6776	6.98E-78	7.15E-77	ppm	0.67406802	1.21E-20		SNARE-like superfamily protein
Sapur.002G197400.1	2719.461502	1.308344559	0.070136145	-18.6544	1.16E-77	9.79E-77	ppm	-0.83779765	1.40E-42	GO:0015979,GO:0009538,GO:0009522	PSAD-2
Sapur.012G059600.1	2979.894654	1.001052818	0.050640075	18.6483	1.30E-77	1.10E-76	ppm	0.805419988	4.55E-37	GO:0006122,GO:0005750	Cytochrome bc1 ubiquinol oxidase, 14kDa subunit
Sapur.005G251000.1	335.4931174	-0.768250258	0.048034428	-18.6422	1.48E-77	1.25E-76	ppm	-0.843185656	1.79E-44	GO:0016021,GO:0005886,GO:0009941,GO:0009522	pseudouridine synthase family
Sapur.014G058200.1	14.90662097	1.825350561	0.097915812	-18.642	1.47E-77	1.24E-76	ppm	-0.84609609	3.34E-44		Protein kinase superfamily protein
Sapur.005G144000.1	186.4805041	-0.811164377	0.043611194	-18.6417	1.48E-77	1.24E-76	ppm	-0.845247048	4.93E-44	GO:0055114,GO:0016655	NDH-M	NADH dehydrogenase/quinone dehydrogenase complex
Sapur.008G141700.1	693.2588159	1.159492189	0.062131921	18.63778	1.59E-77	1.33E-76	ppm	0.777850588	4.42E-33	GO:0016459,GO:0005524,GO:0003774,GO:0005886	ATMYA2,MYA2,kr-2,kr-6
Sapur.010G100200.1	20.46682214	4.498804304	0.241415587	18.6315	1.67E-77	1.40E-76	ppm	0.51585435	1.31E-14	GO:0005515,GO:0004672,GO:0000246	Concanavalin A-like lectin protein kinase family protein
Sapur.010G081300.1	631.1684694	0.864712561	0.045329407	-18.635	1.67E-77	1.40E-76	ppm	-0.828451502	7.30E-41		
Sapur.004G088400.1	12.59619055	2.623786927	0.141175475	18.6268	1.85E-77	1.55E-76	ppm	0.514852256	2.52E-14	GO:0016020,GO:0008375	
Sapur.013G116600.1	565.2121687	0.832369216	0.044713425	-18.6156	2.40E-77	2.01E-76	ppm	-0.852205875	8.86E-45		Rhodanese/Cell cycle control phosphatase superfamily protein
Sapur.003G156800.1	8.963683576	3.1324881	0.170017836	18.6008	3.17E-77	2.65E-76	ppm	0.763218869	3.31E-31	GO:0005544,GO:0005509	
Sapur.15WG070380.1	15.15542726	2.502191712	0.137974637	18.59945	3.25E-77	2.72E-76	ppm	0.531839336	7.65E-13	GO:0016021	TET31
Sapur.010G083800.1	89.40384418	2.044642497	0.109858014	18.59093	3.81E-77	3.18E-76	ppm	0.763886046	2.75E-31	GO:0009607,GO:0006952	MLP28
Sapur.010G194600.1	1310.480017	0.604843097	0.035544053	18.58048	4.72E-77	3.94E-76	ppm	0.813255007	3.80E-38		
Sapur.019G061000.1	3659.08543	1.413856915	0.076137234	18.5088	5.63E-77	4.70E-76	ppm	0.789432575	1.14E-34		ATEXPRATEXPAB,ATHEXP A
Sapur.019G085100.1	261.2833151	1.144278628	0.061619082	18.5616	1.37E-76	1.15E-75	ppm	-0.778121058	4.07E-33		
Sapur.008G088800.1	8.731663041	-2.689380376	0.144913525	-18.5585	6.96E-77	5.80E-76	ppm	-0.798501881	3.26E-36	GO:0006607,GO:0006952	
Sapur.010G194600.1	77.18613364	1.839451327	0.099174488	18.54726	8.58E-77	7.15E-76	ppm	0.708423629	2.45E-25		
Sapur.018G071100.1	369.734953	0.732171306	0.039405579	18.5445	9.74E-77	8.11E-76	ppm	0.824883067	3.10E-40	GO:0016773,GO:0005975	
Sapur.003G044100.1	13.18869203	2.074851206	0.111868623	-18.5273	1.24E-76	1.03E-75	ppm	-0.818846051	3.34E-39		
Sapur.008G164000.1	107.9246601	0.870953464	0.047020281	18.52296	1.35E-76	1.12E-75	ppm	0.810894059	6.50E-38		
Sapur.016G131300.1	24.40785131	-1.443088645	0.07794653	-18.514	1.59E-76	1.32E-75	ppm	-0.817965434	4.70E-39		
Sapur.003G029200.1	555.5543514	0.850702403	0.046468204	18.51087	2.05E-76	1.68E-75	ppm	0.806429255	1.60E-37		
Sapur.006G061000.1	333.4288659	0.570667209	0.030847846	-18.4988	2.11E-76	1.75E-75	ppm	-0.821643266	1.12E-39		Emsy N Terminus (ENT) / plant Tudor-like domains-containing protein
Sapur.010G083200.1	173.6282664	1.296065513	0.070062191	-18.4985	2.12E-76	1.76E-75	ppm	-0.812498966	1.64E-38	GO:0055114,GO:0016655	Inorganic carbon transport protein-related
Sapur.009G027100.1	611.1316829	-1.199955174	0.064873895	-18.4967	2.19E-76	1.82E-75	ppm	-0.80756802	2.26E-37		plastid transcriptionally active 16
Sapur.005G199800.1	999.4704619	1.000241359	0.053725416	18.49537	2.56E-76	2.12E-75	ppm	-0.831373152	2.34E-41		NAD+ transporter 1
Sapur.008G051200.1	92.37751885	1.265457321	0.176163587	18.49456	2.58E-76	2.13E-75	ppm	0.578236348	2.18E-15	GO:0005885,GO:0016021	Major facilitator superfamily protein
Sapur.008G152600.1	1593.813397	-0.766886443	0.04152082	-18.4803	2.97E-76	2.46E-75	ppm	-0.82005627	3.76E-41		
Sapur.005G012700.1	8.818621556	1.892365988	0.210705297	18.47303	3.40E-76	2.81E-75	ppm	-0.756679598	2.08E-30	GO:0048544,GO:0006468,GO:0005524,GO:0004672	
Sapur.005G134700.1	417.2623766	0.843005979	0.045639899	-18.463	4.10E-76	3.38E-75	ppm	-0.815738832	1.46E-42	GO:0016787	B120
Sapur.001G123600.

Sapur.017G085900.1	60.17640551	-1.181061533	0.065662955	-17.9868	2.47E-72	1.93E-71	open	-0.823323886	5.79E-40	GO:0006351;GO:0003899;GO:0003677	DNA/RNA polymerases superfamily protein
Sapur.016G309200.1	1769.243121	-1.107724735	0.061595519	-17.9839	2.61E-73	2.03E-72	open	-0.847636327	1.63E-44	GO:0016020;GO:0015979;GO:0009522	photosystem I subunit G
Sapur.013G340600.1	185.4492688	0.607476051	0.038801899	17.67531	3.04E-72	2.37E-71	open	-0.81928093	2.52E-38	GO:0005488;GO:0004672	calcium-dependent kinase
Sapur.004G036800.1	10.46910052	-2.913018596	0.162056823	-17.9753	3.04E-72	2.37E-71	open	-0.830960019	2.58E-41		NA
Sapur.006G140400.1	1937.165168	0.608821833	0.033875854	17.9733	3.12E-72	2.41E-71	open	-0.79884269	4.84E-36		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.006G116200.1	778.3527766	0.774664459	0.043097569	17.97421	3.13E-72	2.42E-71	open	-0.788809866	1.35E-34		UDP-Glycosyltransferase superfamily protein
Sapur.016G190800.1	3.228619451	5.132265431	0.285577562	17.97184	3.24E-72	2.52E-71	open	-0.691143339	1.27E-23		EXORDIUM like 2
Sapur.005G157000.1	693.5898234	0.714924893	0.039788755	17.96781	3.48E-72	2.71E-71	open	-0.790767606	7.34E-35	GO:0055114;GO:0016491;GO:0006633;GO:0005506	sphingoid base hydroxylase 2
Sapur.008G059800.1	983.017901	0.514266004	0.028604792	17.95572	4.33E-72	3.36E-71	open	-0.820652091	1.66E-39	GO:0006886	alpha-soluble NSF attachment protein 2
Sapur.010G151200.1	107.6610984	-3.767417934	0.207452184	-17.949	4.88E-72	3.79E-71	open	-0.797116162	8.30E-36		hypothetical protein
Sapur.005G118700.1	439.6723874	0.853484727	0.047575005	17.93988	5.75E-72	4.46E-71	open	-0.79602561	1.27E-35	GO:0008152;GO:0008324	nicotinamidase 1
Sapur.004G026600.1	400.3607607	-1.257097285	0.080146025	-17.9307	6.88E-72	5.27E-71	open	-0.801296616	2.09E-39	GO:0016787;GO:0005524;GO:0003677;GO:0005515;GO:0016891;GO:0006396;GO:0004652	endoribonuclease dicer-like protein
Sapur.005G194700.1	144.9084318	-0.922541284	0.051458284	-17.9274	7.20E-72	5.58E-71	open	-0.84253188	1.73E-43		hypothetical protein
Sapur.013G061500.1	5.059829573	4.487862573	0.252882173	17.92683	7.28E-72	5.64E-71	open	-0.72312183	5.68E-27		NA
Sapur.013G008100.1	228.119559	-0.753360075	0.042025581	-17.9249	7.53E-72	5.83E-71	open	-0.821483805	1.20E-39		hypothetical protein
Sapur.004G176000.1	838.0568232	0.612266532	0.032808948	17.86561	1.07E-71	8.24E-71	open	-0.806453864	3.87E-39		proteinase inhibitor I4, serpin; emp24/gp25L/p24
Sapur.016G234400.1	7.038945899	3.917795079	0.218838429	17.90268	1.12E-71	8.68E-71	open	-0.75716719	1.82E-30	GO:0016021;GO:0005215	purine permease 10
Sapur.005G162900.1	2011.782258	-0.755931502	0.046636945	-17.9009	1.16E-71	8.96E-71	open	-0.818262213	4.18E-39	GO:0019898;GO:0015979;GO:0009654;GO:0009523;GO:0005509	photosystem II subunit P-1
Sapur.004G171900.1	24.96042999	1.394865469	0.107609189	17.89616	1.24E-71	9.75E-71	open	-0.765072048	9.75E-31		NA
Sapur.018G045700.1	38.8029169	2.548751995	0.142423907	17.89541	1.28E-71	9.88E-71	open	-0.855020842	4.68E-46	GO:0009733	SAUR-like auxin-responsive protein family
Sapur.006G069700.1	488.3054536	0.955272422	0.054166652	-17.8567	1.56E-71	1.20E-70	open	-0.82503201	2.96E-39		Transmembrane protein
Sapur.010G011000.1	142.4201653	1.819560131	0.101740894	17.88426	1.56E-71	1.21E-70	open	-0.706030451	5.36E-25	GO:0005737;GO:0005094	Immunoglobulin E-set superfamily protein
Sapur.005G060700.1	322.5455243	1.290927413	0.072326611	17.87899	1.72E-71	1.32E-70	open	-0.780682823	2.01E-33		copine (Calcium-dependent phospholipid-binding protein) family
Sapur.007G069500.1	318.2419263	-1.010166022	0.062008391	-17.878	1.75E-71	1.35E-70	open	-0.783815693	6.82E-34	GO:0045454;GO:0015035;GO:0006662	thioredoxin X
Sapur.002G052200.1	225.4442207	0.818111	0.046802138	17.87656	1.80E-71	1.38E-70	open	-0.771093535	2.36E-32	GO:0005515	F-box family protein
Sapur.012G263300.1	41.90992016	7.985338783	0.446844219	17.87052	2.00E-71	1.54E-70	open	-0.571522009	5.41E-15		Protein of unknown function (DUF1278)
Sapur.010G035300.1	14.06515471	-2.461635213	0.136646798	-17.8682	2.09E-71	1.60E-70	open	-0.754095105	4.22E-30		Plant protein of unknown function (DUF247)
Sapur.002G026100.1	13.83400472	-2.962082232	0.137515179	-17.866	2.17E-71	1.67E-70	open	-0.799384626	4.05E-36		NA
Sapur.004G061000.1	105.6659172	-1.01472628	0.056807556	-17.8627	2.30E-71	1.77E-70	open	-0.837909692	1.33E-42	GO:0016887;GO:0005524;GO:0019538	casein lytic proteinase B3
Sapur.016G309700.1	233.5447152	1.391880489	0.079522889	17.86181	2.34E-71	1.80E-70	open	-0.77229559	1.27E-32		hypothetical protein
Sapur.004G039800.1	692.7375472	0.81032403	0.045881846	17.85768	2.53E-71	1.94E-70	open	-0.85522344	5.23E-37	GO:000641;GO:0006914;GO:0005737	ubiquitin-like modifier-activating enzyme ATG7
Sapur.004G183300.1	1.554165091	5.955274237	0.354546652	-17.8567	2.56E-71	1.97E-70	open	-0.825675202	2.26E-40		WD domain, G-beta repeat protein
Sapur.014G039800.1	13.20685075	6.608601995	0.370305427	17.85207	2.79E-71	2.14E-70	open	-0.53961083	3.05E-13		NA
Sapur.008G042200.1	414.9732877	-2.228232204	0.128866188	-17.8404	3.43E-71	2.63E-70	open	-0.851839007	2.75E-45	GO:0003697;GO:0006260	Primosome PriB/single-strand DNA-binding protein
Sapur.T142100.1	6.609085727	2.671929381	0.205976041	17.82697	4.36E-71	3.34E-70	open	-0.72131336	1.37E-26		NA
Sapur.003G000300.1	373.6247633	0.9128	0.051213	17.82184	5.13E-71	4.27E-70	open	-0.805296609	2.26E-37	GO:0005515;GO:0006842	ubiquitin protein ligase 5
Sapur.003G061600.1	3302.346194	1.108156582	0.061908885	17.79876	7.23E-71	5.52E-70	open	-0.781355179	1.50E-33	GO:0016887;GO:0005134;GO:0015085;GO:0042626;GO:0016021;GO:0006810	ABC transporter family 8 protein, group MDR/PGP protein PpABCB18 protein
Sapur.009G075900.1	105.3230804	1.802256562	0.056332592	-17.7981	7.31E-71	5.58E-70	open	-0.8055363	6.68E-37		stress enhanced protein 1
Sapur.017G057700.1	6.964857609	-3.911488384	0.219412833	-17.7967	7.43E-71	5.82E-70	open	-0.818636681	1.64E-39		DCD (Development and Cell Death) domain protein
Sapur.159G114500.1	50.28968813	1.354314885	0.076480199	17.79216	8.13E-71	6.21E-70	open	-0.812293645	4.00E-38		DNA/ heat shock N-terminal domain-containing protein
Sapur.016G113000.1	502.8285011	-0.757860398	0.042662261	-17.7917	8.18E-71	6.25E-70	open	-0.818347466	4.21E-39	GO:0006886	alpha-soluble NSF attachment protein 2
Sapur.006G107200.1	2082.30878	0.8682889	0.048810945	17.78882	8.63E-71	6.58E-70	open	-0.795194699	1.68E-35		PLACE family protein
Sapur.009G046200.1	3.765632626	3.621757413	0.207664488	17.78643	9.00E-71	6.87E-70	open	-0.692600501	1.90E-24	GO:0006355;GO:0003677	RAC-like, activator for FKB/PI
Sapur.001G107800.1	107.3547136	1.993960215	0.112165045	17.77702	1.06E-70	8.11E-70	open	-0.77630398	7.09E-32		NA
Sapur.003G066200.1	32.80413063	1.620795584	0.091175661	17.7763	1.07E-70	8.18E-70	open	-0.710322001	4.84E-28	GO:0003227;GO:0008378;GO:0006888;GO:0006886	Sec23/Sec24 protein transport family protein
Sapur.018G020900.1	131.3924853	1.032128899	0.058093721	17.76627	1.29E-70	9.81E-70	open	-0.813374061	1.88E-38	GO:0016021;GO:0016020	Eamh-like transmitter family
Sapur.014G149300.1	62.36956247	1.992001024	0.112166996	17.7527	1.59E-70	1.20E-69	open	-0.832687953	4.19E-41		Regulator of chromosome condensation (RCC1) family protein
Sapur.013G038500.1	179.0154088	-1.959382865	0.06329757	-17.7614	1.41E-70	1.07E-69	open	-0.819863229	2.19E-39	GO:0046931;GO:0015986	protein phosphatase 2A-3
Sapur.006G178800.1	976.4460559	0.907059852	0.051009791	17.76117	1.41E-70	1.07E-69	open	-0.763563759	3.00E-31	GO:0008270;GO:0005515	RING/U-box superfamily protein
Sapur.006G111200.1	288.3263837	-0.196490153	0.047187567	-17.7551	1.57E-70	1.18E-69	open	-0.83013831	2.42E-42	GO:0005515	NA
Sapur.001G139300.1	932.7667926	0.535488936	0.03015854	17.75447	1.59E-70	1.21E-69	open	-0.80662035	1.38E-37	GO:0008509	alpha/beta-Hydrolases superfamily protein
Sapur.016G144800.1	1431.175212	0.538800508	0.08175834	17.7449	1.89E-70	1.43E-69	open	-0.82367702	2.26E-40		Photosystem II 5 kD protein
Sapur.006G045900.1	14.46132007	-2.048577587	0.115446837	-17.7448	1.89E-70	1.43E-69	open	-0.779276885	2.46E-33		hypothetical protein
Sapur.004G126600.1	542.8572297	0.524602232	0.029608786	17.74118	2.01E-70	1.52E-69	open	-0.81305111	7.52E-38		hypothetical protein
Sapur.017G067700.1	211.6283195	0.724092213	0.040831567	17.74029	2.05E-70	1.55E-69	open	-0.81801827	1.75E-36	GO:0005515	Non-S-locus F-box protein, putative
Sapur.015G072200.1	806.6040782	1.024957688	0.0158555	17.7353	2.31E-70	1.75E-69	open	-0.788042022	1.38E-33	GO:0016020;GO:0006886	Vesicle transport v-SNARE protein
Sapur.008G164900.1	9.892031927	4.596030618	0.259195612	17.73296	2.33E-70	1.76E-69	open	-0.663972083	2.59E-21		NA
Sapur.012G068600.1	81.1965254	-0.951161994	0.059206134	-17.7273	2.58E-70	1.95E-69	open	-0.84326561	1.23E-43		RING domain ligase2
Sapur.009G054505.1	280.115207	0.983353446	0.056047244	17.72019	2.85E-70	2.16E-69	open	-0.749194216	1.38E-29		NA
Sapur.005G139900.1	44.62812014	-1.479472653	0.083503471	-17.7175	3.07E-70	2.32E-69	open	-0.821738075	1.08E-39		Trm112p-like protein
Sapur.019G117300.1	158.9571016	0.98705166	0.055615244	17.7127	3.35E-70	2.52E-69	open	-0.782261764	1.13E-33		Lsm1/SM/RNA binding domain-containing protein
Sapur.003G165200.1	2419.617594	0.380215791	0.021494439	17.68903	5.09E-70	3.83E-69	open	-0.811132058	6.15E-38	GO:0016787	protein phosphatase 2A-3
Sapur.003G064600.1	6.318568223	-3.190149227	0.180063349	-17.6843	5.46E-70	4.16E-69	open	-0.588138611	5.00E-16	GO:0006208;GO:0004252	Subtilisin family
Sapur.T068100.1	11.7639828	2.243507218	0.126879159	17.68224	5.75E-70	4.32E-69	open	-0.768326352	7.63E-32		NA
Sapur.005G088900.1	746.0220378	-0.634728188	0.036773518	-17.6378	6.03E-70	4.54E-69	open	-0.777272795	5.56E-33		Rhodanese/Cell cycle control phosphatase superfamily protein
Sapur.013G261000.1	21.70274564	1.347622888	0.077519149	17.67765	6.23E-70	4.68E-69	open	-0.574778695	2.49E-15		expansin-B3
Sapur.006G044800.1	640.2831133	-0.436962869	0.051817986	-17.6687	7.17E-70	5.38E-69	open	-0.805068632	5.53E-37	GO:0042254;GO:0005622	Ribosomal protein L30 family protein
Sapur.016G150300.1	227.2053884	0.857391705	0.048532988	17.66616	7.64E-70	5.73E-69	open	-0.770294976	4.28E-32		DNA-binding storekeeper protein-related transcriptional regulator
Sapur.014G134800.1	21.68353138	-1.863884762	0.105522669	-17.6634	8.03E-70	6.02E-69	open	-0.82091245	5.76E-41		hypothetical protein
Sapur.019G141600.1	47.45605949	-2.614374568	0.091449224	-17.6572	8.94E-70	6.72E-69	open	-0.827744937	1.52E-40	GO:0005524	TCP-1/cpn60 chaperonin family protein
Sapur.003G139900.1	72.28854673	-0.793396125	0.04493561	-17.6563	9.10E-70	6.82E-69	open	-0.810762439	7.00E-38		
Sapur.004G012200.1	2627.100584	0.477189947	0.028258667	17.64871	1.05E-69	7.87E-69	open	-0.81305111	7.52E-38		GTGPT2;GPT2
Sapur.007G079400.1	26.79169929	-1.691489609	0.095859416	-17.6455	1.10E-69	8.25E-69	open	-0.78056881	1.91E-32		NA
Sapur.015G272000.1	400.9323886	1.007496663	0.062605599	17.6346	1.34E-69	9.88E-69	open	-0.764315726	6.24E-31		ATMTP11;MTP11
Sapur.004G154400.1	138.1610977	-1.030604928	0.058769506	-17.6326	1.38E-69	1.03E-68	open	-0.822796107	7.11E-40	GO:0005515	Plant regulator RWP-RK family protein
Sapur.016G188900.1	7.137672201	-1.74904268	0.138496295	-17.6254	1.57E-69	1.17E-68	open	-0.818369326	1.30E-39		NA
Sapur.008G168200.1	3.025241686	4.596210904	0.262824245	-17.6219	1.67E-69	1.25E-68	open	-0.755523871	2.96E-30	GO:0004983	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.002G187200.1	422.0109899	0.611580198	0.034938723	17.61745	1.81E-69	1.35E-68	open	-0.816277241	7.40E-39	GO:0008270	proteolysis 1
Sapur.009G016005.1	925.6801752	-0.980707961	0.055657425	-17.616	1.86E-69	1.38E-68	open	-0.838376766	1.08E-42		Duplicated homeodomain-like superfamily protein
Sapur.017G052900.1	3.368376965	5.074704691	0.2882316	17.60634	2.20E-69	1.64E-68	open	0.6487265	1.06E-21		
Sapur.004G047800.1	2516.357984	-0.415837733	0.080431828	-17.605	2.24E-69	1.68E-68	open	-0.797643808	7.35E-36	GO:0004857;GO:0042545;GO:0030599;GO:0005618	pectin methylesterase 3
Sapur.019G017400.1	18.91003893	1.611164425	0.091535056	17.60161	2.39E-69	1.78E-68	open	-0.779428312	2.72E-33	GO:0005515;GO:0006488;GO:0004672	Leucine-rich repeat transmembrane protein kinase
Sapur.010G268600.1	10.18891504	-2.467895267	0.138306613	-17.6	2.46E-69	1.83E-68	open	-0.808674409	1.51E-37		Histone deacetylase-like hydrolase (HDAH) superfamily protein
Sapur.014G050500.1	108.2085116	-0.715655556	0.040684151	-17.5904	2.92E-69	2.17E-68	open	-0.805074662	5.52E-37		NA
Sapur.004G150900.1	550.7440007	-0.621241288	0.037047737	-17.5887	2.95E-69	2.19E-68	open	-0.823747107	1.57E-40	GO:0016020	CAAX amino terminal protease family protein
Sapur.017G041700.1	289.5592076	0.886412453	0.050408786	17.58448	3.24E-69	2.40E-68	open	-0.763383703	1.79E-31		RNI-like superfamily protein
Sapur.004G028800.2	7.644847476	-2.480238805	0.1411112	-17.5855	3.34E-69	2.48E-68	open	-0.774078861	2.19E-32	GO:0005515;GO:0005634;GO:0005524;GO:0032502;GO:0006351	growth-regulating factor 1
Sapur.006G001300.1	62.34247721	1.030005025	0.121208063	17.57313	3.96E-69	2.93E-68	open	-0.715529869	1.24E-25		Copper transport protein family
Sapur.016G189100.1	79.28160609	1.25081646	0.07123952	17.56058	4.94E-69	3.66E-68	open	-0.798858917	6.85E-36		List/CRA/RING-U-box domain-containing protein
Sapur.019G031900.1	4590.684635	0.612735197	0.034909785	17.55446	5.52E-69	4.07E-68	open	-0.81805605	8.20E-39	GO:0005515;GO:0008270	ubiquitin-associated/translation elongation factor EF-1B-containing protein / octicosapentaoleoyl/Phca/Bemo1 (PB1)-domain-contai	zinc ion-binding protein; positive
Sapur.008G057500.1	1856.090936	1.080800071	0.057426932	17.55346	5.60E-69	4.14E-68	open	-0.77725456	5.30E-33	GO:0008152;GO:0008824	acyl-activating enzyme 7
Sapur.008G084900.1	2469.880584	0.563458287	0.030258664	17.53966	5.75E-69	4.25E-68	open	-0.747693377	2.34E-30	GO:0007165	CBL-interacting Serine/Threonine-kinase, putative
Sapur.006G171000.2	16.0830055	-1.706489005	0.097237829	-17.5496	5.99E-69	4.43E-68	open	-0.755467627	2.88E-30	GO:0006414;GO:0005525;GO:0046820;GO:0008312	signal recognition particle 54 kDa protein
Sapur.019G240700.1	12.48137306	-2.46681015	0.140521849	-17.5494	6.01E-69	4.45E-68	open	-0.817739074	1.56E-39	GO:0005515	MYM-type DNA-binding protein
Sapur.013G139100.1	168.1236889	-1.663168233	0.094796008	-17.5445	6.15E-69	4.84E-68	open	-0.74808237	2.97E-29		Duplicated homeodomain-like superfamily protein
Sapur.006G125400.1	434.1180514	-0.393481617	0.02242946	-17.5433	6.68E-69	4.94E-68	open	-0.818131397	4.46E-39	GO:0016591;GO:0016576;GO:0006368	RNA polymerase II assessory factor cdc73p
Sapur.003G089100.1	220.0498078	1.629369762	0.092902778	17.53844	7.29E-69	5.38E-68	open	-0.744797232	5.05E-29	GO:0016021;GO:0004252;GO:0006508	RHOMBOID-like 2
Sapur.006G087900.1	134.3864877	1.640326868	0.094060587	17.53684	7.48E-69	5.52E-68	open	-0.818368842	6.55E-23		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.015G171000.2	86.62018571	1.288937181	0.073556439	17.53522	7.72E-69	5.69E-68	open	-0.668894801	8.52E-22	GO:0006629	PATATIN -like protein 6
Sapur.006G115400.1	51.47426777	1.196103308	0.068219456	17.53327	7.98E-69	5.89E-68	open	-0.786865295	2.53E-34	GO:0051260	BTB/POZ domain with WD40/YVTN repeat-like protein
Sapur.010G017300.1	464.9774848	0.522202065	0.029788529	17.53101	8.26E-69	6.09E-68	open	-0.822312388	2.01E-40	GO:0005488;GO:0005524;GO:0004672	Protein kinase superfamily protein
Sapur.018G012700.1	513.6881355	0.562307828	0.032109886	17.51466	1.11E-68	8.15E-68	open	-0.821197366	1.34E-39	GO:0008270	ubiquitin-specific protease 22
Sapur.004G061200.1	5.658461627	4.425850564	0.252771633	17.50928	1.21E-68	8.86E-68	open	-0.771341619	5.32E-32		NA
Sapur.015G072600.1	376.6767656	-1.10753603	0.063276084	-17.5032	1.35E-68	9.95E-68	open	-0.779055687	2.05E-33		DNA-binding storekeeper protein-related transcriptional regulator
Sapur.T104600.1	25.12378367	1.526529026	0.087232376	17.49656	1.55E-68	1.14E-67	open	-0.718441394	1.25E-26	GO:0055114;GO:0009186	ribonucleotide reductase 2A
Sapur.159G115900.1	190.2927517	1.242460519	0.07101749	17.49515	1.58E-68	1.15E-67	open	-0.763014796	1.12E-31	GO:0003677;GO:0006355;GO:0003700	WRKY transcription factor, putative
Sapur.014G263700.1	575.0864205	-0.832373667	0.047601138	-17.4846	1.54E-68	1.17E-67	open	-0.80183732	4.32E-37	GO:0009512	cytochrome b6f complex subunit [petM], putative
Sapur.019G081100.1	44.75215231	1.976102758	0.112964899	17.49307	1.62E-68	1.19E-67	open	-0.70642469	7.25E-25	GO:0005085;GO:0016020;GO:0015297;GO:0015138;GO:0006855	MATE efflux family protein
Sapur.013G139800.1	134.5263978	-1.954864431	0.111852497	-17.4916	1.66E-68	1.22E-67	open	-0.814251206	1.93E-38		hypothetical protein
Sapur.004G154600.1	1586.625537	-0.625145486	0.032175503	-17.4854	1.85E-68	1.36E-67	open	-0.80154753	1.90E-38	GO:0005515	ubiquitin family protein
Sapur.001G104300.1	395.1299691	0.852802394	0.037325079	17.48428	1.89E-68	1.38E-67	open	-0.80134511	2.05E-38		autophagy 3 (ATG3)
Sapur.006G085000.1	1326.616097	0.591717	0.033881663	17.4567	2.18E-68	1.60E-67	open	-0.793968387	2.59E-35	GO:0016021;GO:0004659	Ubiquitin protease family protein
Sapur.015G143300.1	55.06269532	-1.286808308	0.073707895	-17.4369	2.43E-68	1.81E-67	open	-0.801265023	2.10E-36	GO:0055114;GO:0050897;GO:0016836;GO:0010024	phytochromobilin/biliverdin oxidoreductase, chloroplast / phytochromobilin synthase [HY2]
Sapur.004G047200.1	88.40414152	-0.667720916	0.04048582	-17.4333	2.46E-68	1.80E-67	open	-0.838865072	2.47E-42	GO:0005515	CCCH-type zinc finger protein with ARM repeat domain
Sapur.012G080800.1	307.9437633	-0.607028781	0.034875178	-17.4329	4.65E-68	3.39E-67	open	-0.819438379	3.12E-42	GO:0006779;GO:0006396;GO:0003723	Polynucleotide adenylyltransferase family protein
Sapur.008G218800.1	92.73672679	-0.642227425	0.046604914	-17.4287	5.06E-68	3.64E-67	open	-0.816164906	5.20E-39		Ribosomal protein S8 family protein
Sapur.012G204200.1	12.27326702	-2.141136223	0.123929554	-17.4176	6.07E-68	4.42E-67	open	-0.810012936	9.28E-38	GO:0005515	enoyl-CoA hydratase/isomerase family protein
Sapur.003G065700.1	375.5171327	-0.587361765	0.036331363	-17.4167	6.17E-68	4.49E-67	open	-0.796063444	1.14E-35	GO:0008270;GO:0005622;GO:0005515	3h32K-dihydroxy-2-naphthoyl-CoA synthase
Sapur.016G279900.1	153.5153232	1.112930653	0.069093455	17.41594	6.24E-68	4.55E-67	open	-0.749714352	1.37E-29		B-box type zinc finger protein with CCT domain
Sapur.006G162300.1	11.72274425	2.804393937	0.196981536	17.41271	6.61E-68	4.81E-67	open	-0.654778837	1.39E-20		formin homology5
Sapur.013G120100.1	144.0372896	-0.021463301	0.015860517	-17.4105	6.87E-68	5.00E-67	open	-0.828482133	1.04E-41	GO:0043531	LRR and NB-ARC domains-containing disease resistance protein
Sapur.019G089800.1	26.53292005	1.47907705	0.086954431	17.41024	6.90E-68	5.02E-67	open	-0.789524765	1.11E-34		Leucine-rich repeat transmembrane protein kinase
Sapur.001G041300.1	20.34527789	5.026477	0.3064608	17.4048	7.56E-68	5.50E-67	open	-0.775997054	7.79E-33		NA
Sapur.016G151900.1	369.5404957	0.568196731	0.032646583	17.40283	7.85E-68	5.71E-67	open	-0.817938777	4.75E-39		reduced lateral root formation
Sapur.008G108400.1	4.196318863	3.240888842	0.301144373	17.40158	7.98E-68	5.80E-67	open	-0.675818525	2.72E-22	GO:0016758;GO:0008152	UDP-glucose glucosyltransferase
Sapur.008G045900.1	87.75913313	1.717461274	0.098698772	17.3978	8.57E-68	6.22E-67	open	-0.760820059	6.56E-31	GO:0004648;GO:0005524;GO:0004672;GO:0030246	Concanavalin A-like lectin protein kinase family protein
Sapur.005G244600.1	41.41622214	1.800877317	0.103488673	17.39883	9.19E-68	6.67E-67	open	-0.827832224	2.09E-42	GO:0005515	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.002G223100.1	931.1244889	-0.51045286	0.029356005	-17.3884	1.01E-67	7.33E-67	open	-0.819661912	2.43E-39	GO:0008270;GO:0003676	serine/arginine-rich 22
Sapur.014G082900.1	35.21578865	0.930575562	0.054557492	-17.3811	1.11E-67	8.32E-67	open	-0.835323758	4.05E-42		hypothetical protein
Sapur.004G094300.1	15.26266776	-1.824022198	0.10512072	-17.3781	1.21E-67	8.76E-67	open	-0.739928627	1.76E-28		NA
Sapur.001G185800.1	561.2796205	-0.538752229	0.03100769	-17.3738	1.30E-67	9.44E-67	open	-0.827363699	1.14E-40		acetyltransferase (GNAT) domain protein
Sapur.002G082100.1	16.83994846	2.555183082	0.147150433	17.36426	1.54E-67	1.11E-66	open	-0.697097651	3.22E-24		NA
Sapur.016G165500.1	487.145691	-0.588074278	0.033916927	-17.3564	1.77E-67	1.28E-66	open	-0.802439726	7.40E-37		Phosphatidate cytidylyltransferase family protein
Sapur.017G107600.1	57.31107607	-1.364364275	0.079257149	-17.3524	1.84E-67	1.34E-66	open	-0.760694523	2.30E-22	GO:0006950	Adenine nucleotide alpha hydrolases-like superfamily protein
Sapur.010G047700.1	131.283553	0.745818885	0.042986449	-17.3501	1.97E-67	1.42E-66	open	-0.829915802	3.99E-41		Kinase interacting (KIP1-like) family protein
Sapur.009G209100.1	16.8628731	2.183852791	0.132256108	17.34282	2.23E-67	1.61E-66	open	-0.768275197	2.50E-31	GO:0003677;GO:0003677	Dof type zinc finger protein
Sapur.002G017500.1	1399.564827	1.401015531	0.080832391	17.33848	2.41E-67	1.74E-66	open	-0.738793449	2.35E-28	GO:0004672;GO:0003755;GO:0000413	rotamase CYP 3
Sapur.018G006600.1	15.22109669	2.387041515	0.142638958	17.33349	2.81E-67	2.03E-66	open	-0.682687863	1.85E-17	GO:0005509	calcium-binding EF-hand family protein
Sapur.020G167200.1	8.223376642	3.346903416	0.20815149	17.32459	3.07E-67	2.21E-66	open	-0.669636169	8.95E-22		Pectin lyase-like superfamily protein
Sapur.009G063600.1	930.7860513	0.814834403	0.047038738	17.32337	3.13E-67	2.26E-66	open	-0.78994786	9.60E-35	GO:0016020;GO:0008515;GO:0005215	Major facilitator superfamily protein
Sapur.010G075700.1	147.5018210	-0.617486027	0.037368606	-17.3138	3.76E-67	2.66E-66	open	-0.787424195	2.17E-34	GO:0055114;GO:0006097;GO:0016491;GO:0008152	polyphenol oxidase
Sapur.159G145400.1	562.185146	0.650977951	0.037616872	17.3064	4.29E-67	3.03E-66	open	-0.808657527	1.41E-37		F-box protein PP2-A13
Sapur.007G039700.1	21.67947668	-1.354834194	0.078258323	-17.3064	4.29E-67	3.03E-66	open	-0.835252128	1.04E-42		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.159G113400.1	161.0657577	1.4262541	0.082339231	17.3016	4.58E-67	3.29E-66	open	-0.723007847	1.79E-26		nucleic acid-binding protein, putative
Sapur.016G276400.1	1922.184107	0.562401396	0.032611942	17.29086	5.41E-67	3.89E-66	open	-0.800930809	2.97E-37		NA
Sapur.001G084200.1	12.06445	-2.11355801	0.122463158	-17.2895	5.65E-67	4.06E-66	open	-0.772207014	2.08E-32	GO:0009058;GO:0005524;GO:0016874	Translation initiation factor SUI1 family protein
Sapur.013G120100.1	264.3774435	0.88317064	0.051032043	17.2866	5.93E-67	4.26E-66	open	-0.829482133	1.04E-41	GO:0043531	LRR and NB-ARC domains-containing disease resistance protein
Sapur.003G080600.2	1.25845708	3.970993889	0.229273135	-17.2861	5.98E-67	4.29E-66	open	-0.836496823	8.32E-42		Leucine-rich repeat transmembrane protein kinase
Sapur.001G041300.1	306.0182147	0.662457461	0.038315164	17.28526	6.37E-67	4.56E-66	open	-0.779997054	7.79E-33		NA
Sapur.009G024000.1	50.30188086	1.361603276	0.07875111	17.28319	6.36E-67	4.52E-66	open	-0.81626796	5.31E-38	GO:0006355;

Sapur.007G116300.1	681.1251628	0.683114756	0.040597693	16.82644	1.56E-63	1.06E-62	cyan	0.764514851	2.30E-31	GO:0043565,GO:0006355,GO:0003700	AT1G06070.1		Basic-leucine zipper (bZIP) transcription factor family protein	transcription factor RF2a
Sapur.019G111600.1	540.3181631	0.772502544	0.045910864	16.82614	1.57E-63	1.07E-62	cyan	0.785836496	3.63E-34		AT3G51620.2		PAP/OAS1 substrate-binding domain superfamily	nucleic acid-binding protein, putative
Sapur.001G068800.1	1998.818066	1.175217422	0.069845499	16.82596	1.57E-63	1.07E-62	cyan	0.769501688	5.41E-32	GO:0009055	AT1G64640.1	AtENODL8,ENODL8	early nodulin-like protein 8	plastocyanin-like domain protein
Sapur.002G184700.1	1151.58705	0.730128696	0.043403315	16.82196	1.68E-63	1.15E-62	cyan	0.773991351	1.43E-32		AT3G07480.1		2Fe-2S ferredoxin-like superfamily protein	2Fe-2S ferredoxin
Sapur.009G079100.1	17.9433942	-1.482386593	0.088139802	-16.8186	1.78E-63	1.21E-62	cyan	-0.808125354	1.85E-37		AT4G33985.1		Protein of unknown function (DUF1685)	DUF1685 family protein
Sapur.15WG095000.1	9.559123886	-2.827143944	0.16810189	-16.818	1.80E-63	1.23E-62	cyan	-0.738476031	2.54E-28		AT5G14750.1	ATMYB66.MYB66.WER.WEI	myb domain protein 66	Myb transcription factor
Sapur.002G190500.1	147.5630119	-0.697361146	0.041513468	-16.7984	2.51E-63	1.70E-62	cyan	-0.82202439	9.68E-40		AT3G07210.1			hypothetical protein
Sapur.004G087900.1	312.0032771	-0.781552683	0.046534517	-16.7951	2.65E-63	1.80E-62	cyan	-0.820817452	1.55E-39	GO:0006468,GO:0005524,GO:0004672	AT1G10940.1	ASK1 SNRK2-4 SNRK2.4 SRK	Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.006G070800.1	2903.283373	0.687188412	0.04093629	16.78678	3.05E-63	2.07E-62	cyan	0.79960233	3.75E-36		AT3G09300.1	ORP3B	OSBP(oxysterol binding protein)-related protein 3B	oxysterol-binding protein-related protein 3B
Sapur.016G298700.1	25.68218563	-1.381763777	0.082334434	-16.7823	3.29E-63	2.23E-62	cyan	-0.800983138	2.33E-36		AT1G73720.1	SMU1	transducin family protein / WD-40 repeat family protein	NA
Sapur.007G121400.1	16.65401505	-1.436473733	0.085602243	-16.7808	3.37E-63	2.29E-62	cyan	-0.804430919	6.94E-37		AT5G44150.1			NA
Sapur.006G015900.1	91.58858274	-1.56803944	0.093446997	-16.78	3.42E-63	2.32E-62	cyan	-0.760854394	6.50E-31		AT3G22210.1			transmembrane protein, putative
Sapur.013G131000.1	3.667759526	4.768279059	0.284243803	16.77531	3.70E-63	2.51E-62	cyan	0.703275784	9.73E-25	GO:0005515	AT3G18150.1		RNI-like superfamily protein	F-box protein
Sapur.013G061800.1	4.012319139	4.89211533	0.291654887	16.77364	3.80E-63	2.58E-62	cyan	0.659497469	5.90E-21					NA
Sapur.010G077300.1	48.89677379	-1.806877268	0.107738363	-16.771	3.98E-63	2.69E-62	cyan	-0.792597138	4.01E-35	GO:0055085,GO:0016020,GO:0006810,GO:0005215	AT5G62890.3		Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.013G115900.1	866.4966975	1.158425194	0.069082814	16.76865	4.14E-63	2.80E-62	cyan	0.686732805	3.13E-23	GO:0016787	AT1G18480.1		Calcineurin-like metallo-phosphoesterase superfamily protein	ser/thr phosphatase family protein
Sapur.006G030800.1	211.1057977	2.004022629	0.119541645	16.76422	4.46E-63	3.02E-62	cyan	0.625759881	1.91E-18		AT2G41380.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NA
Sapur.014G060100.1	4.499885132	4.438292695	0.264803252	16.76072	4.73E-63	3.20E-62	cyan	0.734941039	6.18E-28	GO:0005515	AT2G45760.1	BAL,BAP2	BON association protein 2	BON1-associated protein, putative
Sapur.002G179500.1	334.7592398	0.629472615	0.037570129	16.7546	5.24E-63	3.54E-62	cyan	0.793861479	2.63E-35	GO:0055114,GO:0016491	AT2G43080.1	AT-P4H-1	P4H isoform 1	prolyl 4-hydroxylase alpha subunit, putative
Sapur.008G080900.1	42.70905024	1.911041522	0.114094819	16.74959	5.70E-63	3.85E-62	cyan	0.685125812	4.33E-23		AT5G49525.1			transmembrane protein, putative
Sapur.016G186600.1	158.6098031	-0.80091586	0.04783604	-16.7429	6.38E-63	4.30E-62	cyan	-0.813978808	2.13E-38		AT1G76890.2	AT-GT2,GT2	Duplicated homeodomain-like superfamily protein	GT-like trihelix DNA-binding protein, putative
Sapur.010G096900.2	188.1148037	1.417436496	0.084688075	16.73714	7.03E-63	4.74E-62	cyan	0.766741688	1.21E-31	GO:0016020,GO:0006810,GO:0005215	AT1G68570.1		Major facilitator superfamily protein	peptide transporter
Sapur.006G154200.1	279.4246205	-1.019780092	0.060937331	-16.7349	7.30E-63	4.92E-62	cyan	-0.825007901	2.95E-40	GO:0005524,GO:0003676,GO:0016891,GO:0006396,GO:0004525,GO:0003723	AT5G20320.1	ATDCL4,DCL4	dicer-like 4	endoribonuclease dicer-like protein
Sapur.004G154500.1	193.219458	1.016654837	0.060784733	16.7255	8.55E-63	5.76E-62	cyan	0.739869131	1.79E-28		AT2G17140.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.005G183500.1	1106.310813	-0.501642782	0.029994359	-16.7246	8.68E-63	5.85E-62	cyan	-0.802210365	1.52E-36	GO:0016743,GO:0006520,GO:0016597	AT1G75330.1	OTC	ornithine carbamoyltransferase	ornithine carbamoyltransferase
Sapur.014G095100.1	116.6015306	-0.610974509	0.036535796	-16.7226	8.97E-63	6.04E-62	cyan	-0.80702856	2.74E-37		AT1G02370.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.019G064000.1	606.2034778	-0.574332593	0.03435225	-16.7189	9.54E-63	6.42E-62	cyan	-0.804100963	7.80E-37		AT3G10850.1	GLX2-2,GLY2	Metallo-hydrolase/oxidoreductase superfamily protein	hydroxyacylglutathione hydrolase
Sapur.T177300.1	6.725876706	3.013299399	0.180237638	16.71848	9.61E-63	6.47E-62	cyan	0.718938368	2.89E-26	GO:0005681,GO:0000398,GO:0000387	AT1G54385.2		ARM repeat superfamily protein	NA
Sapur.017G074800.1	33.93367941	-1.146629031	0.068589107	-16.7174	9.80E-63	6.59E-62	cyan	-0.786530685	2.90E-34	GO:0006355	AT4G38180.1	FRS5	FAR1-related sequence 5	NA
Sapur.001G074200.1	4205.356193	1.329257754	0.079575355	16.70439	1.22E-62	8.19E-62	cyan	0.757513525	1.65E-30	GO:0055114,GO:0016616,GO:0006694,GO:0003854	AT4G10960.1	UGE5	UDP-D-glucose/UDP-D-galactose 4-epimerase 5	UDP-glucose 4-epimerase
Sapur.016G197700.1	213.5027002	-0.844981008	0.050587546	-16.7033	1.24E-62	8.33E-62	cyan	-0.794044496	2.48E-35		AT1G12830.1			hypothetical protein
Sapur.012G098000.1	172.3709408	0.89288835	0.053473737	16.6977	1.36E-62	9.15E-62	cyan	0.779724399	2.48E-33		AT1G02000.1	GAE2	UDP-D-glucuronate 4-epimerase 2	UDP-D-glucuronate 4-epimerase
Sapur.016G213600.1	738.0433628	-0.83830845	0.050209048	-16.6964	1.39E-62	9.36E-62	cyan	-0.810678822	7.27E-38	GO:0005515	AT5G14370.1		CCT motif family protein	CCT motif protein
Sapur.012G023100.1	65.84789688	-0.922295826	0.055268712	-16.6875	1.62E-62	1.09E-61	cyan	-0.813541577	2.51E-38	GO:0004518				extracellular ribonuclease
Sapur.005G108700.1	260.2837896	-1.004171613	0.06017995	-16.6861	1.65E-62	1.11E-61	cyan	-0.80789481	2.01E-37		AT2G23360.1		Plant protein of unknown function (DUF869)	myosin-9 protein, putative
Sapur.011G069700.1	45.50080456	1.367319228	0.081959127	16.68294	1.74E-62	1.17E-61	cyan	0.721419141	1.62E-26		AT5G46030.1			transcription elongation factor-like protein
Sapur.001G141900.2	6.273362519	3.082499685	0.184848448	16.67582	1.96E-62	1.32E-61	cyan	0.699281792	2.30E-24	GO:0055114,GO:0016491	AT1G15550.1	ATGA3OX1,GA3OX1,GA4	gibberellin 3-oxidase 1	gibberellin 3-beta-hydroxylase
Sapur.018G098700.1	1794.937603	-1.788968519	0.107305885	-16.6717	2.11E-62	1.41E-61	cyan	-0.784636038	5.32E-34		AT2G10940.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/LTP family protein
Sapur.010G068200.1	379.0086721	-0.93328131	0.055986823	-16.6697	2.18E-62	1.46E-61	cyan	-0.793258478	3.22E-35		AT5G43750.1	NDH18	NAD(P)H dehydrogenase 18	NAD(P)H dehydrogenase
Sapur.013G023700.1	511.202311	1.376400904	0.082628713	16.65766	2.66E-62	1.78E-61	cyan	0.700699654	1.70E-24		AT3G05290.1	PNC1	peroxisomal adenine nucleotide carrier 1	peroxisomal adenine nucleotide carrier protein
Sapur.001G177700.1	399.901312	-0.617962546	0.03711284	-16.6509	2.98E-62	1.99E-61	cyan	-0.836905265	2.06E-42	GO:0005515	AT4G06599.1		ubiquitin family protein	ubiquitin-like domain CTD phosphatase
Sapur.007G000600.1	11.55985736	-2.749385821	0.165227726	-16.64	3.58E-62	2.39E-61	cyan	-0.810609694	7.46E-38					hypothetical protein
Sapur.004G025500.1	425.8504129	1.137150748	0.068351744	16.63675	3.78E-62	2.52E-61	cyan	0.731211276	1.55E-27		AT1G61065.1		Protein of unknown function (DUF1218)	plant/plant protein
Sapur.002G032600.1	68.91404366	1.730701409	0.104033283	16.63604	3.82E-62	2.55E-61	cyan	0.77667972	6.32E-33	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT3G48520.1	CYP94B3	cytochrome P450, family 94, subfamily B, polypeptide 3	cytochrome P450 family-dependent fatty acid hydroxylase
Sapur.018G070400.1	133.3532513	-1.264030749	0.076054508	-16.6201	4.99E-62	3.33E-61	cyan	-0.771034899	3.44E-32		AT5G57520.1	ATZFP2,ZFP2	zinc finger protein 2	zinc finger protein
Sapur.011G056500.1	346.5240596	1.104270255	0.066453701	16.61714	5.24E-62	3.49E-61	cyan	0.775064093	1.03E-32		AT2G34585.1			transmembrane protein, putative
Sapur.010G107800.1	133.1927424	-0.926481154	0.055756682	-16.6165	5.29E-62	3.53E-61	cyan	-0.822207796	9.00E-40	GO:0008236,GO:0006508,GO:0070008,GO:0004252	AT1G69020.1		Prolyl oligopeptidase family protein	prolyl oligopeptidase family protein
Sapur.016G223900.1	678.1402734	-0.462409985	0.027828773	-16.6163	5.32E-62	3.54E-61	cyan	-0.793132512	3.36E-35	GO:0006457,GO:0003755,GO:0000413	AT3G01480.1	ATCYP38,CYP38	cyclophilin 38	peptidyl-prolyl cis-trans isomerase
Sapur.008G057300.1	58.06636714	2.290581734	0.137862335	16.61499	5.43E-62	3.61E-61	cyan	0.620723563	4.27E-18	GO:0045454,GO:0015035,GO:0009055	AT5G58530.1		Glutaredoxin family protein	NA
Sapur.005G063600.1	152.0977788	-1.576295807	0.094928573	-16.6051	6.40E-62	4.26E-61	cyan	-0.814131734	2.01E-38		AT5G65207.1			hypothetical protein
Sapur.007G060500.1	37.86570398	-1.20246692	0.072492966	-16.5874	8.60E-62	5.71E-61	cyan	-0.792553313	4.07E-35	GO:0016021,GO:0006952	AT2G17480.1	ATMLO8,MLO8	Seven transmembrane MLO family protein	NA
Sapur.010G130700.1	12.75361299	-1.589536073	0.095883826	-16.5777	1.01E-61	6.70E-61	cyan	-0.80389631	8.38E-37		AT1G69588.1	CLE45	CLAVATA3/ESR-RELATED 45	hypothetical protein
Sapur.15WG084500.1	372.0752291	-0.819619427	0.049442908	-16.5771	1.02E-61	6.77E-61	cyan	-0.81495975	1.48E-38		AT1G74730.1		Protein of unknown function (DUF1118)	NA
Sapur.002G034000.1	526.811277	-1.285115415	0.077574335	-16.5662	1.22E-61	8.10E-61	cyan	-0.815711881	1.11E-38	GO:0006355,GO:0005634	AT3G04730.1	IAA16	indoleacetic acid-induced protein 16	auxin-responsive protein IAA16, putative
Sapur.004G020600.1	77.66930993	-1.518559288	0.091678338	-16.564	1.27E-61	8.40E-61	cyan	-0.783489772	7.64E-34		AT4G21445.1			receptor-interacting protein, putative
Sapur.003G017900.1	585.7731188	-0.829911925	0.050113625	-16.5606	1.34E-61	8.88E-61	cyan	-0.796534231	1.07E-35		AT1G72810.1		Pyridoxal-5\'-phosphate-dependent enzyme family protein	threonine synthase
Sapur.001G065400.1	45.18081179	-1.551677701	0.093713135	-16.5577	1.41E-61	9.31E-61	cyan	-0.803559882	9.44E-37		AT1G31320.1	LBD4	LOB domain-containing protein 4	LOB domain protein
Sapur.004G029200.1	153.5917139	-1.353143511	0.081738796	-16.5545	1.49E-61	9.83E-61	cyan	-0.786144846	3.29E-34	GO:0006468,GO:0005524,GO:0004672,GO:0030246	AT4G04960.1		Concanavalin A-like lectin protein kinase family protein	lectin-receptor-like kinase
Sapur.004G175600.1	49.77093431	1.757771964	0.106190604	16.55299	1.52E-61	1.01E-60	cyan	0.687333898	2.77E-23		AT3G54200.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.014G130600.1	176.9193308	-0.797961088	0.048218802	-16.5488	1.63E-61	1.08E-60	cyan	-0.809901728	9.67E-38	GO:0009245,GO:0008915	AT2G04560.1		transferases, transferring glycosyl groups	lipid-A-disaccharide synthase
Sapur.004G165600.1	240.2146314	-1.797107613	0.108622423	-16.5445	1.75E-61	1.16E-60	cyan	-0.753733281	4.65E-30		AT5G01750.2		Protein of unknown function (DUF567)	tubby C 2 protein
Sapur.008G042800.1	6.323928739	3.612697058	0.218393573	16.54214	1.82E-61	1.20E-60	cyan	0.697288643	3.51E-24		AT2G16050.1		Cysteine/Histidine-rich C1 domain family protein	DC1; C1-like protein, putative
Sapur.016G212500.1	11.89369405	4.139128497	0.250244607	16.54033	1.88E-61	1.24E-60	cyan	0.535350515	5.06E-13		AT5G40690.1			Hop-interacting protein THI031, putative
Sapur.016G044500.3	29.279246	1.360721925	0.082267665	16.54018	1.88E-61	1.24E-60	cyan	0.772597532	2.16E-32		AT3G12150.1			transmembrane protein, putative
Sapur.001G191900.1	25.13101621	2.291224553	0.13853563	16.53888	1.93E-61	1.27E-60	cyan	0.531795795	7.68E-13	GO:0016787	AT4G19420.1		Pectinacetylesterase family protein	pectinacetylesterase
Sapur.002G069300.1	561.6522494	0.794516171	0.048050557	16.535	2.05E-61	1.35E-60	cyan	0.782124622	1.17E-33		AT4G08230.1		glycine-rich protein	transmembrane protein, putative
Sapur.016G248400.1	702.406342	-0.572669586	0.034640347	-16.5319	2.16E-61	1.43E-60	cyan	-0.808993507	1.35E-37	GO:0005515	AT3G14860.2		NHL domain-containing protein	NHL domain protein
Sapur.002G168200.1	708.0144588	0.714052799	0.043201908	16.52827	2.30E-61	1.51E-60	cyan	0.79010776	9.11E-35		AT3G62240.1		RING/U-box superfamily protein	RING Zn-finger protein
Sapur.004G167500.1	25.0872656	-2.089900148	0.126469528	-16.5249	2.43E-61	1.60E-60	cyan	-0.768332508	7.62E-32		AT2G40475.1			hypothetical protein
Sapur.019G066100.1	66.66855715	-1.090400543	0.066055786	-16.5073	3.25E-61	2.14E-60	cyan	-0.804847936	5.98E-37	GO:0005515	AT2G40815.1		Calcium-dependent lipid-binding (CaLB domain) family protein	C2 domain protein
Sapur.002G018300.1	179.5540417	1.42138855	0.086110464	16.50657	3.29E-61	2.16E-60	cyan	0.726230084	5.19E-27	GO:0009733	AT1G75580.1		SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.T168700.1	56.57166063	-0.984797936	0.059681601	-16.5009	3.62E-61	2.38E-60	cyan	-0.779354498	2.78E-33	GO:0006284	AT3G07930.3		DNA glycosylase superfamily protein	base excision DNA repair protein, HhH-GPD family protein
Sapur.012G053500.1	324.5527855	0.610985527	0.037041761	16.49451	4.02E-61	2.64E-60	cyan	0.820672481	1.65E-39	GO:0006468,GO:0005524,GO:0004674	AT3G08720.1	ATPK19.ATPK2.ATS6K2.S6K2	serine/threonine protein kinase 2	ribosomal protein S6 kinase, putative
Sapur.018G068200.1	163.4560263	-0.768520054	0.046601143	-16.4914	4.23E-61	2.78E-60	cyan	-0.791258456	6.25E-35		AT5G57410.1		Afadin/alpha-actinin-binding protein	afadin and alpha actinin-binding protein
Sapur.011G030300.1	2237.134951	-0.94412911	0.057281079	-16.4824	4.91E-61	3.22E-60	cyan	-0.829872595	4.06E-41		AT4G21620.1		glycine-rich protein	hypothetical protein
Sapur.009G083400.1	28.12052635	-1.138075489	0.069075393	-16.4758	5.47E-61	3.59E-60	cyan	-0.792939295	3.58E-35		AT2G26520.1			transmembrane protein, putative
Sapur.006G115100.1	511.732626	-1.182233433	0.071762075	-16.4743	5.61E-61	3.68E-60	cyan	-0.822016965	9.71E-40	GO:0016020,GO:0009765	AT1G19150.1	LHCA2*1,LHCA6	photosystem I light harvesting complex gene 6	light-harvesting complex I chlorophyll-A/B-binding protein Lhca5
Sapur.005G077600.1	30.94949601	1.779745824	0.108040337	16.47298	5.74E-61	3.76E-60	cyan	0.661756541	3.90E-21	GO:0006355,GO:0003677	AT1G56010.2	anac021,ANAC022,NAC1	NAC domain containing protein 1	NAC transcription factor
Sapur.017G039200.2	30.84530865	-1.691384747	0.102721771	-16.4657	6.47E-61	4.24E-60	cyan	-0.764649966	2.21E-31	GO:0016021,GO:0004659	AT1G60600.1	ABC4	UbiA prenyltransferase family protein	UbiA family prenyltransferase
Sapur.T066700.1	13.78297024	2.554552107	0.155144191	16.46566	6.47E-61	4.24E-60	cyan	0.655565372	1.20E-20					NA
Sapur.001G010900.1	1029.884214	0.423090777	0.025701385	16.46179	6.90E-61	4.52E-60	cyan	0.791821236	5.19E-35		AT5G13030.1			UPF0061 protein TOL2-C18030 protein
Sapur.011G035900.1	143.6461259	-1.246797647	0.075752989	-16.4587	7.26E-61	4.75E-60	cyan	-0.775604848	8.76E-33		AT5G22620.1		phosphoglycerate/bisphosphoglycerate mutase family protein	phosphoglycerate mutase family protein
Sapur.016G092500.1	514.8724733	0.49493535	0.030076756	16.45574	7.63E-61	4.99E-60	cyan	0.77584594	8.14E-33		AT3G53970.1		proteasome inhibitor-related	proteasome inhibitor, putative
Sapur.017G060700.1	4.479108435	3.518045329	0.213795219	16.45521	7.70E-61	5.03E-60	cyan	0.7825374	1.03E-33		AT3G28470.1	ATMYB35,TDF1	Duplicated homeodomain-like superfamily protein	NA
Sapur.013G129900.1	3.852267642	4.468759052	0.271805958	16.44099	9.73E-61	6.36E-60	cyan	0.733370597	9.13E-28		AT4G03320.1	tic20-IV	translocon at the inner envelope membrane of chloroplasts 20-IV	NA
Sapur.006G199400.1	226.017955	-0.926034239	0.05635316	-16.4327	1.12E-60	7.28E-60	cyan	-0.826768055	1.45E-40	GO:0006413,GO:0003743,GO:0003723	AT4G11175.1		Nucleic acid-binding, OB-fold-like protein	translation initiation factor IF-1
Sapur.15WG035100.1	48.48795359	-0.776043534	0.047246699	-16.4253	1.26E-60	8.22E-60	cyan	-0.789723373	1.03E-34	GO:0003676,GO:0017069,GO:0000398	AT2G30260.1	U2B\'\'	U2 small nuclear ribonucleoprotein B	NA
Sapur.T190900.1	5.461306895	2.414816098	0.147018328	16.42527	1.26E-60	8.22E-60	cyan	0.771794248	2.75E-32		AT1G48550.1		Vacuolar protein sorting-associated protein 26	NA
Sapur.006G080200.1	14.71364994	-1.964038006	0.119657319	-16.4139	1.52E-60	9.92E-60	cyan	-0.812188286	4.16E-38		AT3G09032.1			NA
Sapur.017G077100.1	10.73731188	2.740715566	0.167012836	16.41021	1.62E-60	1.05E-59	cyan	0.707541807	3.82E-25	GO:0017025,GO:0008270,GO:0006355,GO:0006352	AT3G10330.1		Cyclin-like family protein	transcription initiation factor IIB
Sapur.013G109600.1	169.9429232	1.891374984	0.115277334	16.40717	1.70E-60	1.11E-59	cyan	0.728604122	2.93E-27		AT2G42570.1	TBL39	TRICHOME BIREFRINGENCE-LIKE 39	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.005G035800.1	57.82634005	-1.266218999	0.077205674	-16.4006	1.89E-60	1.23E-59	cyan	-0.747138741	2.72E-29		AT4G25170.1		Uncharacterised conserved protein (UCP012943)	hypothetical protein
Sapur.002G017700.1	71.57091136	-1.265583529	0.077177558	-16.3983	1.97E-60	1.28E-59	cyan	-0.799363825	4.08E-36	GO:0008168,GO:0008152	AT4G31790.1		Tetrapyrrole (Corrin/Porphyrin) Methylases	diphthine synthase
Sapur.018G006200.1	265.3248019	1.016054676	0.061973679	16.39494	2.08E-60	1.35E-59	cyan	0.754423644	3.86E-30	GO:0005515	AT2G24540.1	AFR	Galactose oxidase/kelch repeat superfamily protein	F-box protein AFR
Sapur.014G098400.1	73.94109919	-0.643782247	0.039274148	-16.392	2.18E-60	1.42E-59	cyan	-0.801627874	1.86E-36		AT2G25920.1			hypothetical protein
Sapur.008G075400.1	56.65142379	-1.43168533	0.087341741	-16.3918	2.19E-60	1.42E-59	cyan	-0.771891147	2.67E-32	GO:0071705	AT2G03530.2	ATUPS2,UPS2	ureide permease 2	ureide permease
Sapur.014G114000.1	7849.928779	-0.578810713	0.035314118	-16.3903	2.24E-60	1.46E-59	cyan	-0.788474344	1.55E-34	GO:0055114,GO:0016620	AT3G26650.1	GAPA,GAPA-1	glyceraldehyde 3-phosphate dehydrogenase A subunit	glyceraldehyde-3-phosphate dehydrogenase
Sapur.004G155100.1	2368.704369	1.074667377	0.065598389	16.38253	2.55E-60	1.65E-59	cyan	0.775659787	8.62E-33		AT2G17230.1	EXL5	EXORDIUM like 5	phosphate-induced protein 1 motif protein
Sapur.15WG086900.1	51.239275	-1.326360337	0.080982266	-16.3784	2.73E-60	1.77E-59	cyan	-0.782742334	9.68E-34	GO:0016853,GO:0005975	AT3G04880.1	DRT102	DNA-damage-repair/toleration protein (DRT102)	NA
Sapur.012G039400.1	289.7701548	1.361105871	0.083124208	16.37436	2.92E-60	1.89E-59	cyan	0.742112905	1.01E-28		AT3G02550.1	LBD41	LOB domain-containing protein 41	NA
Sapur.006G166800.1	44.50520897	1.413201845	0.086316482	16.37233	3.01E-60	1.95E-59	cyan	0.745756638	3.91E-29					hypothetical protein
Sapur.014G116900.1	2.566260081	4.160266528	0.254109116	16.37197	3.03E-60	1.97E-59	cyan	0.779744008	2.47E-33					hypothetical protein
Sapur.15WG107200.1	122.9544355	2.608716298	0.159363706	16.36958	3.15E-60	2.04E-59	cyan	0.66064833	4.78E-21		AT1G24440.1		RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.005G089800.1	126.7108085	-1.077874696	0.06584665	-16.3695	3.16E-60	2.05E-59	cyan	-0.804500744	6.77E-37		AT3G51290.2		Protein of unknown function (DUF630) ;Protein of unknown function (DUF632)	DUF632 family protein
Sapur.012G099100.1	23.25354214	-1.454842724	0.088925728	-16.3602	3.68E-60	2.38E-59	cyan	-0.770974555	3.50E-32					transmembrane protein, putative
Sapur.15WG021900.1	371.7539132	0.760833672	0.046507569	16.35935	3.73E-60	2.41E-59	cyan	0.766573477	1.27E-31		AT5G08200.1		peptidoglycan-binding LysM domain-containing protein	peptidoglycan-binding LysM domain protein, putative
Sapur.005G109600.1	1074.88829	-1.155945573	0.070680074	-16.3546	4.03E-60	2.61E-59	cyan	-0.860706446	2.66E-47		AT5G67070.1	RALFL34	ralf-like 34	NA
Sapur.010G011400.1	157.3054137	-0.995692388	0.060965319	-16.3321	5.83E-60	3.77E-59	cyan	-0.79476674	1.95E-35		AT3G06145.1			hypothetical protein
Sapur.011G055900.1	323.0513213	-0.712390997	0.043625363	-16.3297	6.06E-60	3.91E-59	cyan	-0.796722053	1.01E-35	GO:0006508,GO:0004252	AT4G18370.1	DEG5,DEGP5,HHOA	DEGP protease 5	protease Do-like protein
Sapur.001G164000.1	169.3466576	-1.297935311	0.079488886	-16.3285	6.19E-60	3.99E-59	cyan	-0.789825195	9.99E-35	GO:0051536,GO:0009055	AT3G16250.1	NDF4	NDH-dependent cyclic electron flow 1	electron carrier/electron transporter/iron ion-binding protein
Sapur.016G129700.1	88.19276802	-1.198703445	0.073424416	-16.3257	6.48E-60	4.18E-59	cyan	-0.841070201	3.28E-43	GO:0003676	AT3G46020.1		RNA-binding (RRM/RBD/RNP motifs) family protein	cold-inducible RNA-binding protein
Sapur.016G216600.1	1405.709357	0.512648618	0.031413769	16.31923	7.20E-60	4.64E-59	cyan	0.815525068	1.19E-38	GO:0048280,GO:0006886,GO:0005737,GO:0000139,GO:0016020,GO:0008565,GO:004819	AT3G27530.1	GC6,MAG4	golgin candidate 6	coiled-coil vesicle tethering protein, putative
Sapur.016G294500.1	160.3083119	-0.856315572	0.052482224	-16.3163	7.56E-60	4.87E-59	cyan	-0.800432243	2.82E-36	GO:0006468,GO:0005524,GO:0004672,GO:0030246	AT5G06740.1		Concanavalin A-like lectin protein kinase family protein	lectin-like kinase, putative
Sapur.003G022800.1	3.708345618	4.779068523	0.293010629	16.31022	8.35E-60	5.38E-59	cyan	0.665056191	2.12E-21					NA
Sapur.005G160400.1	90.77387682	-1.209562958	0.074159812	-16.3102	8.35E-60	5.38E-59	cyan	-0.789280888	1.19E-34		AT1G06475.1			transmembrane protein, putative
Sapur.014G059500.2	8.803367818	2.252335743	0.13812889	16.30604	8.94E-60	5.75E-59	cyan	0.752457591	6.58E-30	GO:0008168	AT4G00750.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	dehydration-responsive family protein
Sapur.003G062500.1	361.487025	0.608580057	0.037323819	16.30541	9.03E-60	5.81E-59	cyan	0.772712847	2.09E-32		AT1G32260.1			hypothetical protein
Sapur.010G206400.1	700.2311675	-0.599795608	0.036800851	-16.2984	1.01E-59	6.51E-59	cyan	-0.806601127	3.20E-37		AT5G08380.1	AGAL1,AtAGAL1	alpha-galactosidase 1	alpha-galactosidase/alpha-N-acetylgalactosaminidase, putative
Sapur.014G136700.1	236.1374727	-1.087669574	0.06675916	-16.2924	1.12E-59	7.18E-59	cyan	-0.788557445	1.51E-34		AT4G14540.1	NF-YB3	nuclear factor Y, subunit B3	nuclear transcription factor Y subunit B-3
Sapur.010G088100.1	18.06103931	2.545504669	0.156259422	16.29025	1.16E-59	7.44E-59	cyan	0.64815127	4.47E-20	GO:0008270	AT2G01275.1		RING/FYVE/PHD zinc finger superfamily protein	membrane associated RING finger protein 1%2C8, putative
Sapur.011G003200.1	602.1163372	0.794523698	0.04879714	16.28218	1.32E-59	8.48E-59	cyan	0.73338897	9.09E-28	GO:0005737,GO:0000045	AT1G62040.2	ATG8C	Ubiquitin-like superfamily protein	gaba(A) receptor-associated protein, putative
Sapur.002G048500.1	7.145574992	-2.065041389	0.126861025	-16.278	1.41E-59	9.08E-59	cyan	-0.80002654	3.24E-36	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G42850.1	CYP718	cytochrome P450, family 718	cytochrome P450 family protein
Sapur.010G064900.1	136.0604782	-1.50766583	0.092638836	-16.2747	1.49E-59	9.59E-59	cyan	-0.783905174	6.70E-34	GO:0005515	AT3G22800.1		Leucine-rich repeat (LRR) family protein	Serine/Threonine kinase, plant-type protein%2C putative
Sapur.002G192200.1	156.6391923	-1.021828091	0.062793558	-16.2728	1.54E-59	9.88E-59	cyan	-0.73715788	3.55E-28		AT3G07310.1		Protein of unknown function (DUF760)	DUF760 family protein
Sapur.004G096500.1	14444.34992	-0.889573071	0.054667086	-16.2726	1.55E-59	9.92E-59	cyan	-0.77355958	1.62E-32		AT1G67090.1	RBCS1A	ribulose bisphosphate carboxylase small chain 1A	ribulose bisphosphate carboxylase small chain
Sapur.010G145100.1	226.4097717	1.458118762	0.089608036	16.27219	1.56E-59	9.97E-59	cyan	0.65851069	7.06E-21	GO:0006468,GO:0004672	AT5G07150.1		Leucine-rich repeat protein kinase family protein	tyrosine kinase domain protein
Sapur.004G134500.1	21.38115793	-1.254663514	0.0771102	-16.271	1.58E-59	1.02E-58	cyan	-0.811310017	5.76E-38		AT4G35130.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.009G127900.1	60.21876526	-0.847925772	0.052145433	-16.2608	1.87E-59	1.20E-58	cyan	-0.802607458	1.32E-36		AT2G27470.1	NF-YB11	nuclear factor Y, subunit B11	histone-like transcription factor and archaeal histone protein
Sapur.002G108800.1	261.4586224	0.830712459	0.051090286	16.25969	1.91E-59	1.22E-58	cyan	0.771831287	2.72E-32	GO:0016559,GO:0005779	AT1G47750.1	PEX11A	peroxin 11A	peroxisomal biogenesis factor 11
Sapur.007G107400.1	24.24394762	2.884746669	0.177424739	16.25899	1.93E-59	1.24E-58	cyan	0.531510766	7.94E-13	GO:0009055	AT2G32300.1	UCC1	uclacyanin 1	plastocyanin-like domain protein
Sapur.010G027100.1	350.1326249	-0.765340059	0.047081161	-16.2558	2.03E-59	1.30E-58	cyan	-0.826176444	1.84E-40		AT1G60790.1	TBL2	Plant protein of unknown function (DUF828)	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.016G005400.1	278.6884704	0.650257689	0.040008963	16.2528	2.13E-59	1.37E-58	cyan	0.786483547	2.95E-34	GO:0016787	AT5G47650.1	ATNUDT2.ATNUDX2.NUDT	nudix hydrolase homolog 2	nudix hydrolase
Sapur.014G016900.1	16.17232895	-1.807284199	0.11120595	-16.2517	2.17E-59	1.39E-58	cyan	-0.759935339	8.41E-31		AT1G45207.2		Remorin family protein	remorin
Sapur.008G047800.1	278.8118222	0.533241894	0.032817212	16.24885	2.28E-59	1.46E-58	cyan	0.783326305	8.05E-34	GO:0016020	AT2G39805.2		Integral membrane Yip1 family protein	NA
Sapur.009G063900.1	744.1459709	0.660790044	0.040669034	16.24799	2.31E-59	1.48E-58	cyan	0.755682667	2.73E-30		AT5G64510.1			nicotiana tabacum ORF protein
Sapur.15WG083300.1	57.70746675	-1.013507858	0.062394172	-16.2436	2.48E-59	1.58E-58	cyan	-0.76539074	1.79E-31	GO:0003676,GO:0017069,GO:0000398	AT2G30260.1	U2B\'\'	U2 small nuclear ribonucleoprotein B	NA
Sapur.010G204100.1	302.2121303	-0.762720587	0.046955338	-16.2435	2.48E-59	1.59E-58	cyan	-0.809385187	1.17E-37		AT1G16860.1		Ubiquitin-specific protease family C19-related protein	cysteine-type endopeptidase/ubiquitin thiolesterase
Sapur.006G043400.1	69.80523359	-1.706749038	0.105086515	-16.2414	2.57E-59	1.64E-58	cyan	-0.752438911	6.61E-30					transmembrane protein, putative
Sapur.005G197100.1	1025.80536	-1.391736075	0.085704573	-16.2388	2.68E-59	1.71E-58	cyan	-0.795769454	1.39E-35		AT1G76100.1	PETE1	plastocyanin 1	NA
Sapur.001G069700.1	169.6056995	0.820305589	0.0505247	16.23573	2.82E-59	1.80E-58	cyan	0.763108862	3.43E-31	GO:0016021,GO:0005789	AT5G42000.1		ORMDL family protein	ORMDL family protein
Sapur.005G190800.1	591.7057307	-0.865425442	0.053305423	-16.2352	2.84E-59	1.81E-58	cyan	-0.778277304	3.88E-33		AT5G42560.1		Abscisic acid-responsive (TB2/DP1, HVA22) family protein	HVA22-like protein I
Sapur.004G163700.1	781.3951839	-0.743073041	0.045781654	-16.2308	3.05E-59	1.95E-58	cyan	-0.815278723	1.31E-38	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G44890.1	RPL9	ribosomal protein L9	50S ribosomal protein L9
Sapur.017G107800.1	126.4468191	-1.22306399	0.075375318	-16.2263	3.29E-59	2.09E-58	cyan	-0.798497559	5.49E-36	GO:0007264,GO:0005525	AT5G37680.1	ARLA1A,ATARLA1A	ADP-ribosylation factor-like A1A	ADP-ribosylation factor-like protein
Sapur.013G125800.1	79.69358383	-1.004349473	0.061913876	-16.2217	3.54E-59	2.26E-58	cyan	-0.79861189	5.28E-36		AT1G03670.1		ankyrin repeat family protein	ankyrin repeat protein
Sapur.004G144400.1	13.6552895	4.929068497	0.303921786	16.21821	3.75E-59	2.39E-58	cyan	0.642375111	1.21E-19					NA
Sapur.006G105700.1	206.695108	1.551653668	0.095708567	16.21228	4.13E-59	2.63E-58	cyan	0.729879293	2.15E-27		AT3G09770.1		RING/U-box superfamily protein	E3 ubiquitin-protein ligase, putative
Sapur.001G099300.1	617.8389944	0.983862156	0.060702167	16.20802	4.43E-59	2.81E-58	cyan	0.726266777	5.14E-27		AT4G22580.1		Exostosin family protein	exostosin family protein
Sapur.013G111400.1	585.3837717	0.651289148	0.040183785	16.20776	4.44E-59	2.83E-58	cyan	0.76556705	1.70E-31		AT3G54680.1		proteophosphoglycan-related	plant/T5N23-40 protein, putative
Sapur.005G182300.1	133.7920319	-1.074613346	0.066311403	-16.2056	4.61E-59	2.93E-58	cyan	-0.813517788	2.54E-38	GO:0016567,GO:0004842	AT4G36550.1		ARM repeat superfamily protein	ubiquitin-protein ligase, putative
Sapur.009G124800.1	1933.334927	0.808929338	0.049934259	16.19989	5.05E-59	3.21E-58	cyan	0.756760547	2.03E-30	GO:0016705,GO:0016117	AT3G10230.1	LYC	lycopene cyclase	capsanthin/capsorubin synthase, chromoplast protein
Sapur.001G187400.1	212.1956338	-0.797686317	0.049252068	-16.196	5.38E-59	3.42E-58	cyan	-0.785126966	4.55E-34	GO:0005524	AT5G49840.1		ATP-dependent Clp protease	ATP-dependent Clp protease ATP-binding subunit CLPX protein, putative
Sapur.019G052100.1	1810.170462	0.724903818	0.044772925	16.19067	5.87E-59	3.72E-58	cyan	0.755159738	3.15E-30	GO:0016787,GO:0008299,GO:0004452	AT3G02780.1	IDI2,IPIAT1,IPP2	isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase 2	isopentenyl diphosphate isomerase
Sapur.007G091100.1	224.4089255	0.746942458	0.046156532	16.18281	6.67E-59	4.23E-58	cyan	0.761415806	5.55E-31	GO:0007034	AT5G09260.1	VPS20.2	vacuolar protein sorting-associated protein 20.2	NA
Sapur.008G103100.1	423.9584209	0.543826058	0.033607398	16.18174	6.79E-59	4.30E-58	cyan	0.774060662	1.40E-32	GO:0016020,GO:0008375	AT1G71070.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	acetylglucosaminyltransferase, putative
Sapur.007G058000.1	441.1011395	-0.714023424	0.044139459	-16.1765	7.38E-59	4.67E-58	cyan	-0.798118722	6.25E-36		AT1G79190.1		ARM repeat superfamily protein	Tel2-interacting protein
Sapur.016G049700.1	4.144712867	5.365826201	0.331888734	16.16755	8.54E-59	5.40E-58	cyan	0.683451981	6.07E-23	GO:0006355,GO:0003677	AT1G69490.1	ANAC029,ATNAP,NAP	NAC-like, activated by AP3/PI	NAC domain protein
Sapur.005G127900.1	374.530047	0.978004293	0.060498202	16.16584	8.78E-59	5.56E-58	cyan	0.753476989	4.99E-30	GO:0045454	AT1G34780.1	APRL4,ATAPRL4	APR-like 4	5'-adenylylsulfate reductase-like protein
Sapur.T009500.1	5.856553354	3.43694097	0.212692085	16.15923	9.78E-59	6.18E-58	cyan	0.695319126	5.32E-24					NA
Sapur.011G082700.1	3392.326358	0.608842162	0.037685379	16.15592	1.03E-58	6.52E-58	cyan	0.758976678	1.10E-30	GO:0010155,GO:0005886,GO:0005783	AT4G27500.1	PPI1	proton pump interactor 1	DNA double-strand break repair rad50 ATPase, putative
Sapur.009G129000.1	57.08272876	1.122816037	0.069561482	16.14135	1.31E-58	8.25E-58	cyan	0.738264986	2.68E-28		AT3G44510.2		alpha/beta-Hydrolases superfamily protein	alpha/beta hydrolase family protein
Sapur.003G129900.1	2.274221708	4.592648707	0.284574764	16.13864	1.37E-58	8.62E-58	cyan	0.669307627	9.53E-22	GO:0000160	AT3G04280.2	ARR22,RR22	response regulator 22	NA
Sapur.007G059000.1	78.67307528	-0.91914719	0.056966829	-16.1348	1.45E-58	9.17E-58	cyan	-0.801057457	2.27E-36		AT1G79060.1			hypothetical protein
Sapur.008G083600.1	100.8683989	-1.764189712	0.109365059	-16.1312	1.54E-58	9.71E-58	cyan	-0.814954566	1.48E-38		AT4G24972.1	TPD1	tapetum determinant 1	DNA-directed RNA polymerase, putative
Sapur.006G169500.1	135.96671	-0.89868946	0.055717709	-16.1293	1.59E-58	1.00E-57	cyan	-0.831865484	1.77E-41	GO:0016787,GO:0008152	AT3G02875.1	ILR1	Peptidase M20/M25/M40 family protein	IAA-amino acid hydrolase ILR1, putative
Sapur.001G059900.5	10.69535353	-1.874017067	0.11619475	-16.1282	1.62E-58	1.02E-57	cyan	-0.790883409	7.07E-35	GO:0006457	AT5G45680.1	ATFKBP13,FKBP13	FK506-binding protein 13	peptidyl-prolyl cis-trans isomerase
Sapur.012G041600.1	8.568869674	-2.043209002	0.126685948	-16.1281	1.62E-58	1.02E-57	cyan	-0.773197496	1.81E-32					hypothetical protein
Sapur.001G049800.1	556.5377599	1.632493434	0.101256445	16.12237	1.78E-58	1.12E-57	cyan	0.72730861	4.01E-27	GO:0008081,GO:0006629	AT5G41080.1		PLC-like phosphodiesterases superfamily protein	NA
Sapur.007G045500.1	517.6765019	0.814186725	0.050507176	16.12022	1.84E-58	1.16E-57	cyan	0.746587389	3.14E-29	GO:0005515	AT5G67250.1	SKIP2,VFB4	SKP1/ASK1-interacting protein 2	F-box protein SKIP2
Sapur.003G130900.1	1129.380563	0.642392723	0.03986645	16.11362	2.05E-58	1.29E-57	cyan	0.78150621	1.43E-33		AT1G04630.1	MEE4	GRIM-19 protein	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex protein
Sapur.004G052800.1	7652.009698	0.829865244	0.051501388	16.11345	2.05E-58	1.29E-57	cyan	0.772502158	2.23E-32	GO:0030170,GO:0019752,GO:0016831	AT5G17330.1	GAD,GAD1	glutamate decarboxylase	glutamate decarboxylase
Sapur.005G203300.1	656.3202815	0.51250018	0.031809873	16.11136	2.12E-58	1.33E-57	cyan	0.776364465	6.96E-33	GO:0003824,GO:0006470,GO:0004722	AT2G33700.1		Protein phosphatase 2C family protein	protein phosphatase 2C, putative
Sapur.008G035300.1	101.1562179	-0.704043103	0.043700393	-16.1107	2.15E-58	1.35E-57	cyan	-0.78603074	3.41E-34	GO:0033588	AT4G10090.1	ELP6	elongator protein 6	elongator complex protein
Sapur.001G037500.1	512.924973	0.568406238	0.035300958	16.10172	2.48E-58	1.56E-57	cyan	0.756430444	2.23E-30	GO:0005634	AT1G80780.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	CCR4-associated factor, putative
Sapur.005G205200.1	10.94998257	-1.73902187	0.108022487	-16.0987	2.61E-58	1.64E-57	cyan	-0.797758151	7.07E-36	GO:0046872,GO:0030001	AT3G56891.1		Heavy metal transport/detoxification superfamily protein	NA
Sapur.007G108200.1	132.3139527	-1.403299897	0.087171879	-16.0981	2.63E-58	1.65E-57	cyan	-0.742870472	8.27E-29		AT3G21870.1	CYCP2;1	cyclin p2;1	cyclin-U1-1 protein
Sapur.016G023000.1	4799.614046	0.918896412	0.05712047	16.08699	3.15E-58	1.97E-57	cyan	0.772041262	2.55E-32		AT2G27030.3	ACAM-2,CAM5	calmodulin 5	calmodulin cam-203
Sapur.008G082500.1	215.3098857	1.301284477	0.080917911	16.08154	3.44E-58	2.15E-57	cyan	0.726744496	4.59E-27	GO:0005509	AT5G49480.1	ATCP1,CP1	Ca2+-binding protein 1	nacl-inducible Ca2+-binding protein
Sapur.15WG004000.1	223.0415786	-0.867012252	0.053924383	-16.0783	3.62E-58	2.27E-57	cyan	-0.810779143	7.01E-38		AT5G24500.1			hypothetical protein
Sapur.014G087100.1	340.1998944	1.054307493	0.065612576	16.06868	4.23E-58	2.65E-57	cyan	0.738683871	2.41E-28		AT1G28200.1	FIP1	FH interacting protein 1	NA
Sapur.004G033000.1	36.18629825	1.917224008	0.119329907	16.06658	4.38E-58	2.74E-57	cyan	0.670474296	7.64E-22	GO:0006468,GO:0004672	AT5G46080.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.017G039800.1	3341.909815	1.354800141	0.084330953	16.06528	4.47E-58	2.79E-57	cyan	0.662451812	3.43E-21		AT5G64260.1	EXL2	EXORDIUM like 2	phosphate-induced protein 1 motif protein
Sapur.018G040100.1	360.8218069	0.832647723	0.051874478	16.0512	5.61E-58	3.50E-57	cyan	0.759091832	1.06E-30		AT2G26070.1	RTE1	Protein of unknown function (DUF778)	green-ripe protein
Sapur.002G171500.1	70.38906058	-1.239254969	0.077266908	-16.0386	6.87E-58	4.28E-57	cyan	-0.805471822	4.79E-37	GO:0005524,GO:0004797	AT3G07800.1		Thymidine kinase	thymidine kinase
Sapur.017G050100.1	19448.07995	0.890825917	0.055548027	16.03704	7.04E-58	4.39E-57	cyan	0.760798828	6.60E-31	GO:0055114,GO:0051287,GO:0006730,GO:0004013	AT4G13940.1	ATSAHH1.EMB1395.HOG1.M	S-adenosyl-L-homocysteine hydrolase	S-adenosyl-L-homocysteine hydrolase
Sapur.016G260600.1	144.1745746	-1.451955084	0.090542599	-16.0362	7.14E-58	4.45E-57	cyan	-0.757324599	1.74E-30		AT4G27460.1		Cystathionine beta-synthase (CBS) family protein	NA
Sapur.019G068600.1	1478.619903	0.469111387	0.029264825	16.02987	7.90E-58	4.93E-57	cyan	0.800767561	2.51E-36	GO:0005525,GO:0003924	AT1G59610.1	ADL3,CF1,DL3,DRP2B	dynamin-like 3	NA
Sapur.15WG002200.1	9.695440057	-2.237313453	0.139649598	-16.0209	9.13E-58	5.68E-57	cyan	-0.75386694	4.49E-30		AT4G27660.1			hypothetical protein
Sapur.013G087100.1	7.028969968	2.977578477	0.185895733	16.01747	9.65E-58	6.01E-57	cyan	0.685264983	4.21E-23					NA
Sapur.011G075200.1	330.3158717	0.387192219	0.024176356	16.01533	9.99E-58	6.21E-57	cyan	0.792863972	3.67E-35		AT1G78800.1		UDP-Glycosyltransferase superfamily protein	alpha-1%2C3-mannosyltransferase ALG2
Sapur.017G003300.1	312.8894794	-0.671859724	0.04195926	-16.0122	1.05E-57	6.53E-57	cyan	-0.801304988	2.08E-36		AT2G43950.1	ATOEP37,OEP37	chloroplast outer envelope protein 37	outer envelope pore protein
Sapur.012G057900.1	362.478589	-0.750704317	0.046897543	-16.0073	1.14E-57	7.06E-57	cyan	-0.802099558	1.58E-36	GO:0006396,GO:0004525,GO:0003723	AT1G24450.1	NFD2	Ribonuclease III family protein	ribonuclease-III-like protein
Sapur.004G141400.1	62.10358965	1.271206129	0.079445459	16.00099	1.26E-57	7.81E-57	cyan	0.710555908	1.96E-25		AT2G27770.1		Plant protein of unknown function (DUF868)	DUF868 family protein
Sapur.15WG129400.1	129.4525953	-1.062273072	0.066406774	-15.9965	1.35E-57	8.40E-57	cyan	-0.796387481	1.13E-35	GO:0055114,GO:0008113,GO:0030091,GO:0016671,GO:0006979	AT4G25130.1	PMSR4	peptide met sulfoxide reductase 4	peptide methionine sulfoxide reductase
Sapur.011G029600.1	1111.108246	0.621615931	0.038860674	15.99602	1.36E-57	8.46E-57	cyan	0.752038775	7.36E-30	GO:0055114,GO:0016491,GO:0008270	AT4G21580.1		oxidoreductase, zinc-binding dehydrogenase family protein	NADPH quinone oxidoreductase, putative
Sapur.15ZG035800.1	12.71728501	2.144078112	0.134112368	15.98718	1.57E-57	9.74E-57	cyan	0.674056435	3.84E-22	GO:0006468,GO:0005524,GO:0004672	AT5G63610.1	ATCDK8,CDKE;1,HEN3	cyclin-dependent kinase E;1	cyclin-dependent kinase E-1
Sapur.007G055200.1	19.93656143	-1.497591582	0.093692644	-15.9841	1.65E-57	1.02E-56	cyan	-0.75978274	8.78E-31		AT2G17510.1	EMB2763	ribonuclease II family protein	NA
Sapur.016G262900.1	6.895915796	-2.286537395	0.143051631	-15.984	1.65E-57	1.02E-56	cyan	-0.769230294	5.86E-32		AT1G52855.1			hypothetical protein
Sapur.018G078700.1	487.9226711	0.801785301	0.05017428	15.98001	1.76E-57	1.09E-56	cyan	0.755513969	2.86E-30		AT4G30790.1			autophagy-related protein
Sapur.011G105300.1	8085.140657	-0.910279315	0.056972245	-15.9776	1.83E-57	1.13E-56	cyan	-0.800331526	2.92E-36	GO:0042651,GO:0015979,GO:0009654,GO:0009523	AT1G79040.1	PSBR	photosystem II subunit R	photosystem II 10 kDa protein
Sapur.011G054600.1	244.7514176	-1.212308886	0.075878215	-15.977	1.85E-57	1.14E-56	cyan	-0.798680677	5.15E-36	GO:0006355,GO:0005739,GO:0003690	AT2G34620.1		Mitochondrial transcription termination factor family protein	mTERF-like protein
Sapur.012G105700.1	17.44117703	-2.88330427	0.180523714	-15.9719	2.01E-57	1.24E-56	cyan	-0.680624553	1.07E-22	GO:0016788	AT1G29670.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-lipase, putative
Sapur.013G066700.1	337.6178783	1.36988194	0.085770019	15.97157	2.02E-57	1.25E-56	cyan	0.641420834	1.43E-19					NA
Sapur.002G108100.1	294.2165544	1.13817204	0.071280918	15.96742	2.16E-57	1.33E-56	cyan	0.714876525	7.37E-26	GO:0016757	AT1G19300.1	ATGATL1.GATL1.GLZ1.PARV	Nucleotide-diphospho-sugar transferases superfamily protein	glycosyltransferase family GT8 protein
Sapur.009G007100.1	153.46259	-0.7907931	0.049545038	-15.9611	2.39E-57	1.48E-56	cyan	-0.782052086	1.20E-33	GO:0008289,GO:0003677	AT5G60690.1	IFL,IFL1,REV	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein	NA
Sapur.001G142000.1	11.07183016	2.823897292	0.177100212	15.94519	3.08E-57	1.90E-56	cyan	0.596312621	1.72E-16					NA
Sapur.002G125900.1	29.80398398	-1.276548873	0.080072721	-15.9424	3.22E-57	1.99E-56	cyan	-0.770458821	4.08E-32	GO:0006355,GO:0003677	AT1G33060.2	ANAC014,NAC014	NAC 014	NAC domain protein
Sapur.008G113600.1	135.8669429	-0.812729866	0.051019251	-15.9299	3.93E-57	2.43E-56	cyan	-0.784308018	5.90E-34		AT1G68130.1	AtIDD14,IDD14	indeterminate(ID)-domain 14	C2H2L domain class transcription factor
Sapur.019G081100.1	397.9625315	0.598005987	0.03754549	15.92751	4.08E-57	2.52E-56	cyan	0.765274632	1.85E-31		AT1G71940.1		SNARE associated Golgi protein family	SNARE associated protein
Sapur.003G100600.1	78.40783397	-0.88235541	0.055407415	-15.9249	4.26E-57	2.63E-56	cyan	-0.760461458	7.26E-31	GO:0006396,GO:0005622	AT5G41770.1		crooked neck protein, putative / cell cycle protein, putative	cell cycle control protein crooked neck-like protein, putative
Sapur.016G291500.1	79.56395587	-1.332463611	0.083673848	-15.9245	4.28E-57	2.64E-56	cyan	-0.775652278	8.63E-33		AT1G61570.1	TIM13	translocase of the inner mitochondrial membrane 13	import inner membrane translocase subunit Tim13, putative
Sapur.005G134700.1	1321.738681	-0.736625934	0.04627793	-15.9174	4.80E-57	2.95E-56	cyan	-0.785018796	4.71E-34	GO:0006412,GO:0005840,GO:0005622,GO:0003735,GO:0003723	AT5G14320.1		Ribosomal protein S13/S18 family	30S ribosomal protein S13
Sapur.006G139300.4	12.86361852	-1.406489373	0.088402325	-15.9101	5.39E-57	3.32E-56	cyan	-0.79967961	3.66E-36	GO:0030170,GO:0008483	AT5G57590.1	BIO1	adenosylmethionine-8-amino-7-oxononanoate transaminases	NA
Sapur.004G076400.1	846.6071023	0.738909898	0.046473048	15.89975	6.36E-57	3.91E-56	cyan	0.744323987	5.68E-29	GO:0003333	AT3G30390.1		Transmembrane amino acid transporter family protein	amino acid transporter
Sapur.002G196900.1	27.25598025	-2.105872426	0.132448818	-15.8995	6.39E-57	3.92E-56	cyan	-0.736901674	3.79E-28	GO:0000160	AT5G26594.1	ARR24,RR24	response regulator 24	extra response regulator
Sapur.010G009000.1	681.1093712	1.011851394	0.063641237	15.8993	6.41E-57	3.94E-56	cyan	0.725054739	6.87E-27	GO:0005515	AT4G15840.1		BTB/POZ domain-containing protein	BTB/POZ domain protein
Sapur.001G046700.1	2830.802748	1.114597574	0.070104635	15.89906	6.43E-57	3.95E-56	cyan	0.7514212	8.70E-30	GO:0005783	AT1G27350.1		Ribosome associated membrane protein RAMP4	ribosome associated membrane protein RAMP4
Sapur.002G136000.1	96.14760401	0.951647499	0.059864634	15.89666	6.68E-57	4.10E-56	cyan	0.72802515	3.37E-27		AT4G01575.1		serine protease inhibitor, Kazal-type family protein	serine-type endopeptidase inhibitor, putative
Sapur.016G232300.1	171.2908107	-0.501044928	0.031523873	-15.8941	6.96E-57	4.27E-56	cyan	-0.780263349	2.10E-33		AT1G55880.1		Pyridoxal-5\'-phosphate-dependent enzyme family protein	cysteine synthase
Sapur.017G030200.1	44.0708443	-1.777361726	0.111827612	-15.8938	7.00E-57	4.30E-56	cyan	-0.767405018	9.98E-32		AT3G22070.1		proline-rich family protein	transmembrane protein, putative
Sapur.007G129900.1	47.94443794	-0.810064324	0.050972751	-15.8921	7.19E-57	4.41E-56	cyan	-0.791540321	5.69E-35	GO:0005975,GO:0004649	AT2G31870.2	TEJ	Poly (ADP-ribose) glycohydrolase (PARG)	NA
Sapur.014G079900.1	13.64725356	2.771668335	0.174479917	15.88531	8.01E-57	4.91E-56	cyan	0.671916673	5.80E-22		AT4G27745.1		Yippee family putative zinc-binding protein	Fad NAD-binding oxidoreductase, putative
Sapur.008G093600.1	455.5961915	-1.654171362	0.104142323	-15.8838	8.21E-57	5.03E-56	cyan	-0.725413841	6.31E-27	GO:0050662,GO:0003824	AT1G75290.1		NAD(P)-binding Rossmann-fold superfamily protein	NA
Sapur.002G096200.1	198.6887775	1.762172918	0.110952688	15.8822	8.42E-57	5.16E-56	cyan	0.760238419	7.72E-31		AT1G27730.1	STZ,ZAT10	salt tolerance zinc finger	Cys2-His2 type zinc finger protein, putative
Sapur.016G148000.1	211.6565328	-0.895449157	0.056380731	-15.8822	8.42E-57	5.16E-56	cyan	-0.791288705	6.18E-35	GO:0016740,GO:0008033	AT1G51310.1		transferases;tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferases	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
Sapur.019G066200.1	1551.755897	0.33375906	0.021022178	15.87652	9.21E-57	5.64E-56	cyan	0.753696818	4.70E-30	GO:0055114,GO:0016491,GO:0008270	AT3G56460.1		GroES-like zinc-binding alcohol dehydrogenase family protein	zinc-binding dehydrogenase family oxidoreductase
Sapur.004G163900.1	964.1244771	0.604149207	0.038054546	15.87587	9.31E-57	5.70E-56	cyan	0.74335741	7.30E-29	GO:0055114,GO:0051537,GO:0016491,GO:0010277	AT3G44880.1	ACD1,LLS1,PAO	Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain	pheophorbide A oxygenase
Sapur.012G056700.1	141.417072	-1.348687757	0.085050183	-15.8576	1.25E-56	7.62E-56	cyan	-0.778356261	3.78E-33		AT5G50090.2			NA
Sapur.T045800.1	106.1371616	-0.712138679	0.044911127	-15.8566	1.27E-56	7.73E-56	cyan	-0.79376403	2.72E-35	GO:0005634	AT3G25430.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	poly(A)-specific ribonuclease PARN protein
Sapur.010G125600.1	197.4746074	-1.108238561	0.069906196	-15.8532	1.34E-56	8.16E-56	cyan	-0.832903516	1.14E-41	GO:0051301,GO:0032955	AT1G69390.1	ARC12,ATMINE1,MINE1	homologue of bacterial MinE 1	cell division topological specificity factor MinE
Sapur.T127700.1	6.018183259	2.199880196	0.138768214	15.85291	1.34E-56	8.20E-56	cyan	0.788888566	1.36E-34					NA
Sapur.T154200.1	6.617725609	3.366815164	0.212551432	15.84	1.65E-56	1.01E-55	cyan	0.717489056	4.05E-26					NA
Sapur.012G043200.1	17.20331863	-1.808296856	0.114193628	-15.8354	1.77E-56	1.08E-55	cyan	-0.751286068	9.02E-30		AT5G11040.1	AtTRS120,TRS120	TRS120	NA
Sapur.003G092300.1	125.1033809	-1.282467194	0.081022718	-15.8285	1.98E-56	1.21E-55	cyan	-0.742866112	8.28E-29	GO:0055114,GO:0016491	AT4G23340.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2OG-Fe(II) oxygenase family oxidoreductase
Sapur.016G046000.1	753.4159066	0.792799137	0.050088152	15.82808	1.99E-56	1.22E-55	cyan	0.769731376	5.06E-32		AT2G42310.1			ESSS subunit of NADH:ubiquinone oxidoreductase (complex I) protein
Sapur.15WG000200.1	530.2685389	0.661379659	0.041791812	15.82558	2.07E-56	1.26E-55	cyan	0.789620914	1.07E-34		AT3G49590.2		Autophagy-related protein 13	autophagy-related protein
Sapur.004G067400.1	70.82484599	-1.417635916	0.089586695	-15.8242	2.12E-56	1.29E-55	cyan	-0.774911932	1.08E-32					transmembrane protein, putative
Sapur.009G063300.1	264.4242307	0.90453293	0.057162954	15.82376	2.13E-56	1.30E-55	cyan	0.752279731	6.90E-30	GO:0055114,GO:0050661,GO:0033014,GO:0008883	AT1G58290.1	HEMA1	Glutamyl-tRNA reductase family protein	glutamyl-tRNA reductase

Sapur.01G0077800.1	621.8703992	0.8543752	0.054010949	15.81671	2.39E-56	1.45E-55	cpm	0.742404932	9.33E-20		GO:0140180		LIV-stimulated scaffold A-like protein, putative
Sapur.01G0073900.1	263.430946	-0.649760472	0.041088249	-15.8188	2.50E-56	1.52E-55	cpm	-0.796865471	9.58E-16	GO:0003723	GO:0009290		THUMP domain protein
Sapur.01G0183000.1	82.2133768	0.551928716	0.037402042	14.8501	2.96E-56	1.80E-55	cpm	0.800201287	3.56E-20	GO:0005681	GO:0005840		transcriptional regulator of BRA pdrl1, SAGA, subunit
Sapur.01G0698200.1	26.3908284	2.353947332	0.148998426	15.79847	3.13E-56	1.94E-55	cpm	0.82603652	1.95E-40		GO:0048630	PCR11	PLANT CADMIUM RESISTANCE 11
Sapur.01G0281300.1	355.0154606	0.810403362	0.051330874	15.7939	3.42E-56	2.08E-55	cpm	-0.780866237	1.72E-33	GO:0005515	GO:0003370.1		C2 calcium/lipid-binding and GRAM domain containing protein
Sapur.01G0640000.1	187.4604662	0.994156795	0.062953922	15.79182	3.54E-56	2.15E-55	cpm	-0.724998708	6.96E-27	GO:0005622;GO:0003779;GO:0030042;GO:0015629	GO:0005890	ADF4;ATADF4	actin depolymerizing factor 4
Sapur.01G0260300.1	1478.413845	0.662066898	0.04192869	15.78981	3.66E-56	2.22E-55	cpm	0.773851957	2.67E-32		GO:0020152.1		
Sapur.T040000.1	172.9032204	1.664398646	0.105433092	15.7863	3.87E-56	2.35E-55	cpm	0.792716113	1.36E-24		GO:0016020.1		Integral membrane HRF1 family protein
Sapur.T146100.1	7.108425987	2.367032447	0.21343137	15.7786	4.37E-56	2.65E-55	cpm	0.70820246	3.30E-25				NA
Sapur.007G0199200.1	82.33668736	1.162457346	0.074297986	15.7763	4.53E-56	2.74E-55	cpm	0.728032339	2.97E-27		GO:0007581.1		Myb-like DNA-binding domain protein, putative
Sapur.01G0269700.1	182.8082435	0.686028019	0.043458304	15.77584	4.54E-56	2.76E-55	cpm	0.73861956	2.65E-28		GO:0005739.1		Protein of unknown function (DUF3639)
Sapur.01G0047100.1	2.246887142	-0.47182776	0.29400217	15.7506	5.46E-56	3.32E-55	cpm	0.517170179	4.08E-12		GO:0016740.1		Protein family protein
Sapur.006G1395600.1	444.4857586	1.461671155	0.092789973	15.75247	6.63E-56	3.96E-55	cpm	0.707546891	3.82E-25		GO:0016787		Polyketide cyclase/dehydrase and lipid transport superfamily protein
Sapur.006G0994000.1	52.13376818	0.760774428	0.048305519	15.7159	8.73E-56	5.06E-55	cpm	0.752546884	6.63E-30		GO:0016540.1		NA
Sapur.02G0357800.1	132.0932456	-1.578575289	0.100233705	-15.7484	7.04E-56	4.25E-55	cpm	-0.761665329	5.47E-31	GO:0009055	GO:0020850.1	ARPN	transmembrane protein, putative
Sapur.01G0461200.1	140.3304512	0.9832423	0.062421671	15.75469	7.39E-56	4.46E-55	cpm	-0.784548807	8.96E-26	GO:0004888	GO:0005524;GO:0009507;GO:0004672	MAPKKK18	plantacyanin
Sapur.003G0794000.1	109.3378088	-0.583621201	0.037071168	-15.7433	7.64E-56	4.61E-55	cpm	-0.781738399	1.31E-33		GO:0005185;GO:0005886		mitogen-activated protein kinase kinase kinase 18
Sapur.01G0256700.1	1391.083899	0.668697947	0.041086725	15.74255	7.73E-56	4.66E-55	cpm	0.767996683	8.40E-32	GO:0016149;GO:0006415;GO:0005737	GO:0003743	ERF1-3	zinc finger (CCHC-type) family protein
Sapur.005G1321001.1	60.5140476	-0.490278431	0.079696417	-15.7319	8.96E-56	5.40E-55	cpm	-0.720128973	1.36E-24	GO:0043565;GO:0006355;GO:0005730	GO:0003700		eukaryotic release factor 1-3
Sapur.T025500.1	1333.457272	0.458406088	0.029142903	15.73147	9.20E-56	5.55E-55	cpm	0.778208972	3.96E-33		GO:0046085.1		Basic-leucine zipper (bZIP) transcription factor family protein
Sapur.02G0169200.1	122.1164312	1.127457346	0.15469445	15.7109	9.51E-56	5.73E-55	cpm	-0.646014124	2.29E-18	GO:0046983	GO:0016491	ATMRC2;AR1;JIN1;MYC2;RE	transcription factor (bHLH) DNA-binding family protein
Sapur.01G0144400.1	2476.469918	0.909889548	0.057852835	-15.7277	9.78E-56	5.89E-55	cpm	-0.774166797	1.35E-32	GO:0015979;GO:0009538;GO:0009522	GO:0012800.1	PSAL	Basic-helix-loop-helix (bHLH) DNA-binding family protein
Sapur.01G0203500.1	695.1775883	0.804821784	0.053881746	-15.7268	9.93E-56	5.97E-55	cpm	-0.69918805	2.55E-24	GO:0007165;GO:0005515;GO:0043531	GO:0016020.2		photosystem I reaction center subunit XI
Sapur.01G0205800.1	724.0766122	0.395888617	0.025179071	15.72633	9.98E-56	6.01E-55	cpm	-0.782909547	9.18E-34	GO:0016787	GO:0003700		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.01G0071500.1	186.3919369	0.760774428	0.048348888	15.73028	1.38E-55	8.30E-55	cpm	-0.76917015	2.04E-32		GO:0016301.1		Calcineurin-like metallo-phosphoesterase superfamily protein
Sapur.01G0271000.1	95.62215784	-0.619466196	0.039437611	-15.7007	1.49E-55	8.96E-55	cpm	-0.791435596	5.89E-35		GO:0005886	ATSPI4;SPI4	SPI4 domain protein
Sapur.01G0247500.1	27.18894619	-1.213705089	0.077302591	-15.7007	1.50E-55	8.99E-55	cpm	-0.794022719	2.50E-35		GO:0016829		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01G0178800.1	18.16723861	-0.474861952	0.030261377	-15.6863	1.68E-55	1.00E-54	cpm	-0.778828098	1.27E-33	GO:0016021	GO:0016020		Carbohydrate-binding X8 domain superfamily protein
Sapur.01T0268800.1	10.19337652	-1.711904104	0.109033117	-15.6933	1.68E-55	1.01E-54	cpm	-0.786498801	2.93E-34	GO:0055085;GO:0005741	GO:0005886	ATVDAC1;VDAC1	Peroxisomal membrane 22 kDa (Pex19p)(PMP22) family protein
Sapur.01G0231300.1	407.5553814	-0.490278431	0.031172326	-15.6748	1.83E-55	1.10E-54	cpm	-0.788463138	1.56E-34	GO:0005509;GO:0046873;GO:0030001;GO:0016020	GO:0005200		voltage dependent anion channel 1
Sapur.01G0267700.2	22.06503311	1.456764089	0.092937073	15.67642	2.19E-55	1.32E-54	cpm	-0.75253701	6.24E-30	GO:0005515;GO:0005096	GO:2311160.3	AGD12;ZAC	Magnesium transporter CorA family protein
Sapur.006G0948000.1	954.1138861	0.468704308	0.029903313	15.67399	2.28E-55	1.37E-54	cpm	-0.798032344	6.44E-36		GO:0005085.1		Calcium-dependent ARF-type GTPase activating protein family
Sapur.T120700.1	6.110693054	2.144179405	0.136885589	15.67356	2.33E-55	1.39E-54	cpm	0.804433069	6.91E-27	GO:0005515	GO:0016020.1	ATIMR1;FIM1	glucosides 1 beta subunit-like protein
Sapur.01G0617800.1	115.8763074	0.810872844	0.051846332	-15.663	2.75E-55	1.62E-54	cpm	-0.762074661	7.63E-31	GO:0005515	GO:0016180.1		Fimbrin
Sapur.15W0141700.1	69.60313316	0.707535361	0.045180756	-15.6601	2.83E-55	1.70E-54	cpm	-0.792367629	4.33E-35		GO:0016787		F-box only protein
Sapur.01G0289700.1	471.836602	1.156135408	0.074000378	15.65092	2.84E-55	1.70E-54	cpm	0.805127242	6.38E-27		GO:0043481		mediator of RNA polymerase II transcription subunit 30, putative
Sapur.01G0280900.1	1766.6641	1.350105205	0.085326778	15.65669	2.99E-55	1.79E-54	cpm	-0.625601086	1.96E-18	GO:0016787	GO:0003723	ATPAP18;PAP18	RING/U-box superfamily protein
Sapur.01G0254000.1	1111.582344	0.878834863	0.056134418	-15.6559	3.08E-55	1.85E-54	cpm	-0.79413657	2.25E-35		GO:0016020.1	PSRP5	purple acid phosphatase 18
Sapur.00B0261000.1	421.9609661	0.811589344	0.052484888	15.65601	3.14E-55	1.88E-54	cpm	-0.76917015	2.04E-32		GO:0016787		plastid-specific 50S ribosomal protein 5
Sapur.01G0072200.1	34.59198243	2.167803671	0.138508883	15.65025	3.31E-55	1.98E-54	cpm	-0.686024746	3.51E-23		GO:0016020.1		Oligosaccharyltransferase (OST) subunit
Sapur.00B0269100.1	605.4463539	0.524750386	0.033530857	15.64874	3.36E-55	2.01E-54	cpm	0.752917159	5.79E-30		GO:0016829.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.00B0249500.1	50.49658185	1.241184859	0.079318719	-15.6481	3.42E-55	2.05E-54	cpm	-0.816478674	8.30E-39	GO:0006355;GO:0003677	GO:0020330.1	BLH9;BLH-4B-4;LSN PHY.BP	Family of unknown function (DUF572)
Sapur.00G1499000.1	1513.768507	0.268047248	0.016325255	15.6475	3.48E-55	2.08E-54	cpm	-0.74609454	3.81E-29		GO:0008080.1	PSAD	POX (plant homeobox) family protein
Sapur.01G0322400.1	515.672017	0.703085042	0.045009555	-15.6408	3.84E-55	2.29E-54	cpm	-0.787463023	2.14E-34	GO:0006508;GO:0004176	GO:0005840	ATP	photosystem I subunit D
Sapur.01G0267600.2	9.77461003	2.998571265	0.191267867	-15.6362	4.13E-55	2.46E-54	cpm	-0.801663227	2.06E-36		GO:0016887.2	LYM1	ATP-dependent protease LA domain protein
Sapur.00G1469500.1	34.2612838	1.541906079	0.098624836	15.63405	4.27E-55	2.54E-54	cpm	-0.729469858	2.38E-27		GO:0016020.1		lysM domain GPI-anchored protein 2 precursor
Sapur.01G0172500.1	108.0562581	0.815001507	0.05211247	15.6243	4.37E-55	2.60E-54	cpm	-0.783572968	7.45E-34		GO:0005515		RING/U-box superfamily protein
Sapur.01G0243200.1	62.7598354	0.357715867	0.0869074	-15.6225	5.11E-55	3.05E-54	cpm	-0.764153825	2.55E-31	GO:0006355;GO:0005739;GO:0030630	GO:0005840		Integral membrane HPP family protein
Sapur.00G1330600.1	67.23078824	-1.734892221	0.111033894	-15.6204	5.29E-55	3.15E-54	cpm	-0.5204527	1.14E-29		GO:0016020.1	ICL	Mitochondrial transcription termination factor family protein
Sapur.01G0269400.1	667.7577773	0.445264227	0.028508231	15.61691	5.44E-55	3.24E-54	cpm	-0.7954614	1.79E-35	GO:0005524	GO:0016491;GO:0051116;GO:0018180		isocitrate lyase
Sapur.01G0093500.1	20.78214734	-1.291764073	0.082748158	-15.6105	6.17E-55	3.67E-54	cpm	-0.782321221	4.30E-32	GO:0006468;GO:0006472	GO:0016740		DNA-binding storekeeper protein-related transcriptional regulator
Sapur.00B0281100.1	681.0738864	-0.524750386	0.033530857	-15.6102	6.20E-55	3.69E-54	cpm	-0.79417801	2.27E-35	GO:0016887;GO:0005524;GO:0016020;GO:0006810;GO:0005215	GO:0004016;GO:0006810.1		Protein kinase protein with tetratricopeptide repeat domain
Sapur.01G0203300.1	49.03413632	1.181691234	0.075171161	15.60789	6.43E-55	3.83E-54	cpm	-0.733783433	8.24E-28		GO:0005215.1		ABC transporter family protein, SmbABCD protein, putative
Sapur.01G0186900.1	178.1453924	0.407733284	0.026117735	-15.6061	6.73E-55	4.00E-54	cpm	-0.725808608	2.28E-26	GO:0016597;GO:0008152;GO:0551154;GO:0050661;GO:0016491;GO:006530	AK-HSDH;AK-HSDH II	aspartate kinase-homoserine dehydrogenase II	hypothetical protein
Sapur.01G0294000.1	70.81271709	-1.549387143	0.099308294	-15.6018	7.08E-55	4.21E-54	cpm	-0.789204463	1.34E-34	GO:0005515	GO:0016787.1	AK-HSDH;AK-HSDH II	aspartokinase/homoserine dehydrogenase
Sapur.01G0154400.1	261.7533729	-0.951434051	0.076011127	-15.6015	7.11E-55	4.22E-54	cpm	-0.779226988	7.03E-33		GO:0016020.1		Protein of unknown function (DUF538)
Sapur.01G0136400.1	244.4659045	-0.979462855	0.069207171	-15.5976	7.56E-55	4.49E-54	cpm	-0.820103296	2.06E-39		GO:0005481.1		histone deacetylase complex subunit SAP30 Sin3-binding protein
Sapur.01G0128000.1	112.8357034	0.916894578	0.058860388	-15.5772	1.04E-54	6.17E-54	cpm	-0.74184581	1.08E-28	GO:0016021;GO:0006810;GO:0005337	GO:0016020.1		Amidase family protein
Sapur.01G0240200.1	788.2888617	0.556422555	0.035520071	15.57122	1.14E-54	7.75E-54	cpm	-0.743184581	1.08E-28	GO:0016021;GO:0006810;GO:0005337	GO:0016020.1		equilibrative nucleoside transporter 1
Sapur.01G0141700.1	91.99099807	-0.854084537	0.110081489	-15.5699	1.17E-54	6.92E-54	cpm	-0.775825757	8.19E-33		GO:0070310.1	ATST2A;ST2A	sulfotransferase 2A
Sapur.01G0264200.1	91.51594122	0.7911689	0.053132247	15.5643	1.16E-54	7.68E-54	cpm	-0.775831166	8.19E-33	GO:0006629;GO:0008033;GO:0551154;GO:0016491	GO:0005886		FAD-dependent oxidoreductase family protein
Sapur.15W0284700.1	57.99160598	-1.267987769	0.080193765	-15.5607	1.15E-54	7.98E-54	cpm	-0.737014283	1.68E-28		GO:0016020.1		Integral membrane HPP family protein
Sapur.01G0175300.1	26.00240309	1.701863355	0.43073898	15.5193	1.38E-54	9.14E-54	cpm	0.546924311	6.91E-16	GO:0019752;GO:0004451	GO:0005829.1	ICL	isocitrate lyase
Sapur.T157200.1	2.850883263	4.671123815	0.303654453	15.5525	1.53E-54	9.05E-54	cpm	0.652165157	2.21E-20		GO:0043760.1		DNA-ear I-like superfamily protein
Sapur.01T0209800.1	537.0289449	0.921164468	0.059516683	15.5429	1.64E-54	9.81E-54	cpm	-0.775831166	8.19E-33	GO:0006629;GO:0551154;GO:0018180	GO:0016491		Aldolase-type TIM barrel family protein
Sapur.01G0264500.1	85.60916575	-0.748296892	0.048133103	-15.5464	1.68E-54	9.96E-54	cpm	-0.774062458	1.40E-32		GO:0016020.1		DNA-binding storekeeper protein-related transcriptional regulator
Sapur.01G0344300.1	656.8519526	0.576283287	0.051418899	-15.5453	1.71E-54	1.01E-53	cpm	-0.828381815	1.11E-41	GO:0009041;GO:0006221	GO:0005840		Aminoacyl-tRNA synthetase family protein
Sapur.01G0128500.1	166.9996693	-1.713151528	0.102211778	-15.5442	1.74E-54	1.03E-53	cpm	-0.762339313	4.28E-31	GO:0019888;GO:0015979;GO:0009654;GO:0009523;GO:0005509	GO:0016020		Aminoacyl-tRNA synthetase family protein
Sapur.T010400.1	28.25066302	2.037090879	0.121123848	15.5268	2.18E-54	1.29E-53	cpm	-0.701226786	1.52E-24		GO:0016890.1		Uridylyltransferase, putative
Sapur.00G1135400.1	554.4663963	0.768692883	0.045527828	15.5262	2.24E-54	1.33E-53	cpm	-0.792515483	1.28E-35	GO:0005515	GO:0016020.1		Exostosin family protein
Sapur.01G0102200.1	78.83817877	-1.996657984	0.12870545	-15.5134	2.83E-54	1.66E-53	cpm	-0.789736542	1.03E-34		GO:0170351.1		F-box family protein with a domain of unknown function (DUF295)
Sapur.01G0276500.1	513.8278877	-0.752622621	0.051333891	-15.5102	2.93E-54	1.72E-53	cpm	-0.758347693	1.31E-30		GO:0016491	SLP3	SUBTILISI-like serine protease 3
Sapur.01G0281600.1	656.1509263	0.800713182	0.051673869	-15.4955	3.73E-54	2.19E-53	cpm	-0.809963118	1.34E-40	GO:0006412;GO:0005840;GO:0005622;GO:0003735;GO:0005761	GO:0003723		IAAD-superfamily hydrolase, subfamily IG, D/I-nucleotidase
Sapur.01G0088400.1	1145.547324	2.721575175	0.171151721	15.4951	3.74E-54	2.20E-53	cpm	-0.742868023	4.38E-29		GO:0016020.1	LCN8;PDF12.3	ribosomal protein L29 family protein
Sapur.01G0207200.1	14.17376334	-3.310443204	0.149141333	-15.4916	3.95E-54	2.32E-53	cpm	-0.801065404	2.26E-36		GO:0016740.1		low-molecular-weight cysteine-rich 68
Sapur.01G0244000.1	102.9077288	-0.880147417	0.063018226	-15.4755	5.07E-54	2.98E-53	cpm	-0.755316548	2.28E-29	GO:0006468;GO:0004672	GO:0005829	RKF1	transmembrane protein, putative
Sapur.01G0286200.1	19.91319921	-1.618463882	0.106232183	-15.4695	5.57E-54	3.27E-53	cpm	-0.795423719	1.56E-35	GO:0006468;GO:0004672	GO:0005975;GO:0004553	CES101	receptor-like kinase in flowers 1
Sapur.01G0230700.1	294.0656886	0.789889547	0.051079712	15.45884	6.47E-54	3.79E-53	cpm	-0.748372253	1.78E-29		GO:0160330.1	ATPPDK2;PDPCK2;PPCK2	cellulose synthase-like protein E6
Sapur.01G0141700.1	549.5478078	-0.791368652	0.051292276	-15.4537	7.12E-54	4.17E-53	cpm	-0.793087675	4.57E-35	GO:0016740	GO:0006426.1		phosphoenolpyruvate carboxylase kinase 2
Sapur.01G0072600.1	2883.307658	-0.678883224	0.042585811	-15.4467	7.95E-54	4.65E-53	cpm	-0.753092881	5.54E-30		GO:0016020		RNA-recognition motif (RRM)-containing protein
Sapur.01G0207800.1	325.7517663	-0.74469582	0.048246658	-15.4424	8.47E-54	4.95E-53	cpm	-0.768397023	4.08E-32	GO:0005506	GO:0005525.1		cytochrome b561 and DOMON domain-containing protein
Sapur.01G0272000.1	65.67295145	1.009792652	0.071888811	-15.4419	8.55E-54	5.00E-53	cpm	-0.752773358	6.04E-30	GO:0016829;GO:0008152			rubredoxin
Sapur.00B0260500.1	2864.88238	-0.945729243	0.061245813	-15.4416	8.60E-54	5.03E-53	cpm	-0.82745603	1.06E-40	GO:0016740		SHM4;SHMT1;STM	KDRG and WHG aldolase
Sapur.01G0349500.1	1014.328525	0.627606013	0.040615247	15.44036	8.76E-54	5.12E-53	cpm	-0.753880097	4.47E-30	GO:0008138;GO:0004770			serine hydroxymethyltransferase
Sapur.01G0139300.1	1042.893505	0.531882283	0.031104653	15.41888	8.98E-54	5.26E-53	cpm	-0.781312276	1.02E-34	GO:0016491;GO:0016740	GO:0004648;GO:0004767	AFC1;AMC2;FC1	Phosphotyrosine protein phosphatases superfamily protein
Sapur.01G0403300.1	479.6980642	0.855514079	0.05142304	-15.4361	9.16E-54	5.47E-53	cpm	-0.778914166	3.20E-33	GO:0005992;GO:0004751	GO:0004790.1		FUS6-cytochrome b-like protein
Sapur.01G0411400.2	21.52719648	-0.573181822	0.100904704	-15.4342	9.38E-54	5.60E-53	cpm	-0.78550325	8.6E-27		GO:0005525.1		Ribose 5-phosphate isomerase, type A protein
Sapur.00G0555500.1	49.55562192	-1.24512627	0.080747197	-15.4201	1.23E-53	7.00E-53	cpm	-0.763691442	5.13E-31		GO:0016491.1		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.00G1327000.1	273.7521771	0.709887704	0.046038887	-15.4184	1.23E-53	7.17E-53	cpm	-0.774900742	1.08E-32	GO:0005515	GO:0016020.1	VIP3	Transducin/WD40 repeat-like superfamily protein
Sapur.01G0187200.1	921.6168547	0.304887837	0.020527607	-15.4167	1.16E-53	8.75E-53	cpm	-0.763362154	1.8E-31	GO:0016740	GO:0016020.1		Tetraspanin family protein
Sapur.01G0177900.1	250.1851861	0.795891803	0.05167303	15.4025	1.57E-53	9.18E-53	cpm	-0.743804634	7.81E-29	GO:0016021;GO:0006810	GO:0016020		Eukaryotic protein of unknown function (DUF914)
Sapur.15W0202800.1	1341.014934	0.636731395	0.037620518	15.39937	1.61E-53	9.42E-53	cpm	-0.762367013	3.44E-31	GO:0005515;GO:0009435;GO:0008897	GO:0005829	OLD5;QS;SUFE3	quinolinate synthetase A protein
Sapur.01G0161800.1	15.15499379	-1.434392346	0.093180712	-15.3937	1.81E-53	1.05E-52	cpm	-0.779212928	2.91E-33	GO:0016491;GO:0016491	GO:0016810.1	AT2XG1;ATGA2OXO1;GA2OX2	gibberellin 20 oxidase 2
Sapur.01G0119600.1	1946.122798	0.778271915	0.050275277	15.3883	1.94E-53	1.13E-52	cpm	-0.722092372	9.61E-27	GO:0003924;GO:0007017;GO:0005874	GO:0005200.1	TUB2	tubulin beta chain
Sapur.01G0469800.2	15.65089499	-1.73807788	0.112968761	-15.3855	2.05E-53	1.19E-52	cpm	-0.767938457	8.55E-32	GO:0016788	GO:0033370.2		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.01G0144700.1	442.6484758	0.699318276	0.045452156	15.3822	2.16E-53	1.25E-52	cpm	-0.802836621	8.38E-37		GO:0007120.1		NTM2-like protein
Sapur.01G0291200.1	13.53615194	-0.982515256	0.063003309	-15.375	2.41E-53	1.40E-52	cpm	-0.78649878	2.93E-34		GO:0046880.1		Pentatricopeptide repeat (PPR-like) superfamily protein
Sapur.01G0123000.1	91.58537293	-0.804087831	0.054238193	-15.371	2.46E-53	1.49E-52	cpm	-0.78213966	1.37E-33		GO:0016020.1		thylakoid lumenal17.2 protein
Sapur.15W0143400.1	760.6740044	-0.665516369	0.043311958	-15.3656	2.78E-53	1.62E-52	cpm	-0.806182256	3.72E-37	GO:0005515;GO:0051087	GO:0005737	ATBAG3;BAG3	BAG family molecular chaperone regulator
Sapur.00G0230900.1	1417.663468	1.947053995	0.126736054	15.36446	2.83E-53	1.66E-52	cpm	-0.554205224	5.08E-14	GO:0008168;GO:0008150	GO:0005829		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.01G0241600.1	251.9924723	-0.874606654	0.056895776	-15.3631	2.88E-53	1.68E-52	cpm	-0.785126305	5.42E-34		GO:0016020.1	BOB1	HSP20-like chaperones superfamily protein, putative
Sapur.01G0179400.1	175.2361987	0.978352126	0.063395524	15.35763	3.15E-53	1.83E-52	cpm	-0.717493551	4.04E-26		GO:0016491		nuclear migration protein nudc protein
Sapur.01G0122400.1	353.9889506	-0.528317302	0.034419838	-15.3434	3.92E-53	2.27E-52	cpm	-0.763337652	1.62E-31	GO:0043565;GO:0006355;GO:0003700;GO:0005515	GO:0003700;GO:0005515	BZIP45;TGA6	ENTH/VHS family protein
Sapur.01G0211600.1	262.9300502	0.923659331	0.06020761	15.34124	4.05E-53	2.35E-52	cpm	-0.691454184	1.19E-23	GO:0005515;GO:0009916		TGA2;TGA6	TGA2.2 and TGA6 bZIP transcription factors family protein
Sapur.01G0207000.1	665.3576617	0.525681011	0.034281659	15.3385	4.54E-53	2.63E-52	cpm	-0.788491652	1.56E-34		GO:0016491	IMUM1	Alternative oxidase family protein
Sapur.004G0272000.1	99.1337605	0.684565513	0.044627786	-15.3329	4.63E-53	2.67E-52	cpm	-0.80472069	6.26E-37		GO:0016020.1		SAND family protein
Sapur.01G0238000.2	28.03073584	-2.081344604	0.136375154	-15.3327	4.63E-53	2.68E-52	cpm	-0.708058051	2.91E-22	GO:0005975;GO:0004650	GO:0004857.1		Pectin lyase-like superfamily protein
Sapur.01G0232100.1	1660.977663	0.59686665	0.038919266	15.3314	4.72E-53	2.72E-52	cpm	0.803201802	1.62E-36		GO:0004240.1	SEC	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.007G0130300.1	1467.528241	0.521585653	0.034227786	15.3263	4.85E-53	2.81E-52	cpm	-0.7351256	4.50E-32		GO:0016020		UDP-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase, putative
Sapur.01G0246800.1	628.8223133	0.767601764	0.051867022	15.3175	4.95E-53	2.86E-52	cpm	-0.719327434	1.26E-27	GO:0007034	GO:0005198	VPS2.1	f-box/ankyrin repeat protein 5KP35
Sapur.01G0254800.4	8.677264192	-1.856702126	0.121140165	-15.3269	5.08E-53	2.92E-52	cpm	-0.74471205	5.12E-29		GO:0005515	HCF101	charged multivesicular body protein 2a
Sapur.01G0282800.1	34.58012332	1.127457346	0.073235854	-15.3167	5.56E-53	3.20E-52	cpm	-0.779904042	4.04E-32		GO:0016787	ATP	nucleotide-binding (ISG) ATPase, putative
Sapur.01G0107000.1	1901.992882	0.724014707	0.04724576	15.3161	5.63E-53	3.50E-52	cpm	0.754611009	8.27E-30		GO:0016491		organelle transport processing protein, putative
Sapur.01G0133000.1	13.58576823	-1.677177987	0.10953459	-15.3147	5.68E-53	3.52E-52	cpm	-0.731924744	1.20E-27	GO:0005515;GO:0016614;GO:0050660;GO:0016430	GO:0005829	EDA12;AHR	NADH dehydrogenase 1 beta subcomplex subunit 8, putative
Sapur.01G0074000.1	72.27528476	0.729273521	0.047404183	15.30805	6.76E-53	4.20E-52	cpm	-0.74532868	4.16E-29		GO:0016491		Glucose-methanol-choline (GMC) oxidoreductase family protein
Sapur.01G0166400.1	154.3071177	0.525681011	0.034281659	15.3049	6.98E-53	4.33E-52	cpm	-0.768027177	3.36E-34		GO:0016020.1	ATHD7;HD7;PDG2	Nucleotide-diphospho-sugar transferase family protein
Sapur.01G0219600.1	234.7984548	-0.549470564	0.035911231	-15.3008	7.53E-53	4.35E-52	cpm	-0.809563615	1.12E-37		GO:0016020.1	PDV5	homogentisate phytyltransferase
Sapur.01G0150600.1	77.49461668	-0.756321304	0.050113192	-15.2893	8.45E-53	4.88E-52	cpm	-0.788091166	3.36E-34	GO:0007165;GO:0005515	GO:0016491		plastid division5
Sapur.00G0272900.1	5.100794616	-2.579254884	0.168687115	-15.2902	8.89E-53	5.12E-52	cpm	-0.750525881	1.26E-29		GO:0016020	ZFP7	Rho GTPase activating protein with PAK-box/PJ21-Rho-binding domain
Sapur.00G0250900.1	183.1375791	-0.851969448	0.055729668	-15.2875	9.26E-53	5.33E-52	cpm	-0.793642281	2.83E-35	GO:0003676	GO:0016020		zinc finger protein 7
Sapur.01T0258100.1	98.27995261	-1.431511288	0.092417188	-15.2872	9.31E-53	5.36E-52	cpm	-0.757634043	4.30E-30	GO:0006470	GO:0004721	ABC4	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.15W0204800.1	10.79968776	-1.066264455	0.06845441	-15.2838	9.81E-53	5.64E-52	cpm	-0.735802682	4.99E-28	GO:0003676;GO:0017008;GO:0000398	GO:0000398	U2B'';U	Ubiquitin family protein
Sapur.01B0275000.1	2331.214969	0.82652129	0.057839468	15.28044	1.02E-52	5.87E-52	cpm	0.742673292	1.04E-29	GO:0016021	GO:0016020.1	TBT8	U2 small nuclear ribonucleoprotein B
Sapur.01G0135900.1	1878.069467	0.689585896	0.11868007	15.26907	1.23E-52	7.06E-52	cpm	0.721573623	1.51E-26	GO:0005114;GO:0016491;GO:0005937	GO:0016021	SKU5	transmembrane protein
Sapur.01G0137100.1	110.511795	2.051378332	0.13306514	15.2689	1.23E-52	7.08E-52	cpm	-0.742904008	2.9E-29		GO:0016020.1	CYCP2;2	SKU5 similar 5
Sapur.004G0489400.1	239.6152848	0.777569912	0.050950071	-15.2614	1.38E-52	7.93E-52	cpm	-0.77333387	3.44E-32	GO:0016758;GO:0008152	GO:0016540.2	UGT88A1	cyclin cp2.2
Sapur.01G0184300.1	282.8582202	0.697168504	0.052679065	-15.2557	1.51E-52	8

Sapur.01G0264900.1	1267.161846	-0.597334428	0.040084444	-14.9012	3.24E-50	1.78E-49	Open	-0.769049969	6.18E-32	GO:0005992;GO:0003824	ATSG76581	ATTPS1;TPS1	trehalose-6-phosphate synthase
Sapur.01G0288200.1	722.9489399	5.599414991	0.040233754	14.89681	3.45E-50	1.90E-49	Open	-0.748703356	1.77E-29	GO:0045454;GO:0055114;GO:0016972	ATSG01270.1	AKGDX2;QSOX2	quiescin-sulfhydryl oxidase 2
Sapur.01G0118400.1	13.33680604	3.978841984	0.13287776	14.89322	3.70E-50	2.03E-49	Open	0.6693725	1.82E-07	GO:0055114;GO:0050660;GO:0016491	ATSG01280.1	FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.T1436001.1	11.13483901	1.773630384	0.119122488	14.88953	3.88E-50	2.13E-49	Open	0.75309523	5.53E-30		ATSG35700.1	FIM2	fimbrin-like protein 2
Sapur.01G0220400.1	96.36639665	1.000565471	0.067193085	14.8859	4.07E-50	2.24E-49	Open	-0.773376314	1.52E-32		ATSG18800.1		transmembrane protein, putative
Sapur.0BG0245000.1	231.9548045	1.200855971	0.08070666	14.88037	4.42E-50	2.42E-49	Open	-0.714470215	8.08E-26		ATSG02220.1		hypothetical protein
Sapur.01G0230500.1	40.59937574	0.932139318	0.062646981	-14.8792	4.50E-50	2.47E-49	Open	-0.7559815	9.38E-31				hypothetical protein
Sapur.0D0230400.1	69.11787994	1.041380626	0.069988524	-14.8781	4.57E-50	2.51E-49	Open	-0.777589988	4.79E-33		ATSG47830.1		hypothetical protein
Sapur.0D4G0270900.1	22.22032139	5.730422922	0.385281899	14.8741	4.85E-50	2.66E-49	Open	0.59289166	2.83E-16	GO:0006629	ATSG18550.1		phospholipase A1
Sapur.0D7G0262300.1	33.84448038	3.265382374	0.2196115	14.87276	5.45E-50	2.99E-49	Open	0.710367061	2.46E-25		ATSG19740.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.0D2G0149800.1	26.62740327	-4.630674237	0.096249688	-14.8642	5.63E-50	3.08E-49	Open	-0.781059673	1.64E-32				hypothetical protein
Sapur.01G0213800.1	1197.026259	5.662367777	0.381051309	14.85074	6.88E-50	3.76E-49	Open	-0.777381607	1.50E-32	GO:0016021;GO:0015031	ATSG30840.1		Secretory carrier membrane protein (SCAMP) family protein
Sapur.0D3G0099500.1	83.52591423	-1.744683379	0.117546086	-14.8422	7.82E-50	4.27E-49	Open	-0.799054657	4.51E-36	GO:0006355;GO:0003700	ATSG23750.1	CRF2;TMD3	cytokinin response factor 2
Sapur.01G0212100.1	210.5958037	1.329707168	0.089671889	-14.7969	1.14E-49	6.24E-49	Open	-0.743278761	2.60E-29	GO:0008270;GO:0005515	ATSG40080.1		RING/U-box superfamily protein
Sapur.0D4G1270001.1	4549.323039	-1.021387044	0.068844577	-14.8361	8.56E-50	4.67E-49	Open	-0.743615992	1.13E-28	GO:0006457;GO:0003755;GO:0000413	ATSG16600.1	ROC3	rotamase CYP 3
Sapur.01G0119300.1	63.68056422	-0.963258324	0.065604329	-14.8329	8.97E-50	4.89E-49	Open	-0.758356663	3.68E-28		ATSG15010.1		Mitochondrial substrate carrier family protein
Sapur.01G0111500.1	268.1144098	-0.729156879	0.049188787	-14.8277	9.70E-50	5.30E-49	Open	-0.752804676	5.99E-30		ATSG48400.1		zinc knuckle (CCHC-type) family protein
Sapur.0D0G0122000.1	236.6158618	0.591626682	0.039927972	14.81735	1.13E-49	6.18E-49	Open	0.758631168	2.21E-30		ATSG16440.1		fermodoxin hydrogenases
Sapur.01G0881100.1	13.97941595	5.017440386	0.339317329	14.80995	1.24E-49	6.8E-49	Open	0.750290688	6.42E-30	GO:0005515	ATSG27261.1		F-box/Rho-like/FAD-like domains-containing protein
Sapur.0D3G0197000.1	2470.546162	0.462583302	0.02988843	14.80785	1.30E-49	7.11E-49	Open	-0.748115371	2.10E-29	GO:0007034	ATSG11730.1	CHMP1B;VPS46.1	vacuolar protein sorting-46.1
Sapur.0D6G0068000.1	2.966645422	1.000164357	0.067551	14.8021	1.31E-49	7.34E-49	Open	-0.764851561	2.98E-31	GO:0006457;GO:0003677	ATSG07150.1	ATJ2;DF2.4;DOF2.4	DNA binding with one finger 2.4
Sapur.01G0910300.1	905.3519512	6.527197007	0.441009707	14.80531	1.51E-49	7.38E-49	Open	0.775482863	9.06E-33	GO:0006872	ATSG61690.1		phosphoinositide binding
Sapur.0D6G0040100.1	293.8293028	2.381466402	0.180150561	-14.799	1.49E-49	8.10E-49	Open	-0.738819424	2.12E-28		ATSG08988.1		hypothetical protein
Sapur.T0D5600.1	443.9248855	0.940191864	0.061532978	14.79735	1.52E-49	8.30E-49	Open	-0.751253036	9.10E-30	GO:0550B;GO:0016020;GO:0006810;GO:0015171;GO:0003333	ATSG58030.1	CAT2	cationic amino acid transporter 2
Sapur.01G0259900.1	12.75618172	3.329707168	0.225187189	14.7969	1.54E-49	8.47E-49	Open	-0.758533443	9.31E-30		ATSG27320.1		Phosphatidylserine synthase function (DUF1645)
Sapur.01C1G1250B0.1	13.41084975	-3.348643736	0.091153529	-14.7953	1.57E-49	8.55E-49	Open	-0.743883568	6.37E-29	GO:0008080	ATSG03650.1		Acyl-CoA N-acyltransferases (NAT) superfamily protein
Sapur.01B0275200.1	61.08263884	1.235273842	0.083491388	14.79522	1.57E-49	8.56E-49	Open	0.687183922	3.59E-24		ATSG30320.1		CAP (Cysteine-rich secretory protein, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein
Sapur.0D1G0754000.1	7851.314854	0.526210116	0.044325441	14.79192	1.61E-49	9.06E-49	Open	-0.72365028	4.14E-28		ATSG40320.1	BIP;BIP2	Heat shock protein 70 (Hsp 70) family protein
Sapur.1S9G0240000.1	87.17740831	-1.02051343	0.06900797	-14.7853	1.82E-49	9.91E-49	Open	-0.831404304	5.10E-38		ATSG14410.1		hypothetical protein
Sapur.0D6G1240000.1	147.9702751	-0.6377497	0.0867989	-14.7851	1.83E-49	9.93E-49	Open	-0.744927305	4.85E-29		ATSG27861.1	ATET2;ET2	effector of transcription2
Sapur.01B0297900.1	610.6814261	0.529518473	0.035829374	-14.7811	1.94E-49	1.05E-48	Open	-0.758348562	1.31E-30	GO:0006413;GO:0003743	ATSG24560.1		Translation initiation factor 3 protein
Sapur.0D1G0180900.1	682.191846	1.365805179	0.08564542	14.7805	1.95E-49	1.06E-48	Open	0.707538486	1.68E-25		ATSG44860.1		hypothetical protein
Sapur.0D3G1370800.1	68.54895628	-4.464882011	0.09117023	-14.7778	2.04E-49	1.11E-48	Open	-0.767214091	1.06E-31	PSAP;PS-P;TACL;TMP14	ATMG68200.1		photosystem I P subunit
Sapur.0D1G0142200.1	238.4426131	0.973118183	0.065860588	-14.7755	2.11E-49	1.14E-48	Open	-0.74740976	2.32E-29		ATSG40150.1		hypothetical protein
Sapur.1S9G0160600.1	31.702645	2.248842427	0.28451144	-14.7725	2.20E-49	1.20E-48	Open	-0.743339904	7.33E-29	GO0062B4	ATSG07930.3		DNA glycosylase superfamily protein
Sapur.0D6G0617000.1	18.75438756	1.286485	0.098	14.7516	2.98E-49	1.62E-48	Open	-0.746028184	5.26E-29		ATSG27240.1	OBPNC	Oligosaccharyltransferase protein(s)-related protein 4C
Sapur.0D2G0179000.1	276.6655697	0.960198809	0.065862211	-14.7466	3.25E-49	1.85E-48	Open	-0.790727676	7.46E-35	GO:0005975;GO:0004553	ATSG19940.1	AtGH9B5;GH9B5	glycosyl hydrolase 9B5
Sapur.01T0298700.1	31.31724871	1.327885761	0.088174341	-14.7618	2.58E-49	1.40E-48	Open	-0.763607347	2.98E-31				hypothetical protein
Sapur.0D9G0247000.4	21.52016607	-1.118591393	0.075796014	-14.7574	2.76E-49	1.49E-48	Open	-0.763782231	1.76E-31	GO:0016987;GO:0006355;GO:0006352;GO:0003700;GO:0003677	ATSG13730.1	SIG4;SIG0	sigma factor 4
Sapur.1S9G0570000.1	2.317188291	-0.058135604	0.275030677	-14.7552	2.85E-49	1.54E-48	Open	-0.689074877	1.94E-23		ATSG18570.1		Oleosin family protein
Sapur.01B0250500.1	18.03749884	2.062835164	0.139637958	-14.7544B	2.88E-49	1.56E-48	Open	-0.59232016	1.56E-16		ATSG75181.1		
Sapur.01B0001800.1	20.82608791	1.213515339	0.08217582	14.75329	2.93E-49	1.59E-48	Open	-0.73615537	4.39E-28				hypothetical protein
Sapur.0D6G1140200.1	12.24843502	1.226449195	0.083815074	-14.7517	3.00E-49	1.62E-48	Open	-0.723860281	1.07E-27	GO:0006457;GO:0003755;GO:0000413	ATSG46020.1	CYP71	cyclophilin71
Sapur.01G0213000.1	975.5519397	-0.717287975	0.048626687	-14.7516	3.01E-49	1.63E-48	Open	-0.761868633	5.14E-31	GO:0016597;GO:0008152;GO:0055114;GO:0051287;GO:0016616	ATSG34200.1	EDA9	D-3-phosphoglycerate dehydrogenase
Sapur.01G0159400.1	6.210064213	-3.619164407	0.129278788	-14.7513	3.02E-49	1.63E-48	Open	-0.748065429	2.13E-29		ATSG21570.1		Protein of unknown function (DUF1012)
Sapur.01G0243900.1	9.008730132	2.925487793	0.198367494	14.76782	3.18E-49	1.72E-48	Open	-0.582436214	1.22E-15		ATSG49880.1		Nucleotide-diphospho-sugar transferases superfamily protein
Sapur.0D6G1310000.1	4.930806788	5.185154944	0.351707583	14.74275	3.43E-49	1.85E-48	Open	-0.547232213	1.21E-13	GO:0016767	ATSG03390.1		HXXXD-type acyl-transferase family protein
Sapur.0D6G0180300.1	99.81809023	-0.905638304	0.050098876	-14.7376	3.66E-49	1.97E-48	Open	-0.788840001	7.75E-34	GO:0006810;GO:0005215	ATSG47190.1	DEAD2	DEAD and ATPase domain protein 2
Sapur.01B0290600.1	647.8284675	-0.850902006	0.057747143	-14.7365	3.78E-49	2.03E-48	Open	-0.777614486	4.99E-32	GO0063344;GO0006486;GO0360777;GO0000786	ATSG06320.2		winged-helix DNA-binding transcription factor family protein
Sapur.01B0680600.1	224.9103568	-1.329707168	0.085350569	-14.7358B	3.88E-49	2.09E-48	Open	-0.746188117	3.48E-29	GO:0016491;GO:0006355;GO:0003700;GO:0003677	ATSG04080.1		C2 calcium/lipid phospholipid and phosphatidylserine/serine family protein
Sapur.01G1179400.1	4.28605607	3.810487339	0.258276667	14.73079	4.09E-49	2.21E-48	Open	-0.689608278	1.94E-23		ATSG49800.1		transmembrane protein, putative
Sapur.01G0131400.1	1355.902713	-0.614164966	0.100007685	-14.728	4.24E-49	2.30E-48	Open	-0.711830304	1.74E-25	GO:0016747;GO:0008610	ATSG19100.1	ATCHS;CHLSYN	Chalcone and stilbene synthase family protein
Sapur.01G0151400.1	836.7243656	0.61570647	0.043165577	14.72648	4.36E-49	2.35E-48	Open	-0.74051587	1.50E-28	GO0055125	ATSG12280.1	ARA8;RGA2;RABG3d	Rab-related GTPase family protein
Sapur.0D6G1160000.1	1225.736315	-0.463848324	0.031648899	-14.7242	4.50E-49	2.42E-48	Open	-0.735544421	1.32E-28		ATSG26020.1	ATHDB;DB;DB1B	Heat shock transcriptional factor family protein
Sapur.0D9G0483000.1	17.56544585	-1.371468719	0.093173224	-14.7199	4.81E-49	2.59E-48	Open	-0.73525484	1.78E-32				hypothetical protein
Sapur.0D6G0453000.1	7.460869671	-4.018444827	0.116577137	-14.7104	5.16E-49	2.78E-48	Open	-0.609539288	1.36E-17	GO:0043531	ATSG07040.1	RPM1;RPS3	NB-ARC domain-containing disease resistance protein
Sapur.01G0287100.1	21.55697762	-1.141349082	0.077743122	-14.7042	6.06E-49	3.26E-48	Open	-0.764557999	1.27E-31	GO0055115	ATSG70280.2		NHL domain-containing protein
Sapur.0B0139200.1	41.29847887	-1.740872028	0.118748798	-14.6938	7.06E-49	3.80E-48	Open	-0.672414043	5.27E-22		ATSG14640.1	CAM8	calmodulin 8
Sapur.0D9G0150500.1	4804.364734	0.514531022	0.036265745	14.68783	7.71E-49	4.15E-48	Open	0.745015151	1.48E-28		ATSG70030.2	ACAM-2;CAM5	calmodulin 5
Sapur.01T0289000.1	173.0710739	-1.021365948	0.069678222	-14.6846	8.09E-49	4.35E-48	Open	-0.754935211	1.38E-30	GO0010170;GO0004834;GO0000162	ATSG38530.1	TSRtrp2	tryptophan synthase beta-like 2
Sapur.0D7G0061300.1	644.0302	-0.748397671	0.056193033	-14.6847	8.09E-49	4.35E-48	Open	-0.75008707	1.34E-29	GO0043531;GO0006355;GO0007030;GO0003677	ATSG27961.1	ARP	Homeobox-leucine zipper protein
Sapur.01G0351000.1	6.075257	2.087618886	0.143185956	-14.6694	1.01E-48	5.44E-48	Open	-0.767888777	8.42E-32	GO0005524	ATSG18190.1		TCP-1/cpn60 chaperonin family protein
Sapur.0D4G0280300.1	86.79605974	-1.551878345	0.108530357	-14.6689	1.02E-48	5.47E-48	Open	-0.687347417	2.76E-23		ATSPR2;SPR2	SPR	SPR domain gene 2
Sapur.0D9G0819900.1	211.6418888	0.968639035	0.066046673	14.66642	1.06E-48	5.68E-48	Open	-0.738697563	2.41E-28		ATSG19100.1		alpha/beta-Hydrolases superfamily protein
Sapur.01B0680200.1	106.8980714	-0.639401	0.043665219	-14.6601	1.14E-48	6.12E-48	Open	-0.739187991	6.60E-34		ATSG47420.1		alpha/beta-Hydrolases superfamily protein
Sapur.01G0149400.1	98.8530884	0.950601793	0.072263922	14.65533	1.25E-48	6.68E-48	Open	-0.71513449	1.57E-25	GO:0016020;GO:0008375	ATSG11330.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
Sapur.0D6G1330000.1	21.53860883	-1.154952394	0.078809112	-14.6551	1.29E-48	6.71E-48	Open	-0.795281813	1.58E-35		ATSG71350.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.0D7G0918B0.1	77.37505522	-0.989849377	0.067560711	-14.6513	1.32E-48	7.09E-48	Open	-0.772310553	2.36E-32		ATSG09370.2		transmembrane protein, putative
Sapur.01G1231900.1	19.95893342	1.602294399	0.110159156	14.63814	1.60E-48	8.59E-48	Open	-0.677308825	1.27E-22	AtMYB103;ATMYB80;MS188	MYB103;MYB80;MS188		myb domain protein 103
Sapur.01G0231500.1	24.71884671	-1.329707168	0.079185954	-14.6372	1.82E-48	8.70E-48	Open	-0.752382762	1.76E-30	GO:0006355;GO:0003723	ATSG31180.1	NUTL;NOV;Yor-like	nutrition protein / antiterrorismin Nuak1 domain-containing protein
Sapur.01T0200000.1	57.98848855	-0.847007705	0.057952969	-14.631	1.78E-48	9.51E-48	Open	-0.75852607	1.98E-30		ATSG29300.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.0D6G1770000.1	38.82867504	-1.143884324	0.078184453	-14.6301	1.86E-48	9.61E-48	Open	-0.79811944	2.34E-36		ATSG27110.1		Pentatricopeptide repeat (PPR)-containing protein
Sapur.0D3G1197000.1	1496.789725	-0.497793214	0.034026826	14.62943	1.92E-48	9.75E-48	Open	-0.73162569	8.82E-28	GO0005975	ATSG13420.1		Aldolase-type TIM barrel family protein
Sapur.0D6G0410200.1	6.269944859	1.867188395	0.127678304	14.62419	1.97E-48	1.01E-47	Open	-0.781263881	1.53E-32		ATSG27880.1		Lis0/CLIP/CRA1/Gid domains-containing protein
Sapur.1S9G0584B00.1	922.5624976	0.931607763	0.063709203	14.62279	2.01E-48	1.07E-47	Open	-0.686061783	3.59E-23	GO0003677;GO0043565;GO0006355;GO0003700	ATSG01470.1	ATHB-1;ATHB1;HAT5;HB-1	homeobox 1
Sapur.01B0176000.1	10.86176604	-2.296256488	0.157009083	-14.6268	2.06E-48	1.10E-47	Open	-0.642818167	4.08E-21	GO0006468;GO0005524;GO0004672	ATSG60600.1	BLR2	receptor-like protein kinase 1
Sapur.01G1100800.1	104.4243831	-0.687238651	0.047009578	-14.6192	2.12E-48	1.13E-47	Open	-0.783315942	8.08E-34	GO0080270	ATSG19100.1		Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein
Sapur.0D3G1041000.1	173.2109214	-0.830808458	0.05719156	-14.6181	2.13E-48	1.15E-47	Open	-0.778181933	3.99E-33		ATSG44450.1		Glycine-rich protein family
Sapur.0D5G1117000.1	286.9319241	-0.548391761	0.037518866	-14.61648	2.19E-48	1.18E-47	Open	-0.737284638	2.28E-28		ATSG29530.1		Target SNAREs and domain protein
Sapur.01B0122300.1	108.8892088	-1.292787326	0.088443616	-14.6163	2.21E-48	1.18E-47	Open	-0.729295495	2.48E-27	GO:0051301;GO:0031110;GO:0008017;GO:0007067;GO:0007059;GO:0005876;GO:0000094	ATSG26970.1		hypothetical protein
Sapur.01G1313000.1	127.4077267	0.281408488	0.061577664	14.61054	2.67E-48	1.44E-47	Open	-0.725281795	2.46E-27		ATSG25760.1		Duplicated homeodomain-like superfamily protein
Sapur.0B0G0990400.1	75.74.25692	0.953188482	0.061298695	14.60348	2.67E-48	1.42E-47	Open	0.69281683	8.98E-24	GO:0016597;GO:0008152;GO:0055114;GO:0051287;GO:0016616	ATSG17745.1	PGDH	D-3-phosphoglycerate dehydrogenase
Sapur.01T0207000.1	151.0956597	0.782330426	0.053256141	14.60266	2.76E-48	1.46E-47	Open	-0.751446331	8.64E-30		ATSG42150.1		
Sapur.01T0071900.1	6609.61608	0.767176278	0.051308159	14.60262	2.76E-48	1.46E-47	Open	-0.71895286	2.88E-26		ATSG39570.1		latex abundant protein, putative
Sapur.0B0G0880100.1	122.4296452	-0.53224779	0.036545599	-14.5913	3.18E-48	1.70E-47	Open	-0.762725276	3.96E-31	GO0003676	ATSG10110.1		RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.01T0266900.1	129.0088725	1.160197591	0.081171518	14.57903	3.82E-48	2.03E-47	Open	0.686266606	3.44E-23	GO0081352;GO0005975	ATSG47800.1		Galactose mutarotase-like superfamily protein
Sapur.0D3G0418B0.1	4823.074627	-0.703641801	0.049320117	-14.56926	4.41E-48	2.34E-47	Open	-0.735517562	2.02E-28	GO0016570;GO0009508	ATSG27180.1	ALAAT2	alanine aminotransferase 2
Sapur.0D4G1591000.1	383.3496341	-0.614771731	0.042312204	-14.5635	4.79E-48	2.55E-47	Open	-0.769896562	4.68E-32	GO0003677;GO0080289	ATSG60690.1	IFL;IFL1;BEV	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein
Sapur.0D5G0254B00.1	258.2916465	-0.754554638	0.051859367	-14.55	5.46E-48	2.90E-47	Open	-0.78841684	7.44E-32		ATSG52380.1	GCL1	GCR2-like 1
Sapur.1S9G0602B0.1	400.4303067	0.572631302	0.039159808	14.54843	5.58E-48	2.97E-47	Open	-0.738948206	2.25E-28	GO0016020;GO0005506;GO0004571	ATSG07520.1		Glycosyl hydrolase family 47 protein
Sapur.0D6G1889000.1	336.0934964	-0.714723957	0.049134288	-14.5465	6.14E-48	3.26E-47	Open	-0.760338861	7.53E-31		ATSG11890.1		
Sapur.0D4G1347000.1	83.13053661	-1.147427134	0.10197775	-14.5421	6.54E-48	3.47E-47	Open	-0.738917924	2.76E-28	GO0005885;GO0016021	ATSG16080.2		Major facilitator superfamily protein
Sapur.0D6G2219000.1	63.7382818	1.545007733	0.105938581	14.54118	6.62E-48	3.51E-47	Open	-0.755684788	2.73E-30	GO0071665;GO0005155;GO0000160	ATSG10720.1	AHK5;CKI2;HK5	histidine kinase 5
Sapur.0D6G0270000.1	20.68207734	1.991071232	0.136924721	14.54142	6.62E-48	3.51E-47	Open	-0.704837776	1.38E-25		ATSG29281.1		
Sapur.0D4G0740400.1	844.4047589	-0.980609568	0.067452815	-14.5382	6.94E-48	3.67E-47	Open	-0.74021383	1.67E-28		ATSG15780.1		Pollen Ole e 1 allergen and extensin family protein
Sapur.0D4G0180000.1	77.06635604	0.919798162	0.064512148	14.5354	7.23E-48	3.82E-47	Open	-0.787520206	2.11E-34		ATSG21300.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.0D3G0731000.1	4.260952541	6.453370514	0.306406643	14.53418	7.36E-48	3.89E-47	Open	0.666461172	1.62E-21		ATSG61480.1	ATRAD1B;MIM;SMC6B	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.0D1G0156600.1	188.2195603	1.060885237	0.073162267	14.53123	7.68E-48	4.06E-47	Open	0.718168134	1.46E-26	GO0005524	ATSG60140.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.0D3G0520000.2	4.205388318	-2.638404657	0.181574484	-14.5307	7.74E-48	4.09E-47	Open	-0.735123687	1.91E-28	GO0005515;GO0016020	ATSP9111;6N;SPF111		synteaxin of plants 111
Sapur.0D6G0270600.1	49.86762698	-1.16658802	0.080501944	-14.5286	7.98E-48	4.22E-47	Open	-0.717678654	3.87E-26				
Sapur.0B6G1640500.1	236.6122112	0.634820394	0.029920821	14.52577	8.12E-48	4.28E-47	Open	-0.762779095	2.77E-31	GO0008270;GO0005515	ATSG39100.1		RING/U-box superfamily protein
Sapur.01G1114000.2	2.337318823	-2.637082793	0.250409062	-14.5227	8.70E-48	4.59E-47	Open	-0.773563815	1.62E-32		ATSG15670.1		SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
Sapur.0D6G0220200.1	318.0183008	-0.833561888	0.057418814	-14.5172	9.42E-48	4.97E-47	Open	-0.760562	5.66E-31		ATSG49530.2		AT hook motif DNA-binding family protein
Sapur.0D4G0434000.1	448.2076334	0.734035888	0.050572616	14.5155	9.80E-48	5.17E-47	Open	0.724451492	7.97E-27	GO0046872	ATSG29880.1		RING/FYVE/PHD-type zinc finger family protein
Sapur.01G0173800.1	2.451151727	-4.716047234	0.325160225	-14.5089	1.07E-47	5.62E-47	Open	-0.578751719	1.98E-15				
Sapur.01G2150500.1	311.1821826	1.144893068	0.078937327	14.50566	1.12E-47	5.88E-47	Open	-0.678617618	1.52E-22	GO0016758;GO0008152			UDP-Glycosyltransferase superfamily protein
Sapur.0D5G0860500.1	9.786555171	-1.554329378	0.107446381	-14.5035	1.17E-47	6.15E-47	Open	-0.739975511	1.96E-28	GO0016564	ATSG01160.1		
Sapur.01B0207400.1	488.3962692	1.580018099	0.108967528	14.4999	1.21E-47	6.39E-47	Open	-0.70421881	7.92E-25	GO0016758;GO0008152	ATSG15490.3	UGT73B4	UDP-glycosyltransferase 73B4
Sapur.0D7G1330600.1	18.62793375	-0.750426006	0.08172734	-14.4989	1.23E-47	6.47E-47	Open	-0.762078462	6.12E-31		ATSG30700.1		hypothetical protein
Sapur.01G0131200.1	134.9815577	-0.648806794	0.046080713	-14.49625	1.28E-47	6.72E-47	Open	-0.751416607	5.70E-30	GO0016758;GO0008152	ATSG04080.2		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01G1358600.1	350.2326242	-0.712660068	0.049179424	-14.491	1.38E-47	7.26E-47	Open	-0.765498888	1.74E-31	GO0003676	ATSG21190.1		RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.1S9G0B68B00.1	10.04734286	-2.025227	0.125950251	-14.481	1.39E-47	7.26E-47	Open	-0.768832212	7.51E-32	GO0006412;GO0005840;GO0005622;GO0003735	ATSG07090.1		Ribosomal protein L18 family protein
Sapur.01G1239300.1	1110.994276	0.151860642	0.07261008	14.4878	1.45E-47	7.60E-47	Open	0.719812244	2.91E-26	GO0016161;GO0003722	ATSG17080.1	BAMI;BMY8;CT-BMY	chloroplast beta-amylase
Sapur.0D6G0180400.1	606.5742268	0.861303974	0.058066436	14.48675	1.47E-47	7.72E-47	Open	0.751164607	1.27E-30		ATSG11970.1		Protein of unknown function (DUF3511)
Sapur.0D6G1930200.1	1406.182848	0.751617152	0.051889394	14.4868	1.49E-47	7.83E-47	Open	-0.773376776	2.31E-32	GO0046412;GO0005840;GO0003735	ATSG09630.1		Ribosomal protein L4/L1 family
Sapur.0D6G2780B00.1	24.91194819	-2.000487329	0.137425628	-14.4864	1.50E-47	7.87E-47	Open	-0.762278276	4.80E-26	GO0016514;GO0051920;GO0016491;GO0016209	ATPER1;PER1		1-cys peroxiredoxin
Sapur.1S9G0270000.1	91.94723635	-0.707980228	0.048897467	-14.4818	1.58E-47	8.28E-47	Open	-0.736423931	2.49E-31		ATCNGC3;CNGC19		cyclic nucleotide gated channel 19
Sapur.0D5G0920200.1	198.3478688	-0.812861329	0.056158854	-14.4728	1.73E-47	9.05E-47	Open	-0.745630384	4.96E-29	GO0016021	FLO	CHS3;SUR4	CHS3;SUR4 membrane family protein
Sapur.T0173001.1	33.0567746	1.42289152	0.098487778	14.4566	2.21E-47	1.16E-46	Open	-0.694062298	6.92E-24	GO0046685;GO0006672	ATSG16840.2		Leucine-rich repeat transmembrane protein kinase
Sapur.0D2G1690400.1	230.5474026	2.275315873	0.157386953	14.45701	2.24E-47	1.19E-46	Open	-0.591214097	5.58E-16		ATSG63095.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.0D4G1280000.1	269.2928011	-1.647480515	0.113988588	-14.455	2.38E-47	1.20E-46	Open	-0.689737514	1.70E-23		ATSG80640.1		Chaperone-DnaJ-domain superfamily protein
Sapur.0D1G1157000.1	41.02507765	-1.1864705	0.09594149	-14.4512	2.46E-47	1.29E-46	Open	-0.791682879	3.30E-35		ATSG15260.1		ATP-dependent RNA helicase cht1, putative
Sapur.01G1181200.1	55.69585249	-0.9276164	0.069236451	-14.4476	2.60E-47	1.36E-46	Open	-0.769064888	6.18E-32		ATSG29420.1		plant ubiquitin RNA recognition domain protein
Sapur.01G0250400.1	76.99697389	-0.876285191	0.060616396	-14.4451	2.68E-47	1.41E-46	Open	-0.770818858	6.27E-32				
Sapur.01B0187000.1	1248.190725	0.467791333	0.032186122	14.44316	2.76E-47	1.44E-46	Open	0.757256441	1.76E-30		ATSG06900.1		N-acetine dibasic convertase, putative
Sapur.01G0894900.1	328.7876256	-0.706259336	0.048907881	-14.4406	2.87E-47	1.50E-46	Open	-0.76396245	2.69E-31	GO0055125	ATSG45750.1	ARA8RA1;RABA1c	RAB GTPase homolog A1C
Sapur.01G0845000.1	5729.186866	-0.697764142	0.048188199	-14.4347	2.93E-47	1.53E-46	Open	-0.752808745	6.61E-30	GO0015979;GO0009538;GO0009522	ATSG13130.1	PSB28	photosystem I reaction center subunit III
Sapur.01G0223600.1	99.42698446	1.145763604	0.218011822	14.42934	3.18E-47	1.77E-46	Open	0.586155122	7.32E-16	GO0006629	ATSG26560.1	PLA IIA;PLA2A;PLP2	phospholipase A 2A
Sapur.01B0250800.4	4.735691788	3.754882205	0.190936595	14.42884

Sapur.01G0071500.1	275.1482916	-6.55988689	0.03074777	-14.0856	4.68E-45	2.35E-44	cpm	-0.76393043	8.57E-32		Uncharacterized conserved protein (DUF2358)
Sapur.01G0298800.1	388.3578938	-6.64922769	0.04612685	-14.0813	4.95E-45	2.49E-44	cpm	-0.76161587	5.19E-31	GO:0004932;GO:0006281;GO:0005524;GO:0003697	recA DNA recombination family protein
Sapur.T1342001.1	8.05164294	3.72748816	0.34671846	10.0766	5.10E-45	2.57E-44	cpm	-0.81026966	6.76E-17		
Sapur.0040G072200.1	107.3251219	-8.87268693	0.06199152	-14.0755	5.37E-45	2.70E-44	cpm	-0.73664748	4.22E-28		
Sapur.01T0161000.1	138.5693003	1.87937723	0.13362202	14.0665	5.61E-45	2.88E-44	cpm	-0.68580614	4.36E-23	GO:0004648;GO:0005524;GO:0004672	tyrosine kinase domain protein
Sapur.01B0252600.1	167.5378514	-6.02966731	0.04478636	-14.0662	6.12E-45	3.08E-44	cpm	-0.75384852	2.61E-30		SOUL heme-binding protein
Sapur.0040G204000.2	181.0702552	0.79615924	0.05661748	14.0628	6.58E-45	3.27E-44	cpm	0.72570027	5.89E-27	GO:0005524	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related
Sapur.0082B0500.1	82.53953884	1.12163531	0.08784125	14.0603	6.68E-45	3.35E-44	cpm	-0.73817511	2.72E-28		Chaperone DnaJ-domain superfamily protein
Sapur.0096B0990.1	866.2123839	0.50136755	0.03565552	14.0554	6.93E-45	3.48E-44	cpm	-0.75075639	3.23E-30		Nucleotide-diphosphe-sugar transferase family protein
Sapur.0162E0160.1	634.0163104	-6.20234204	0.04412573	-14.0537	7.03E-45	3.53E-44	cpm	-0.77082869	3.66E-32	GO:0005085;GO:0046873;GO:0030001;GO:0016020	metal cation transporter, CPX family protein
Sapur.0096D71700.1	43.92897726	-2.02910485	0.07232825	-14.0535	7.13E-45	3.68E-44	cpm	-0.75127361	5.27E-30		zinc finger SWIM domain protein
Sapur.0002G038200.1	771.8816163	1.38528269	0.04758103	14.0519	7.34E-45	3.79E-44	cpm	-0.72861376	1.38E-27	GO:0008299	geranylgeranyl pyrophosphate synthase 1
Sapur.0046H41800.1	71.3587891	-1.46403789	0.10417622	14.05296	7.39E-45	3.71E-44	cpm	0.66867983	1.07E-21		recA DNA recombination family protein
Sapur.01G2469000.1	2656.923656	5.87606009	0.04677149	14.0516	7.53E-45	3.78E-44	cpm	-0.79878829	7.37E-35	GO:0006412;GO:0005840;GO:0003735	60S ribosomal protein L13
Sapur.01G0191500.1	5.18704732	-8.86197827	0.34600185	14.0495	7.76E-45	3.89E-44	cpm	0.54880171	9.96E-14	GO:0046983;GO:0003677	SRF-type transcription factor (DNA-binding and dimerization domain) protein
Sapur.01T0219000.1	542.3218064	-7.88648429	0.05806007	-14.0483	8.06E-45	4.04E-44	cpm	-0.73721266	3.08E-28		plant/MRG21-7 protein, putative
Sapur.0072G0772500.1	460.5198842	-0.87822088	0.06255290	-14.046	8.15E-45	4.08E-44	cpm	-0.74462047	5.26E-29	GO:0016758;GO:0008152	UDP-glucosyltransferase, putative
Sapur.0072G0747000.1	5138.515119	0.48378638	0.03448126	14.0409	8.43E-45	4.21E-44	cpm	0.73115271	5.58E-27		ATP synthase
Sapur.0096D800800.1	590.3387962	-6.92800344	0.04728672	-14.03729	8.25E-45	4.42E-44	cpm	0.82248565	2.07E-37		Protein of unknown function, DUF584
Sapur.0196D802300.1	29.11749977	-8.87195422	0.06211152	-14.0279	1.05E-44	5.27E-44	cpm	-0.73897005	2.25E-28	GO:0005515	leucine-rich repeat transmembrane protein kinase family protein
Sapur.0162E0170.1	1385.663834	-7.20000025	0.05760409	-14.024	1.11E-44	5.57E-44	cpm	-0.74412254	5.84E-29	GO:0005515;GO:0009765	light-harvesting chlorophyll A/B-binding protein Lhcb3
Sapur.0130H01000.1	53.67758502	-2.37809254	0.08271537	-14.0234	1.12E-44	5.61E-44	cpm	-0.74873003	5.01E-29	GO:0016829;GO:0006530	THA1	threonine aldolase 1
Sapur.0010G0575100.1	5.77351571	-8.74014197	0.38586419	14.0203	1.17E-44	5.86E-44	cpm	0.66870505	1.56E-21		PHD Finger protein-related
Sapur.0110G0467500.1	219.3240032	-0.95381848	0.06803349	-14.0199	1.18E-44	5.89E-44	cpm	-0.79037891	8.36E-35		Protein of unknown function (DUF688)
Sapur.0046G242100.1	356.3474332	-6.87606009	0.04904166	-14.018	1.21E-44	6.04E-44	cpm	-0.79378861	1.07E-34	GO:0004872;GO:0030001	Heavy metal transport/detoxification superfamily protein
Sapur.0103G1340800.1	51.53652528	-2.42004958	0.17675541	-14.0169	1.23E-44	6.14E-44	cpm	-0.75203924	7.36E-30		Auxin-responsive GH3 family protein
Sapur.0096G203800.1	142.5773841	-8.87916689	0.06279859	-14.0153	1.26E-44	6.28E-44	cpm	-0.79289722	3.63E-35		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.0003G360600.1	213.8399122	-8.44076128	0.10058381	-14.0119	1.32E-44	6.58E-44	cpm	-0.72767636	3.70E-27	ATMYB111,MYB111,PFG3	myb-domain protein 111
Sapur.0020G052000.1	139.2434576	-7.17288042	0.08376838	-14.0077	1.40E-44	6.98E-44	cpm	-0.67448946	3.54E-22	GO:0046872;GO:0030001	Heavy metal transport/detoxification superfamily protein
Sapur.0196G801000.1	41.92554462	-2.12164102	0.07922925	-13.98785	1.61E-44	8.02E-44	cpm	-0.7401958	1.67E-28	GO:0005515;GO:0008017	end binding protein 1B
Sapur.0016J175000.1	263.0268033	0.53203113	0.03717028	13.99054	1.78E-44	8.88E-44	cpm	-0.73265843	1.01E-27	GO:0016811;GO:0016021;GO:0006672	SAG18	senescence associated gene 18
Sapur.0110G0607500.1	221.3931687	-0.55052335	0.03936131	-13.9874	1.86E-44	9.28E-44	cpm	-0.75738516	8.31E-30	GO:0005515		
Sapur.0070B01800.1	288.2262537	0.94341747	0.06745971	13.98674	1.88E-44	9.36E-44	cpm	-0.73438849	8.36E-27		Protein of unknown function (DUF861)
Sapur.0096B0400.1	324.4742606	-0.49177832	0.03516720	-13.984	1.95E-44	9.73E-44	cpm	-0.7348008	2.16E-29	GO:0043531	ARR B response regulator family protein
Sapur.0105G0720200.1	117.7507543	0.87400263	0.06261837	13.97202	2.31E-44	1.15E-43	cpm	-0.70608729	5.27E-25	GO:0016746;GO:0008152	2-oxoacid dehydrogenase acyltransferase family protein
Sapur.0160E0000.1	7.115788604	-8.00972197	0.34608717	13.9748	2.32E-44	1.15E-43	cpm	0.60068836	4.25E-20		calcineurin B-like protein
Sapur.0010G0012000.1	1838.425364	5.98996257	0.4202127	13.97005	2.37E-44	1.18E-43	cpm	-0.72591875	5.40E-27	GO:0030955;GO:0006096;GO:0047742;GO:0004887	Pyruvate kinase family protein
Sapur.0021G1390900.1	17.17998711	2.36856393	0.16960034	13.96556	2.53E-44	1.26E-43	cpm	0.63127809	7.80E-19	GO:0005515	BAI,BAP2	BOR association protein 2
Sapur.0186J980500.1	176.6266469	-1.72420186	0.05180797	-13.9624	2.58E-44	1.29E-43	cpm	0.69944089	2.22E-24	GO:0005515		RING/FYVE/PHD zinc finger superfamily protein
Sapur.1596G149200.1	790.7341504	-0.96409241	0.03295823	-13.9601	2.73E-44	1.36E-43	cpm	-0.74761727	2.40E-29	GO:0006378;GO:0005849;GO:0003729	Cleavage/polyadenylation specificity factor, 25kDa subunit	cleavage and polyadenylation specificity factor 5
Sapur.0160G067500.1	97.11605512	-7.01183094	0.06837987	-13.9574	2.84E-44	1.41E-43	cpm	0.68731097	2.90E-23			hypothetical protein
Sapur.0010G1167000.1	21.44932842	-1.85068822	0.13204819	-13.9507	3.12E-44	1.55E-43	cpm	-0.76865403	6.52E-32	GO:0046983	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH96
Sapur.0020G051200.1	87.68854919	-1.16800523	0.09461608	-13.949	3.16E-44	1.58E-43	cpm	-0.81932002	1.03E-38		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate-dependent dioxygenase
Sapur.0051I664000.1	422.0538171	-0.65178096*	0.04431795	-13.945	3.18E-44	1.68E-43	cpm	-0.76631944	1.25E-31			transmembrane protein, putative
Sapur.0110G0607600.1	19.70277181	1.34631833	0.09604102	13.94437	3.46E-44	1.83E-43	cpm	0.72163816	1.54E-26			hypothetical protein
Sapur.0010G2034000.1	1079.699662	-1.06297751	0.07626705	-13.9382	3.71E-44	1.86E-43	cpm	-0.77851772	3.56E-33	GO:0006508;GO:0004190	Eukaryotic aspartyl protease family protein	aspartic proteinase nepenthesin-1 protein
Sapur.0042B71000.1	45.21885622	-0.92145453	0.08054219	-13.9359	3.83E-44	1.95E-43	cpm	-0.75284561	3.32E-30		alpha/beta-hydrolase family protein	alpha/beta hydrolase family protein
Sapur.T134600.1	18.7825242	1.92833701	0.13835594	13.93553	3.85E-44	1.91E-43	cpm	0.64952088	1.52E-20			
Sapur.0096J180800.1	47.90212573	1.20335291	0.08635818	13.93531	3.87E-44	1.92E-43	cpm	0.71309396	1.75E-25	GO:0005509	Calcium-binding EF-hand family protein	EF-hand calcium-binding protein, putative
Sapur.0051I383000.1	189.6930349	-0.94407669	0.06093297	-13.9325	4.00E-44	1.98E-43	cpm	-0.79415434	2.40E-35	GO:0005275	Plant-specific transcription factor family protein	YABBY transcription factor
Sapur.0062H0900.1	305.1384759	0.45310769	0.03268142	13.93187	4.06E-44	2.01E-43	cpm	0.75157025	8.35E-30		TRF-like 10	
Sapur.0010G0607900.1	75.34695547	-1.00630184	0.07223251	-13.9309	4.11E-44	2.04E-43	cpm	-0.75494658	1.34E-30	GO:0008880	Acyl-CoA N-acyltransferase (DUF1298)	NA
Sapur.0051I853500.1	20.53751007	-2.32122247	0.09487572	-13.9257	4.42E-44	2.19E-43	cpm	-0.71864095	3.08E-26		glutamine-rich protein 23	PPR containing protein
Sapur.0105J370500.1	18.23647619	-2.40802024	0.07068498	-13.9253	4.45E-44	2.20E-43	cpm	-0.75181266	7.74E-30		Pentatricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.0162S02500.1	504.2842446	-5.56886807	0.04080407	-13.9221	4.65E-44	2.30E-43	cpm	-0.75870052	1.19E-30	GO:0006779;GO:0004853	HEME1	Uroporphyrinogen decarboxylase
Sapur.0105G0600800.1	31.15057559	-2.80608595	0.13576002	-13.9218	4.67E-44	2.31E-43	cpm	-0.71342284	1.03E-25			hypothetical protein
Sapur.0162B0600.1	1038.678851	-0.63710798	0.04578051	-13.9165	5.03E-44	2.49E-43	cpm	-0.77528371	9.65E-33			plant/P21F.14-40 protein, putative
Sapur.0110G0480600.1	55.56896789	-0.99025047	0.07118242	-13.9114	5.40E-44	2.67E-43	cpm	-0.78427089	6.07E-34		Protein of unknown function (DUF641)	UN11-like protein
Sapur.0096D540500.1	117.7549779	-0.62456115	0.04528822	-13.9092	5.57E-44	2.75E-43	cpm	-0.74174856	1.32E-29		Pentatricopeptide repeat (PPR)-containing protein	PPR containing plant protein
Sapur.0061G12000.1	452.237939	0.61985248	0.04454744	13.90828	5.64E-44	2.79E-43	cpm	-0.71702857	4.92E-26	GO:0046872	RING/FYVE/PHD-type zinc finger family protein	zinc finger protein
Sapur.0046J613000.1	58.88092369	-2.85147149	0.08476026	-13.9067	5.77E-44	2.85E-43	cpm	-0.70246709	9.76E-25			NA
Sapur.0061J630000.1	65.44012109	-2.87621111	0.13698375	-13.8995	6.18E-44	3.15E-43	cpm	-0.81390706	2.20E-38			ovate transcriptional repressor
Sapur.0110G1120900.1	120.5415511	-1.30581284	0.09395548	-13.8985	6.28E-44	3.10E-43	cpm	-0.7432723	1.56E-28		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosylmethionine-dependent methyltransferase, putative
Sapur.0170J018800.1	33.94098025	-1.14967159	0.08735884	-13.8927	7.02E-44	3.46E-43	cpm	-0.74073317	6.06E-29	GO:0007275;GO:0006511;GO:0005634	Protein with RING/U-box and TRAF-like domains	NA
Sapur.0110G0607800.1	372.5429734	-3.68420384	0.12082618	-13.8899	7.24E-44	3.60E-43	cpm	-0.75284597	2.02E-19		Phosphoglycerate mutase family protein	NA
Sapur.0162J004000.1	2210.468817	-0.48870923*	0.03518522	-13.8896	7.32E-44	3.61E-43	cpm	-0.74204599	1.02E-28	GO:0005515	ATEBP,LATG2,EBP1	proliferation-associated protein 2g4
Sapur.0070J120800.1	33.0247944	-1.68493466	0.12170353	-13.8798	8.34E-44	4.14E-43	cpm	-0.66827516	1.57E-21			nucleotide binding protein
Sapur.0062D040800.1	1235.115507	-0.99734369	0.07189433	-13.8724	9.32E-44	4.59E-43	cpm	-0.73898672	2.24E-28	GO:0046872;GO:0030001	Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.0010G1901000.1	533.842001	-0.61632761	0.04463123	-13.8719	9.38E-44	4.62E-43	cpm	-0.81058633	7.52E-38	GO:0016021;GO:0008680;GO:0005783	GO:0007190	B-cell receptor-associated protein 31-like
Sapur.0062H0300.1	24.83664433	-1.62318504	0.08187543	-13.8713	9.48E-44	4.67E-43	cpm	-0.76098877	5.75E-32			NA
Sapur.0062G040400.1	20.7553303	-2.23631863	0.08918233	-13.8688	9.80E-44	4.82E-43	cpm	-0.74029791	1.62E-28			CC-NBS-resistance protein, putative
Sapur.0061J000500.1	12096.18876	-5.93077903	0.04718535	-13.8602	1.01E-43	5.00E-43	cpm	-0.72521186	6.42E-27	GO:0016020;GO:0006810;GO:0005215	GAMMA-TIP,GAMMA-TIP5;1	gamma tonoplast intrinsic protein	aquaporin, MIP family,SC3L BP subfamily protein
Sapur.0140Z014000.1	12.32043836	-5.54005879	0.11079211	13.86451	1.04E-43	5.11E-43	cpm	0.69402988	5.90E-24		Helicase/SANT-associated, DNA binding protein	
Sapur.0162B0100.1	544.1373526	-5.71930139	0.05180985	-13.8614	1.04E-43	5.14E-43	cpm	0.69344587	7.88E-24	ATMYB4,MYB4	myb domain protein 4	MYB transcription factor 3, putative
Sapur.0162J1820.1	836.8567008	0.37437794*	0.07038603	13.859	1.12E-43	5.51E-43	cpm	-0.7836768*	7.21E-34	GO:0046923;GO:0016021;GO:0006621	ERO2B	endoplasmic reticulum retention defective 2B	ER lumen protein retaining receptor
Sapur.0110G0480600.1	372.6292115	-0.87484624	0.06288543	-13.8555	1.18E-43	5.79E-43	cpm	-0.73500371	1.46E-27	GO:0006543;GO:0003755;GO:0006413		peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.0010G0874000.1	1518.975964	-5.11795004	0.09275561	-13.8526	1.22E-43	5.96E-43	cpm	-0.68349124	9.01E-23	GO:0016021;GO:0004252;GO:0006508	GO:0012130	ATRBL2,RBL2	RHOMBOID-like 2
Sapur.0021G1468800.1	145.1512204	1.92980195	0.13934033	13.84785	1.31E-43	6.40E-43	cpm	-0.57330884	2.48E-15		GO:0019370.1	ACSTL5TS	stachyose synthase
Sapur.0010G0218000.2	6.54604077	-7.16272089	0.1684364	-13.8383	1.54E-43	7.55E-43	cpm	-0.72882616	6.57E-28	GO:0016021;GO:0016020;GO:0022857	WAT1	Walls are This	auxin-induced protein 5NG4
Sapur.0020G039000.1	825.8042367	0.46134237	0.03189647	13.83679	1.53E-43	7.50E-43	cpm	-0.74275739	8.52E-29			ubiquitin interaction motif-containing protein
Sapur.0162J0400.1	66.66964986	1.80705327	0.07279139	13.8351	1.57E-43	7.69E-43	cpm	0.66488251	1.26E-21			hypothetical protein
Sapur.0052J010000.3	16.37612317	-2.37260971	0.09205621	-13.8295	1.69E-43	8.29E-43	cpm	-0.49499135	1.40E-11	GO:0043169;GO:0005975;GO:0003824;GO:0004553	GO:3613360.1	BE3;SBE2.1	starch branching enzyme 2.1
Sapur.0051J350500.1	6.96004840	-7.80284323	0.15172573	-13.8268	1.74E-43	8.40E-43	cpm	-0.67767805	2.02E-21		Protein of unknown function (DUF1462)	NAD(P)H-quinone oxidoreductase subunit 6
Sapur.0B0139J100.1	131.4496918	0.99324436	0.07183609	13.82638	1.77E-43	8.65E-43	cpm	-0.66346932	2.84E-21		Family of unknown function (DUF736)	transmembrane protein, putative
Sapur.0010G0218000.1	44.35413819	-2.00178161	0.07888493	-13.8227	1.86E-43	9.10E-43	cpm	-0.75226619	1.87E-30		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.0162B0100.1	29.63742434	-3.19438788	0.09501572	-13.8181	1.98E-43	9.70E-43	cpm	-0.72634086	5.05E-27		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.0105G0680600.1	580.8156849	-0.72174555	0.05463124	-13.8155	1.99E-43	9.76E-43	cpm	-0.74411796	6.80E-29	GO:0006629	alpha/beta-hydrolase superfamily protein	enhanced disease susceptibility protein
Sapur.0105G0800.1	652.8542925	-0.52206149	0.03780608	-13.8089	2.15E-43	1.10E-42	cpm	-0.73454698	1.00E-26		NAD(P)-binding Rossmann-fold superfamily protein	NAD-dependent epimerase/dehydratase family protein
Sapur.0196G146600.1	651.4386662	-0.37882192*	0.02769256	-13.7983	2.61E-43	1.27E-42	cpm	-0.74924764	1.56E-29	GO:0005634;GO:0003677	MBD13	methyl-binding domain protein, putative
Sapur.0010G0813000.1	-5.07266351	-1.88703833	0.13678075	-13.7983	2.61E-43	1.28E-42	cpm	-0.72689516	4.52E-27		WAT1	Walls are This	hypothetical protein
Sapur.0021G1460000.1	4.72206249	-2.99605081	0.21703074	-13.7966	2.67E-43	1.30E-42	cpm	-0.68348283	8.98E-23	GO:0005524		T-complex protein 1 alpha subunit
Sapur.0162J0600.1	6.38087674	-2.37387294	0.17207082	13.76581	2.76E-43	1.34E-42	cpm	0.67481053	1.66E-21	GO:0006281;GO:0004518;GO:0008289;GO:0005634;GO:0004519;GO:0003697	UVH6,UVR1	EV; XP; excision repair protein
Sapur.0B0141G00.1	284.4372288	0.56017775	0.04060744	13.79509	2.73E-43	1.33E-42	cpm	0.7394973	2.01E-28			alpha/beta-Hydrolases superfamily protein	carboxylesterase, putative
Sapur.0010G0813000.1	93.47847387	-1.64620304	0.11872659	-13.7932	2.85E-43	1.39E-42	cpm	0.70744472	1.60E-25		Iron-sulfur cluster biosynthesis protein	iron-sulfur cluster biosynthesis protein
Sapur.0030G063600.1	340.315254	1.34941407	0.09768211	13.78837	3.01E-43	1.47E-42	cpm	0.70302261	1.28E-24	GO:0008064;GO:0016762;GO:0006073;GO:0005618;GO:0005975;GO:0004553	XTH30,XTH4	xyloglucan endotransglucosylase/hydrolase 30	xyloglucan endotransglycosylase/hydrolase
Sapur.0110G0607900.1	8.10082933	1.08272684	0.2226112	13.78605	3.06E-43	1.49E-42	cpm	0.64472422	6.82E-20		ACT11	actin-11	actin
Sapur.0170D0500.1	46.61404204	-0.91256622*	0.06784874	-13.785	3.14E-43	1.52E-42	cpm	-0.73028765	5.96E-28		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.0196G143700.1	96.11146827	1.58317788	0.11532548	13.7796	3.26E-43	1.60E-42	cpm	0.62365829	5.46E-19	GO:0005975;GO:0004553	glycosyl hydrolase family 16	endo-1,3(2),4-beta-glucanase
Sapur.0130G08900.1	1.90214496	4.31208806	0.31311559	13.77514	3.68E-43	1.75E-42	cpm	0.59458874	2.21E-16	GO:0055114;GO:0020037;GO:0008379;GO:0004601	GO:3623031.1	Peroxidase superfamily protein	heme peroxidase, plant/fungal/bacterial
Sapur.0130J08800.1	3.52484928	2.81325384	0.20425576	13.77167	3.77E-43	1.86E-42	cpm	0.69409766	6.87E-24				NA
Sapur.0105G1120500.1	39.07253329	-1.37356634	0.09074642	-13.7712	3.80E-43	1.85E-42	cpm	-0.68941847	1.81E-22	GO:0007275	YAB2	Plant-specific transcription factor YABBY family protein	transcription factor YABBY2
Sapur.0120J0210.1	6.27319298	-2.01149383	0.14651542	-13.7648	4.15E-43	2.02E-42	cpm	-0.72869559	2.87E-27		ATTCP1B,BRC1,TCP18	TCP family transcription factor	transcription factor TCP24
Sapur.0010G0560000.1	635.8950200	-1.61433389	0.04710649	-13.7609	4.38E-43	2.12E-42	cpm	-0.75084844	1.02E-29	GO:0051082;GO:0031072	DNA heat shock protein family	chaperone protein DnaJ-like	chaperone protein DnaJ-like
Sapur.0105G0360600.1	242.4257964	-0.56146444	0.04080849	-13.757	4.62E-43	2.25E-42	cpm	-0.73828365	2.67E-28	GO:0006310;GO:0006302;GO:0005634;GO:0003677	GO:2310102.2	XRCC4	homolog of human DNA ligase iv-binding protein XRCC4	DNA double-strand break repair and V(D)J recombination protein XRCC4
Sapur.0161T660G0.1	45.80424417	-0.64077385	0.0472372	-13.7557	4.73E-43	2.28E-42	cpm	-0.73435147	7.28E-28	GO:0005461	GO:3189630.1		transcriptional regulator of RNA polII, SKIA, suhsm
Sapur.0180B0100.1	50.67098892	-3.39974228	0.10178362	-13.7544	4.79E-43	2.31E-42	cpm	-0.76370674	2.90E-31				hypothetical protein
Sapur.0061A0400.1	845.2178692	-0.67363632	0.04668887	-13.7521	4.94E-43	2.40E-42	cpm	-0.74035314	1.08E-28	GO:0016020;GO:0010531	GO:3187301.1	SCY1	SCY homolog 1	preprotein translocase subunit SecY
Sapur.0040G058200.1	2.80432143	4.29231116	0.31214253	13.75112	5.01E-43	2.44E-42	cpm	0.55389132	8.19E-14					NA
Sapur.0051J867000.1	1177.905513	0.61780356	0.04693313	13.74996	5.10E-43	2.48E-42	cpm	0.75257267	8.38E-30			CPuGR05	conserved peptide upstream open reading frame 5	peptide upstream ORF protein
Sapur.0130J043000.1	24.02337570	-2.27555653	0.09279562	-13.7458	5.40E-43	2.63E-42	cpm	-0.70054693	1.01E-24	GO:0005515	LSH6	light-dependent short hypocotyls protein, putative	light-dependent short hypocotyls protein, putative
Sapur.0180J051500.1	1420.871016	0.46735899	0.02253502	13.7437	5.58E-43	2.70E-42	cpm	-0.72018238	2.17E-26		Protein of unknown function (DUF644)	Protein of unknown function (DUF644)
Sapur.0096D700001.1	221.6268217	-0.98500224	0.07187274	13.7413	5.67E-43	2.87E-42	cpm	-0.67463807	3.40E-22		ST2,DAT10	ST2,DAT10	C2H2-type zinc-finger protein, putative	C2H2-type zinc-finger protein, putative
Sapur.0B0122T00.2	24.07493956	-4.72300025	0.10714631	-13.7386	5.96E-43	2.89E-42	cpm	-0.73188325	1.52E-27	GO:0005515		GO:3615380.1	aexaxthin epoxidase, putative	NA
Sapur.0130J0400.1	14.62478809	1.57253599	0.11460851	13.7384	5.98E-43	2.90E-42	cpm	-0.71530806	6.68E-26		ASAT1,ATSAT1,ATSAT1	ATSAT1	acyl-CoA sterol acyltransferase 1	NA
Sapur.0110J2550G0.1	742.2684748	-0.6574603	0.03196827	-13.7371	6.09E-43	2.95E-42	cpm	-0.75398751	4.34E-30	GO:0005515	CSN6A	COP9 signalosome subunit 6A	COP9 signalosome complex subunit 6	NA
Sapur.0010G0813000.1	208.2524485	-1.08624704	0.09057613	-13.734	6.14E-43	2.98E-42	cpm	-0.73160849	1.61E-27				cis-2,3,7,8,8-carotene protein	NA
Sapur.0070B09000.1	13.68151547	1.89466495	0.13797249	13.73219	6.51E-43	3.16E-42	cpm	0.70574525	5.68E-25		GO:6327320.1	KPL	kokopelli	hypothetical protein
Sapur.0162J0600.1	938.6372035	-0.95785329	0.06970103	-13.7301	6.59E-43	3.20E-42	cpm	-0.74348835	3.62E-28		ATTIC110,TIC110	translocon at the inner envelope membrane of chloroplasts 110	translocon at the inner envelope membrane of chloroplasts 110	NA
Sapur.0020G075500.1	688.0828674	-0.81938994	0.05968883	-13.7278	6.92E-43	3.35E-42	cpm	-0.76898637	6.30E-32	GO:0005975;GO:0004553		GO:3760600.1	Glycosyl hydrolase family protein	xylan 1,4-beta-xylosidase
Sapur.0161J573000.1	136.8086578	0.97623256	0.07123286	13.72585	7.11E-43	3.44E-42	cpm	-0.71932138	2.92E-26	GO:0006468;GO:0005524;GO:0004672	ATMAPK2,ATMPK2,MPK2	mitogen-activated protein kinase 2	MAPK kinase	MAP kinase
Sapur.T097800.1	4.34869182	2.78272766	0.20287217	13.71665	8.07E-43	3.90E-42	cpm	-0.64722265	3.81E-20	GO:0003984;GO:0005737	GO:6341085.1	ARM repeat superfamily protein	ARM repeat protein	NA
Sapur.0021G1450000.1	64.42055455	-0.64654568	0.04713706	-13.716	8.14E-43	3.94E-42	cpm	-0.75265815	6.23E-30	GO:0006355;GO:0005739;GO:0003690	GO:0079000.1	Mitochondrial transcription termination factor family protein	mTERF protein	NA
Sapur.0051I550000.1	273.8695647	-0.62422968	0.03327756	-13.7084	8.94E-43	4.32E-42	cpm	-0.71538187	6.57E-26		ATTIM23-1,TIM23-1	translocase of inner mitochondrial membrane 23	translocase of inner mitochondrial membrane 23	import inner membrane translocase subunit TIM23
Sapur.0062J1700.1	557.4211644	-0.73125505	0.05341299	-13.7089	8.98E-43	4.34E-42	cpm	-0.70729499	8.28E-25			GO:6164101.1		transmembrane protein, putative
Sapur.0070J0380.1	671.5270987	-0.84189744	0.06141101	13.70841	9.04E-43	4.37E-42	cpm	-0.72682837	4.77E-27			GO:6268237.1		transmembrane protein, putative
Sapur.0162A0900.1	417.4918841	-5.96046322	0.14301529	-13.708	9.09E-43	4.39E-42	cpm	-0.67238642	5.30E-22			GO:6240470.1	Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.0110G0480600.1	337.6475635	-0.83819242	0.08737765	-13.7016	9.93E-43	4.80E-42	cpm	-0.75243136	3.98E-30	GO:0030247	Putative membrane lipoprotein	GO:3181881.1		wall-associated receptor kinase galacturonan-binding protein
Sapur.0051J484000.1	67.79478918	1.99373946	0.08752489	13.69735	1.05E-42	5.08E-42	cpm	0.0874415	3.40E-24					NA
Sapur.0052H0100.1	6.37933164	3.89488122	0.28439326	13.69548	1.08E-42	5.21E-42	cpm	0.63193155	5.32E-19			GO:3237663.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.0105G2140400.1	91.88608834	-6.62131325	0.04836707	-13.6892	1.58E-42	5.68E-42	cpm	-0.75244002	6.02E-30			GO:3237526.1		hypothetical protein
Sapur.0086G071100.1	132.226158	-0.86719153	0.06335842	-13.6871	1.23E-42	5.85E-42	cpm	-0.78645218	2.98E-34		GO:6326340.1	ATC85-AJB5		cytochrome protein b5
Sapur.0010G0813000.1	21.79467863	-1.55825148	0.11388736	-13.6824	1.26E-42	6.34E-42	cpm	-0.69881806	2.56E-24			GO:3447234.1		epidermal patterning factor-like protein, putative
Sapur.0020G057500.1	1164.61444	0.3633689	0.02655

Sapur.003G088300.1	119.7169798	-0.76103488	0.05385043	-13.268	2.38E-40	1.10E-39	cpm	-0.7639376677	2.71E-31	GO:0005524	ATSG13160.1	RFC2	replication factor C subunit 2
Sapur.002G084400.1	1200.16951	0.28786429	0.02164758	13.29778	2.38E-40	1.11E-39	cpm	-0.7316208514	1.40E-27		ATSG16550.2		Clathrin adaptor complexes medium subunit family protein
Sapur.013G251100.1	34.69448804	0.8989852	0.06758206	13.30519	2.46E-40	1.14E-39	cpm	-0.7319526213	2.52E-26		ATS11740.1		O-fucosyltransferase family protein
Sapur.009G019500.1	8.51604201	1.96021425	0.14746568	13.29347	2.53E-40	1.17E-39	cpm	-0.6004510404	9.40E-17	GO:0006887;GO:0000145	ATSG19730.2	ATEXO70H7;EXO70H7	exocyst subunit exo70 family protein H7
Sapur.016G075000.1	114.5451613	1.90846553	0.14358849	13.29126	2.91E-40	1.35E-39	cpm	-0.6918680907	1.09E-20	GO:0005524;GO:0020037;GO:0016705;GO:0005506	ATKG31940.1	CYP82C4	cytochrome P450, family 82, subfamily C, polypeptide 4
Sapur.016G046100.5	31.71971162	-1.17246767	0.08823304	-13.2886	2.70E-40	1.25E-39	cpm	-0.6920604564	8.81E-24		ATG42320.2		nucleolar protein gar2-related
Sapur.003G077400.1	110.7047914	0.95108477	0.07158895	13.28485	2.83E-40	1.31E-39	cpm	-0.7129855	1.51E-25		ATG22260.1	ZYP1;ZYP1a	Myosin heavy chain-related protein
Sapur.004G058600.1	136.2321658	0.61050425	0.04617682	-13.2814	2.97E-40	1.38E-39	cpm	-0.7468365959	3.10E-29	GO:0008641	ATSG37530.1		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.010G076400.1	477.6544296	-0.60584428	0.04561623	-13.2812	2.98E-40	1.38E-39	cpm	-0.722041688	1.40E-26		ATSG68660.1		Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein
Sapur.006G056300.2	21.5106638	2.0122438	0.15024323	13.27809	3.12E-40	1.46E-39	cpm	-0.6770631513	4.58E-20	GO:0055114;GO:0008788;GO:0004392	ATHDS.G;IN2.H3;IN5?.H9	ATHDS.G;IN2.H3;IN5?.H9	Flavin hydroxylase (Oxygenase) family protein
Sapur.010G021500.1	672.9517435	0.77382689	0.05820353	-13.2728	3.33E-40	1.56E-39	cpm	-0.7141646666	8.70E-26	GO:0008635;GO:0008399;GO:0003677	ATG22730.1		DNA binding,DNA-directed RNA polymerases
Sapur.004G000900.1	42.5025147	1.26112752	0.09427551	13.37078	3.42E-40	1.58E-39	cpm	-0.6410305151	1.53E-19		ATSG28110.1		nucleic acid binding,ATP-dependent helicase;ATP binding;helicase;ATP-dependent helicases
Sapur.015W0581600.1	10.1862243	1.56266703	0.11783437	13.2627	3.81E-40	1.76E-39	cpm	-0.708793989	2.90E-25	GO:0016887;GO:0005524;GO:0016021;GO:0006810;GO:0005215	ATAT7780.1	ATATHLLATH6	ABC2 homolog 6
Sapur.013G251300.1	33.86643276	1.38400109	0.10442489	13.2404	4.28E-40	1.98E-39	cpm	-0.7272468635	2.07E-24				
Sapur.001G016000.1	2202.753887	-0.42193729	0.03181459	-13.2517	4.41E-40	2.04E-39	cpm	-0.747798888	2.29E-29	GO:0016491;GO:0008152	ATSG05990.2	ENR1;MD01	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.012G084600.1	68.3395719	1.16126409	0.09026868	13.2476	4.67E-40	2.16E-39	cpm	-0.6790908811	2.06E-20	GO:0005524;GO:0003677	ATG31880.1	KN;ATK;KN-ATG1;KNATG5	KN/OTET3-like homeobox gene 6
Sapur.016G180000.1	169.7312206	-0.79628412	0.06013339	-13.2442	4.88E-40	2.25E-39	cpm	-0.681205863	9.38E-23		ATG15270.1		
Sapur.012G086100.1	160.623079	-0.49393586	0.03720754	-13.2428	4.97E-40	2.29E-39	cpm	-0.738132029	7.98E-28		ATGC6240.1		Protein of unknown function DUF455
Sapur.010G138100.1	8.21705004	1.99553525	0.15035038	13.2385	5.24E-40	2.41E-39	cpm	-0.695292073	2.32E-24		ATSG63060.1	RLA17	FAR2/ATA-20 family protein 17 precursor
Sapur.015G067600.1	1303.744677	0.34564705	0.026103947	13.23581	5.60E-40	2.58E-39	cpm	-0.713014567	4.52E-26	GO:0055114;GO:0009396;GO:0004488;GO:0003824	ATSG12260.1		Amino acid dehydrogenase family protein
Sapur.015W0269680.1	1115.764613	0.29108004	0.02198724	13.2287	5.92E-40	2.72E-39	cpm	-0.72131333	5.98E-26	GO:0005966	ATSG10100.1	TAP46	2A phosphatase-associated protein of 46 kD
Sapur.15W0087000.1	230.1092636	-0.51308183	0.03879501	-13.2255	6.26E-40	2.88E-39	cpm	-0.727984509	3.40E-27		ATSG33080.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.003G040600.1	57.21855529	0.25388041	0.01947648	13.2217	6.58E-40	3.03E-39	cpm	-0.75318466	1.36E-32		ATSG16827.1		
Sapur.009G046200.1	44.30695323	0.79129725	0.05872597	13.21634	7.06E-40	3.25E-39	cpm	-0.723484637	9.07E-27		ATSG47940.1		
Sapur.003G105300.3	73.80865943	0.80105147	0.06064057	13.2108	7.25E-40	3.34E-39	cpm	-0.721202014	5.70E-27		ATSG14600.1		Transmembrane amino acid transporter family protein
Sapur.010G076600.1	808.6763464	-0.78079488	0.07408393	-13.2131	7.38E-40	3.40E-39	cpm	-0.790739342	5.30E-29		ATSG60060.1		Serine/threonine-protein kinase WNK (With No Lysine)-related
Sapur.005G111200.1	134.9760761	-0.68806552	0.05219622	-13.2112	7.54E-40	3.46E-39	cpm	-0.739043137	2.20E-28		ATSG11290.1	CRR22	Pentatricopeptide repeat (PPR) superfamily protein
Sapur.005G054005.1	531.5655542	-0.50136147	0.03721919	-13.2108	7.61E-40	3.50E-39	cpm	-0.705836129	5.56E-25	GO:0016747	ATG54570.1		Extensins/Spine/Hibosyntexase family protein
Sapur.013G021000.2	10.6538916	-1.68613306	0.12763828	-13.2081	7.88E-40	3.62E-39	cpm	-0.701516612	1.42E-24		ATSG22630.1		hypothetical protein
Sapur.010G080800.1	2.80272861	1.79793116	0.24075152	13.20577	7.93E-40	3.65E-39	cpm	-0.69704571	3.70E-24		ATSG47920.1		hypothetical protein
Sapur.015G206100.1	609.9662245	-1.30736571	0.09900175	-13.2041	8.20E-40	3.82E-39	cpm	-0.691898511	1.09E-23	GO:0005515;GO:0006096;GO:0004743;GO:0000287	ATSG08570.1		Pyruvate kinase family protein
Sapur.005G132900.1	35.37889741	-0.53220903	0.03281381	-13.1951	9.58E-40	4.30E-39	cpm	-0.7485525	2.16E-29		ATSG18520.1		Extensins/Spine/Hibosyntexase family protein
Sapur.012G289700.2	4.48136736	2.58369193	0.19580713	13.19105	9.88E-40	4.54E-39	cpm	-0.6703157861	7.81E-22		ATSG42130.1		hypothetical protein
Sapur.004G000400.1	122.7875854	-0.32765154	0.02484698	-13.1871	1.04E-39	4.78E-39	cpm	-0.7316818133	4.90E-26	GO:0055114;GO:0016655	ATSG27525.1	NDH-M	subunit NDH-M of NAD(P)H plastoquinone dehydrogenase complex
Sapur.014G080300.1	327.1062887	-0.61002282	0.04627082	-13.1833	1.09E-39	5.03E-39	cpm	-0.708213981	3.26E-25	GO:0046933;GO:0015986	ATSG06650.1	ATPD	ATP synthase delta-subunit gene
Sapur.015G078700.1	15.58870742	-0.92109183	0.07010265	-13.1813	1.12E-39	5.17E-39	cpm	-0.678102061	1.51E-18		ATSG39160.1		Pentatricopeptide repeat (PPR)-containing protein
Sapur.005G076060.1	61.92559173	-0.26635684	0.08837297	-13.1778	1.23E-39	5.40E-39	cpm	-0.695588009	5.10E-24	GO:0055114;GO:0046872;GO:0008800;GO:0004784	ATSG23310.1	FSD3	Fe superoxide dismutase 3
Sapur.010G200300.1	23.46119423	0.80527826	0.28127081	-13.1754	1.28E-39	5.58E-39	cpm	-0.519047756	3.30E-12		ATSG27750.1		Pectate lyase family protein
Sapur.006G035500.1	480.0751166	-0.34380002	0.02604857	-13.1728	1.32E-39	5.77E-39	cpm	-0.72152053	5.60E-27	GO:0004386	ATSG18465.1		RNA helicase family protein
Sapur.010G190900.1	162.7271559	1.14008975	0.08678693	13.17171	1.28E-39	5.85E-39	cpm	0.6334579	5.44E-19		ATSG78955.1		hypothetical protein
Sapur.010G194900.1	494.8654609	0.78574231	0.06118369	13.17008	1.35E-39	5.88E-39	cpm	0.686215689	4.48E-24	GO:0055085;GO:0016020;GO:0008810;GO:0015171;GO:0003333	ATCAT6;CAT6	cationic amino acid transporter 6	cationic amino acid transporter, putative
Sapur.014G240400.1	52.98362609	1.06282569	0.23285508	13.16848	1.33E-39	6.11E-39	cpm	0.5425667	2.14E-13	GO:0006629	ATSG26560.1	PLA IIA;PLA2A;PLP2	phospholipase A 2A
Sapur.004G203200.1	52.03423364	1.02088128	0.09160715	-13.166	1.38E-39	6.32E-39	cpm	-0.711284645	6.62E-25		ATSG29320.1		Protein of unknown function (DUF1635)
Sapur.7G08800.1	2.26022709	3.70916003	0.28183836	13.16221	1.45E-39	6.63E-39	cpm	0.591997674	2.51E-16	GO:0005681;GO:0000398;GO:0003887	ATSG54385.1		ARM repeat superfamily protein
Sapur.003G317900.1	580.160689	-0.95406425	0.07309745	-13.1616	1.47E-39	6.72E-39	cpm	-0.752097988	1.08E-29	GO:0005524;GO:0003824;GO:0004791;GO:0004722	ATSG41640.1		Protein phosphatase 2C family protein
Sapur.017G104000.1	1246.406247	-0.72640844	0.05520187	-13.1594	1.50E-39	6.88E-39	cpm	-0.668800944	1.05E-21		ATSG66330.1		senescence-associated protein
Sapur.006G113200.1	64.65771	0.90809665	0.06903943	-13.1559	1.57E-39	7.20E-39	cpm	-0.737883817	2.95E-28		ATSG19240.1		transmembrane protein, putative
Sapur.010G202600.1	26.97758607	2.26899469	0.18656457	13.14769	1.75E-39	7.99E-39	cpm	0.594197977	2.24E-16	GO:0005516;GO:0046872;GO:0000166	ACA8;ATACA8	autoinhibited Ca(2+)-ATPase 9	calcium-transporting ATPase 9, plasma membrane-type protein
Sapur.016G055500.1	1061.668161	0.80702859	0.06225698	13.14465	1.83E-39	8.35E-39	cpm	-0.705263904	6.31E-25		ATSG58030.2		RING/U-box superfamily protein
Sapur.010G075400.1	290.3920757	-0.35400002	0.02704857	-13.1424	1.84E-39	8.38E-39	cpm	-0.684881639	1.07E-23		ATG37730.2		NAD(P)-linked oxidoreductase superfamily protein
Sapur.008G001300.1	189.6772546	-0.59892802	0.04334166	-13.1441	1.84E-39	8.40E-39	cpm	-0.703967633	8.37E-25		ATSG78955.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.012G240700.1	35.47161223	1.04175349	0.08200604	13.1344	2.06E-39	9.54E-39	cpm	-0.742866788	8.38E-29		ATSG2	SIR2	similar to NCU-one 2
Sapur.018G091600.1	1.65304118	3.568493	0.27177787	13.13048	2.20E-39	1.01E-38	cpm	0.68367823	5.80E-23				
Sapur.016G181800.1	257.2632256	0.58388128	0.05368033	13.12889	2.25E-39	1.03E-38	cpm	-0.721437087	1.62E-26	GO:0006468;GO:0005524;GO:0004672;GO:0005515	ATSG55632.2	BRL1	BRI1 like
Sapur.007G120800.1	481.4572732	0.39142097	0.02981454	13.12821	2.27E-39	1.04E-38	cpm	-0.73074163	1.76E-27		ATSG30710.1		Rpt/Rab-GAP domain of gyp1p superfamily protein
Sapur.003G337200.1	242.4769325	-0.83431236	0.06370661	-13.1252	2.38E-39	1.08E-38	cpm	-0.723121066	1.39E-26	GO:0015979;GO:0009523;GO:0009507	PSBW	PSBW	photosystem II reaction center W
Sapur.009G086200.1	200.7651213	-0.51604792	0.03939315	-13.1217	2.47E-39	1.13E-38	cpm	-0.729345408	2.45E-27	GO:0031683;GO:0010001;GO:0007186;GO:0004871;GO:0003924	ATXG1;XLG1	ATXG1;XLG1	extra-large G protein 1
Sapur.002G067700.1	242.7862285	0.51875985	0.03955504	13.11472	2.71E-39	1.24E-38	cpm	-0.68705521	2.44E-23				transmembrane protein, putative
Sapur.010G202100.1	3272.764878	-0.62729184	0.04783271	-13.1144	2.74E-39	1.26E-38	cpm	-0.771551347	2.95E-32	GO:0055114;GO:0046872;GO:0016491	ACS9;CHL27;CHD1	ACS9;CHL27;CHD1	dicarboxylate diiron protein, putative (CnsE1)
Sapur.003G189400.1	42.02076661	-0.79920739	0.06094535	-13.1127	2.75E-39	1.25E-38	cpm	-0.738870947	2.30E-28		ATSG26860.1		Homeodomain-like superfamily protein
Sapur.006G189300.1	246.4413102	-0.48128108	0.04394075	-13.1103	2.88E-39	1.31E-38	cpm	-0.745064205	5.20E-28		ATSG62520.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.014G195900.1	12.93898552	-1.51187146	0.10598327	-13.1093	2.91E-39	1.33E-38	cpm	-0.703967633	8.37E-25	GO:0005515	ATG62760.1	ATGGTS13	Glutathione S-transferase family protein
Sapur.003G260600.1	1070.094615	-0.28384688	0.02161278	-13.1091	2.92E-39	1.33E-38	cpm	-0.71278058	5.45E-26	GO:0008270	ATSG35050.1		DHHC-type zinc finger family
Sapur.014G144800.1	2.72042165	1.55497844	0.27142551	13.09935	3.32E-39	1.51E-38	cpm	0.683452381	6.07E-23		ATSG36380.1		Melibiase family protein
Sapur.003G073200.1	26.46481262	0.92145264	0.08201516	-13.0975	3.41E-39	1.55E-38	cpm	-0.728486664	6.05E-27		ATSG22620.1		
Sapur.017G027500.1	683.7602332	0.42978889	0.03280735	13.09504	3.51E-39	1.60E-38	cpm	0.730372014	1.91E-27	GO:0005515	ATSG42320.2		Ubiquitin-like superfamily protein
Sapur.016G280300.1	813.3215134	-0.50358182	0.04204781	-13.0946	3.58E-39	1.63E-38	cpm	-0.721979013	1.49E-26		ATSG10055.1		
Sapur.006G234000.1	11.12575127	1.98739121	0.15177761	13.09278	3.62E-39	1.64E-38	cpm	0.6470305	1.46E-21		ATSG75181.1		
Sapur.016G139900.1	512.1354287	-1.44789718	0.10636777	-13.0866	3.93E-39	1.78E-38	cpm	-0.692809224	8.96E-24		ATSG49701.1		thylakoid soluble phosphoprotein TSP9 protein
Sapur.004G080600.1	31.65782283	-0.68483024	0.05196811	-13.0865	3.98E-39	1.81E-38	cpm	-0.759722663	3.02E-31	GO:0006412;GO:0005840;GO:0003735	ATSG57624.1		Ribosomal protein RSP-3/rrc565
Sapur.006G058000.1	197.0548236	-0.60679636	0.04637747	-13.0839	4.07E-39	1.85E-38	cpm	-0.723631669	9.62E-27				
Sapur.005G177600.1	716.0899022	-0.52769518	0.04030556	-13.0838	4.07E-39	1.85E-38	cpm	-0.729397541	1.42E-26	GO:0005515;GO:0005634;GO:0003677	ATSG67330.1		Calmodulin-binding transcription activator protein with CG-1 and Ankyrin domains
Sapur.006G063400.1	1311.895139	-0.38171727	0.02917583	-13.0837	4.08E-39	1.85E-38	cpm	-0.70847616	7.74E-27		ATSG35160.1	CAC2	acetyl-Co-enzyme a carboxylase biotin carboxylase subunit
Sapur.003G032300.1	472.5149667	-0.67681116	0.05236373	-13.083	4.12E-39	1.87E-38	cpm	-0.731411051	1.47E-27	GO:0016021	ATSG10040.1		Cerrik-like protein-interaction kinase protein
Sapur.014G091600.1	94.2557025	-0.76716388	0.05839496	-13.0828	4.13E-39	1.87E-38	cpm	-0.732276846	1.20E-27		ATSG03130.1		BRCT domain-containing DNA repair protein
Sapur.008G000800.1	657.3699046	-0.67025182	0.05123847	-13.0803	4.26E-39	1.93E-38	cpm	-0.757876546	4.98E-32		ATSG18360.1	ATRAP;RAP	RAP domain protein
Sapur.007G112000.1	79.17778291	-0.49725261	0.03804375	-13.0769	4.46E-39	2.02E-38	cpm	-0.739800671	1.82E-28	GO:0000123	ATSG33160.1		DNA-binding domain protein, putative
Sapur.7G40700.1	15.2558865	1.27191851	0.09730452	13.07166	4.78E-39	2.16E-38	cpm	-0.708592268	3.03E-25		ATSG29360.1	EDA10	SEC7-like guanine nucleotide exchange family protein
Sapur.003G035000.1	25.54022269	-0.59845244	0.08248624	-13.0675	5.05E-39	2.29E-38	cpm	-0.749387627	2.88E-29	GO:0016021	ATSR8;RER18;RER18	ATSR8;RER18	endoplasmic reticulum retrieval protein 18
Sapur.007G018300.1	270.3066131	0.94053784	0.14851194	13.0665	5.12E-39	2.31E-38	cpm	-0.627298649	1.49E-18	GO:0008168	ATSG64330.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.003G225200.1	1381.815769	-0.79828441	0.06111659	-13.0658	5.46E-39	2.47E-38	cpm	-0.707917558	3.52E-25	GO:0005524;GO:0015986;GO:0015978	ATSrna_F0;rnaseq_subunit B;F1_bacterial/chloroplast		ATPase, F0/rnaseq_subunit B;F1_bacterial/chloroplast
Sapur.019G209800.1	6.69625597	-2.44171731	0.18694782	-13.061	5.50E-39	2.49E-38	cpm	-0.698368879	2.80E-24				
Sapur.010G080200.1	84.46136907	-0.63828359	0.05154991	-13.061	5.52E-39	2.50E-38	cpm	-0.724904197	2.62E-27	GO:0009245;GO:0008759	ATSG25054.1		UDP-3-O-(R)-N-acetylglucosamine deacetylase family protein
Sapur.015G173900.1	4076.312802	0.70377442	0.05269834	-13.0474	6.58E-39	2.97E-38	cpm	-0.706647959	1.71E-24	GO:0015979;GO:0009523;GO:0009507	PSBW	PSBW	photosystem II reaction center W
Sapur.003G000300.1	17.87974161	-1.11384007	0.08531088	-13.043	6.97E-39	3.15E-38	cpm	-0.74181263	8.95E-29		ATSG16010.1		hypothetical protein
Sapur.005G081900.1	192.6886602	-0.66610536	0.05107579	-13.0421	7.05E-39	3.18E-38	cpm	-0.739278055	2.02E-28		ATSG17525.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.006G135700.1	260.0130703	-0.70158492	0.05619926	-13.038	7.44E-39	3.36E-38	cpm	-0.730872556	1.76E-27		ATSG49320.1		NAD(P)H-dehydrogenase dehydrogenase (quinone)
Sapur.009G080700.1	149.7884356	-1.23017928	0.09437255	-13.0354	7.70E-39	3.47E-38	cpm	-0.735660686	5.17E-28	GO:0003677	ATSG19184.1		RD 3N-binding domain protein
Sapur.003G247700.1	488.3643891	0.81835536	0.06288938	13.0123	1.04E-38	4.69E-38	cpm	0.688362242	1.99E-23		ATSG15190.1	PRA1.F;PRA7	PRA1 (Prenylated rab acceptor) family protein
Sapur.003G035000.1	4.74797744	-2.86226098	0.22766136	-13.0161	1.05E-38	4.73E-38	cpm	-0.605346421	4.57E-17		ATSG46421.1	CAMB	calmodulin, putative
Sapur.019G001200.1	1080.529694	0.67291879	0.05179369	13.01141	1.05E-38	4.74E-38	cpm	0.693813023	7.20E-24	GO:0016491;GO:0008198;GO:0006725	ATSG15091.1		catalytic Ugb subunit of aromatic ring-opening dioxygenase family
Sapur.005G092600.1	6.11955453	1.79425139	0.40293231	13.01139	1.05E-38	4.74E-38	cpm	0.528031587	1.13E-12		ATSG12510.1	CPR30	F-box and ankyrin domain-containing protein
Sapur.15W0512100.1	600.3718853	0.37985475	0.02916787	-13.0107	1.06E-38	4.76E-38	cpm	-0.719951007	2.29E-26	GO:0009001;GO:0006535;GO:0005737	ATSG76760.1	ATSERAT1;1;SAT-S2;SATS.S1	serine acetyltransferase 1;1
Sapur.019G084000.1	15.13910117	0.07080943	0.08294189	13.0082	1.08E-38	4.84E-38	cpm	-0.666510007	1.60E-21	GO:0016567;GO:0004842	ATSG17320.1		RING/U-box superfamily protein
Sapur.015G181200.1	44.8707869	0.91060112	0.07000954	13.0069	1.12E-38	5.03E-38	cpm	-0.754863673	3.40E-30				
Sapur.003G087000.1	582.0824653	0.64081437	0.03796918	13.0056	1.14E-38	5.11E-38	cpm	-0.738756164	1.86E-28	GO:0055114;GO:0016491;GO:0051536;GO:0020037	ATSG40580.1	SIR	sulfite reductase
Sapur.006G230000.1	934.4318711	0.37644278	0.02894668	13.00559	1.14E-38	5.11E-38	cpm	-0.720130779	2.19E-26		ATSG10780.1		Pyridine nucleotide-disulphide oxidoreductase family protein
Sapur.015G284800.1	1450.213643	-0.56409731	0.04320855	-13.005	1.15E-38	5.15E-38	cpm	-0.745418036	6.57E-28	GO:0005660;GO:0008033	ATSG74570.1		O-Glycosyl hydrolases family 17 protein
Sapur.012G026200.2	62.68585583	1.06577264	0.08159705	13.00457	1.15E-38	5.18E-38	cpm	-0.678964949	1.48E-22		ATSG11380.1		PLACE family protein
Sapur.012G089200.1	580.5790974	-0.66782418	0.04982561	-13.0021	1.19E-38	5.33E-38	cpm	-0.74421782	5.84E-29		ATSG15095.1		hypothetical protein
Sapur.005G180200.1	105.9424659	-1.51081693	0.11617933	-13.0019	1.19E-38	5.36E-38	cpm	-0.743192749	3.60E-29	GO:0009733	ATSG75580.1		SAUR-like auxin-responsive protein family
Sapur.018G089400.1	712.7201706	0.49267495	0.03790653	12.9968	1.28E-38	5.72E-38	cpm	0.737032388	3.66E-28	GO:0003676	ATSG09850.1		D111/G-patch domain protein
Sapur.006G209100.1	97.84335036	0.80336161	0.06870683	-12.9969	1.28E-38	5.72E-38	cpm	-0.728657544	2.08E-27		ATSG59320.1		Adenine nucleotide alpha hydrolases-like superfamily protein
Sapur.001G151000.1	9.53583623	2.03525121	0.15681688	12.96489	1.49E-38	6.67E-38	cpm	0.737248351	3.47E-28	GO:0016021	ATSG25737.1		Sulfite exporter TauE/SafE family protein
Sapur.016G075000.1	1348.171217	1.34025162	0.09618696	12.96192	1.51E-38	6.69E-38	cpm	0.70000886	1.97E-24	GO:0006621;GO:0008439;GO:0080059	ATSG37760.1	CER4;FAR1;G7	cuticle and cuticle wax-related male sterility protein
Sapur.003G182100.1	5.40008246	1.69331706	0.16564132	12.9562	1.68E-38	7.53E-38	cpm	-0.55274289	6.11E-14	GO:0080017;GO:0007018;GO:0005524;GO:0003777;GO:0007871	ATSG26370.1	KINESIN-12B;PAKRP1L	phragmoplast-associated kinesin-related protein, putative
Sapur.016G070000.1	161.4170344	0.80500886	0.06235663	12.95461	1.75E-38	7.59E-38	cpm	0.680290258	1.29E-24	GO:0005515	ATSG49400.1		ARM repeat superfamily protein
Sapur.016G172000.1	421.308877	-0.42221557	0.03254147	-12.9744	1.75E-38	7.64E-38	cpm	-0.720247048	2.13E-26	GO:0006470;GO:0006418;GO:0005524;GO:0004812;GO:0000166;GO:0016874	ATSG37630.1		tRNA synthetase class II (D, K and N) family protein
Sapur.001G117200.1	341.5648513	0.82585527	0.06368808	12.97275	1.75E-38	7.81E-38	cpm	0.676317671	2.46E-22		ATSG26981.1		
Sapur.011G180405.1	123.3704874	-0.69407523	0.07171768	-12.9709	1.78E-38	8.00E-38	cpm	-0.715446118	6.79E-27		ATSG36215.2		Domain of unknown function (DUF203)
Sapur.014G143400.1	3427.212958	0.54033641	0.04160185	12.9702	1.81E-38	8.07E-38	cpm	-0.709375662	2.54E-25	GO:0031897;GO:0003723	ATSG39780.1	RNS2	ribonuclease 2
Sapur.015G149100.1	21.14462398	0.82281156	0.09948557	12.96889	1.82E-38	8.12E-38	cpm	0.646844345	2.51E-21	GO:0005634;GO:0003682;GO:0003677	ATSG18812.NFD1	ATSG18812.NFD1	high mobility group B1
Sapur.001G075200.1	8.76040178	1.66387469	0.12839028	12.96823	1.85E-38	8.28E-38	cpm	0.656820053	9.94E-21	GO:0003247;GO:0008270;GO:0005515	ATSG33180.1		RING/U-box superfamily protein
Sapur.016G066800.1	1167.409208	0.54303871	0.04192646	12.95238	2.28E-38	1.02E-37	cpm	-0.731341108	1.86E-25	GO:0003824;GO:0006418;GO:0005524;GO:0004812;GO:0000166	ATSR5-1	ATSR5-1	lysine-tRNA ligase
Sapur.014G082500.1	161.4976645	-0.72676471	0.05618457	-12.9465	2.46E-38	1.10E-37	cpm	-0.737514306	2.21E-28		ATSG76370.2	NAGS2	N-acetyl-glutamate synthase 2
Sapur.019G060100.1	49.62779896	-0.56398192	0.05185125	-12.9432	2.57E-38	1.15E-37	cpm	-0.688275315	1.86E-23	GO:0006284	ATSG47830.1		DNA glycosylase superfamily
Sapur.017G080000.1	2636.156417	0.36343133	0.03107343	12.93813	2.74E-38	1.22E-37	cpm	-0.68835356	2.25E-23		ATSG29780.1	RALR1;7	ral-like 17
Sapur.011G294600.1	4.67159948	1.37337573	0.10618221	12.93507	2.81E-38	1.25E-37	cpm	-0.548733938	1.03E-13	GO:0048544;GO:0006468;GO:0004672	ATSG11330.1		S-locus lectin protein kinase family protein
Sapur.7G05200.1	49.3603979	1.15388426	0.08926275	12.92686	3.17E-38	1.41E-37	cpm	-0.691343159	1.27E-23		ATSG08110.1		nucleic acid binding,ATP-dependent helicases;ATP binding;helicases;ATP-dependent helicases
Sapur.010G244600.1	413.0609203	0.69927238	0.05409862	12.92465	3.26E-38	1.45E-37	cpm	0.671703997	6.04E-22		ATSG33390.1		
Sapur.010G176200.2	24.10618381	1.22388754	0.09469766	12.92409	3.28E-38	1.47E-37	cpm	0.70820392	3.30E-25	GO:0008270;GO:0005515	ATSG27150.1		RING/U-box superfamily protein
Sapur.001G172000.1	159.3626301	-0.67676932	0.05288829	-12.9178	3.57E-38	1.59E-37	cpm	-0.7222788	1.31E-26				
Sapur.018G070200.1	8.78042511	1.62409129	0.12836146	12.9169	3.58E-38	1.61E-37	cpm	0.664441865	2.42E-21		ATSG57530.1		
Sapur.002G237000.1	24.425975	2.40084209	0.18588212	12.91513	3.70E-38	1.65E-37	cpm	0.557615584	3.30E-14	GO:0043531	ATSG27190.1	NB-ARC domain-containing disease resistance protein	
Sapur.004G000500.1	154.5113164	0.51265127	0.0396654	12.9124	3.78E-38	1.68E-37	cpm	-0.705898706	9.76E-30		ATSG41600.1		ARM repeat superfamily protein
Sapur.007G018100.1	1491.756142	0.36332168	0.03792516	12.91138	3.78E-38	1.68E-37	cpm	-0.575464758	3.19E-15	GO:0008168	ATSB4MT1;B5MT1	ATSB4MT1;B5MT1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.003G091300.1	497.1440858	0.55838389	0.04320727	12.91342	3.88E-38	1.73E-37	cpm	-0.705426849	1.85E-25	GO:0005515	ATG03530.1	ERG28	homolog of yeast ergosterol28
Sapur.018G257000.1	105.393951	1.05058497	0.08147268	12.90696	4.11E-38	1.81E-37	cpm	-0.693284653	8.14E-24		ATSG27610.2		hypothetical protein
Sapur.016G077400.1	35.95566836	1.34527271	0.10423193	12.90659	4.13E-38	1.84E-37	cpm	-0.602379312	6.

Sapur.005G027400.1	4.319368861	2.351355174	0.25807426	12.59853	2.15E-36	9.25E-36	cpm	0.617666154	6.90E-18	GO:0016757			ATCG00890.1	PGSIP5	plant glycogenin-like starch initiation protein 5
Sapur.007G096000.1	264.6241918	0.738345609	0.058610355	-12.5975	2.18E-36	9.37E-36	cpm	-0.734214326	7.41E-28	GO:0006412;GO:0005840;GO:0005622;GO:0003735			ATCG00770.1		Ribosomal protein L17 family protein
Sapur.005G123800.1	41.23475627	0.970675158	0.077129115	-12.5873	2.42E-36	1.04E-35	cpm	-0.680848888	6.15E-18	GO:0005622			ATCG00410.1		Protein kinase superfamily protein
Sapur.005G169200.1	24.45559662	1.332832314	0.105897172	12.58729	2.48E-36	1.07E-35	cpm	0.655843569	1.19E-20				ATCG03070.2		Bax inhibitor-1 family protein
Sapur.004G076600.1	75.61836201	0.763085173	0.060651169	12.58554	2.54E-36	1.09E-35	cpm	0.684849402	4.92E-23				ATCG01000.1		Ubiquitin-like superfamily protein
Sapur.010G141000.1	1349.149023	-0.67992358	0.054036889	-12.5826	2.63E-36	1.13E-35	cpm	-0.720093553	2.21E-26				ATCG36700.1	ATPGLP1,PGLP1	2-phosphoglycolate phosphatase 1
Sapur.008G169800.1	471.1242128	0.777009187	0.061808856	12.58087	2.63E-36	1.15E-35	cpm	0.687842599	2.70E-23				ATCG70780.1		senescence-associated protein, putative
Sapur.T080000.1	21.64090609	1.270569991	0.101014519	12.578	2.78E-36	1.20E-35	cpm	0.68973437	1.68E-23				ATCG61190.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.010G089900.1	2932.815255	0.517203389	0.041120057	12.57789	2.79E-36	1.20E-35	cpm	0.701022017	1.58E-24	GO:0006096;GO:0004332			ATCG01140.1		Aldolase superfamily protein
Sapur.U046G121000.1	5977.623847	0.341861156	0.052291629	12.5727	2.98E-36	1.28E-35	cpm	-0.700098412	1.44E-18	GO:0008355;GO:0005634;GO:0003677;GO:0009725			ATCG00620.1	ARF1-BP,ARF2,HSLOR014	auxin response factor, putative
Sapur.003G028800.1	159.3067309	-0.425766334	0.033866161	-12.57	3.01E-36	1.29E-35	cpm	-0.697890063	2.06E-24				ATCG12320.2		
Sapur.010G139500.1	15.96715567	2.336154124	0.185680099	12.5679	3.17E-36	1.36E-35	cpm	-0.734384764	7.10E-28				ATXRCC1,XRCC3	ATXRCC1,XRCC3	homolog of X-ray repair cross complementing 3 (XRCC3)
Sapur.010G227900.1	23.17090077	-1.257539886	0.100061017	-12.5677	3.18E-36	1.36E-35	cpm	-0.680321937	1.15E-22				ATCG45300.1		Protein of unknown function, DUF538
Sapur.005G179900.1	228.3872094	-0.238202189	0.046735719	-12.5649	3.29E-36	1.38E-35	cpm	-0.676208184	2.46E-22				ATCG58100.1		TCP transcription factor
Sapur.003G165400.1	157.9915551	0.612588666	0.048758623	12.5637	3.34E-36	1.40E-35	cpm	0.685210862	1.15E-22				ATCG51280.1		Lipase/lipooxygenase, PLAT/LH2 family protein
Sapur.008G050000.1	271.8518812	0.652235853	0.052367649	12.5537	3.61E-36	1.46E-35	cpm	0.714014016	8.97E-26				ATCG11580.1		Regulator of chromosome condensation (RCC1) family protein
Sapur.018G041200.1	411.8077229	0.369474072	0.029412428	12.56183	3.42E-36	1.47E-35	cpm	0.710747345	1.87E-25	GO:0070552;GO:0070531;GO:0045739			ATCG29681.1		hypothetical protein
Sapur.010G193500.1	2.466509019	-7.710531774	0.615818376	-12.5597	3.52E-36	1.51E-35	cpm	-0.729691604	2.06E-26	GO:0055085;GO:0016020;GO:0015297;GO:0015238;GO:0006855			ATCG56402.2	ATDTX35,DTX35,FFT	detoxifying efflux carrier 35
Sapur.009G201400.1	27.50210586	-0.528465723	0.045217045	-12.5592	3.54E-36	1.52E-35	cpm	-0.723501993	9.94E-27	GO:0016021			ATCG29061.1	TETN	tetraspanin protein
Sapur.012G045500.1	394.6429993	0.430546029	0.034291191	12.55554	3.71E-36	1.59E-35	cpm	0.667684236	1.29E-21	GO:0008270;GO:0005515			ATCG08139.1		RING/U-box superfamily protein
Sapur.005G088600.1	3.69101696	2.108611506	0.184617721	12.5268	4.46E-36	1.92E-35	cpm	0.623147441	1.68E-19	GO:0008270;GO:0005515			ATCG59530.1		zinc finger (C3HC4-type RING finger) family protein
Sapur.009G069900.1	2244.08875	0.278505161	0.022195754	12.54768	4.09E-36	1.75E-35	cpm	0.719720009	2.41E-26				ATCG49970.1	CLPR1,NCLPP5,SVR2	ATP-dependent Clp protease proteolytic subunit
Sapur.U046G121000.1	275.6302003	-0.567593305	0.049767683	-12.546	4.18E-36	1.79E-35	cpm	-0.72338131	1.66E-26				ATCG51580.1	OSH1	gamma interferon responsive lysosomal thiol (GILT) reductase family protein
Sapur.008G031200.1	1570.088663	0.873651323	0.069647368	12.54398	4.29E-36	1.83E-35	cpm	0.659729388	2.82E-20	GO:0016021;GO:0006952			ATCG61560.1	ATMLO6,MLO6	Seven-transmembrane MLO family protein
Sapur.010G064700.1	537.3444117	0.238202187	0.046735719	-12.5409	4.56E-36	1.94E-35	cpm	-0.694294296	2.04E-24	GO:0005085;GO:0016020;GO:0015297;GO:0015238;GO:0006855			ATCG63580.1		MATE efflux family protein
Sapur.005G159500.1	35.01448113	-0.709461776	0.056605828	-12.533	4.93E-36	2.10E-35	cpm	-0.713054956	1.40E-25				ATCG42920.1		Pentatricopeptide repeat (PPR-like) superfamily protein
Sapur.010G196700.1	225.4631598	0.59282289	0.047288514	12.53207	4.98E-36	2.13E-35	cpm	0.659442559	5.96E-21	GO:0016747			ATCG03940.1		HXXXD-type acyl-transferase family protein
Sapur.005G145500.1	14.19872121	-0.924789404	0.081786363	-12.5307	5.07E-36	2.16E-35	cpm	-0.68620471	1.49E-23				ATCG49600.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.003G031300.2	4.452524674	-1.85351491	0.147898181	-12.529	5.18E-36	2.21E-35	cpm	-0.696349886	2.80E-24				ATCG14746.1		hypothetical protein
Sapur.019G011200.1	1061.903238	0.527278512	0.043772204	12.51846	5.21E-36	2.26E-35	cpm	0.707427487	1.92E-25	GO:0008270;GO:0006508;GO:0004177			ATCG60160.1		2n-dependent exopeptidases superfamily protein
Sapur.014G104300.1	13.52556971	-1.397391244	0.11153891	-12.5282	5.23E-36	2.28E-35	cpm	-0.685286511	4.20E-23				ATCG02870.1		ribosome biogenesis protein Nop16
Sapur.003G193300.1	62.11010374	-0.324151177	0.1057012	-12.5262	5.28E-36	2.29E-35	cpm	-0.73850917	4.21E-28	GO:0005789			ATCG49160.1		Pap2-like superfamily protein
Sapur.003G154600.2	8.54487108	2.361939545	0.185955573	12.52483	5.46E-36	2.33E-35	cpm	0.649971164	3.25E-20	GO:0005544;GO:0005509			ATCG12380.1	ANNAT8	annexin 8
Sapur.008G000300.1	111.6642207	0.463249468	0.0337742	-12.5193	5.85E-36	2.50E-35	cpm	-0.710578057	2.26E-26	GO:0005681			ATCG68800.1		
Sapur.T157800.1	16.78916705	1.552157615	0.124008877	12.5165	6.06E-36	2.58E-35	cpm	0.620783627	4.23E-18						transcriptional regulator of RNA polII, SAGA, subunit
Sapur.016G141000.1	555.8008136	0.585225147	0.047000727	12.51609	6.13E-36	2.60E-35	cpm	0.677692769	4.95E-22				ATCG07230.1		Arabidopsis thaliana protein of unknown function (DUF621)
Sapur.009G057700.1	684.1255625	1.580641275	0.126337018	12.51131	6.47E-36	2.76E-35	cpm	0.606614448	3.76E-17	GO:0008270;GO:0005515			ATCG35330.1		RING/U-box superfamily protein
Sapur.T141100.1	3.867006174	1.962269913	0.156844972	12.51076	6.52E-36	2.78E-35	cpm	0.77249693	2.29E-32						
Sapur.013G048200.1	13.69412471	1.627356122	0.114911258	12.50886	6.84E-36	2.91E-35	cpm	0.655019704	1.06E-20						NA
Sapur.017G087000.1	3786.439459	-0.402172233	0.032198881	12.50664	6.87E-36	2.92E-35	cpm	0.691948701	2.07E-23	GO:0055114;GO:0004616;GO:0050661;GO:0006098			ATCG49870.1		6-phosphogluconate dehydrogenase family protein
Sapur.021G018800.1	440.6632041	-0.455422332	0.0354627	12.5066	6.87E-36	2.92E-35	cpm	-0.707394184	3.95E-25	GO:0005622			ATCG13120.1		Leucine rich repeat protein, putative
Sapur.001G183400.1	103.9809218	-0.76719992	0.061419634	-12.4911	8.35E-36	3.55E-35	cpm	-0.7075608	4.16E-25	GO:0006310			ATCG12246.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Sapur.014G039200.1	22.13817513	0.948267409	0.08124253	-12.4712	9.07E-36	3.86E-35	cpm	0.668376116	2.79E-24				ATCG03110.1		Mitochondrial substrate carrier family protein
Sapur.017G091200.1	1.38439405	3.947902161	0.336087081	12.48992	9.47E-36	3.60E-35	cpm	0.62375965	3.62E-18						
Sapur.016G122300.1	765.6554858	0.361329184	0.077134725	12.48892	9.68E-36	3.44E-35	cpm	0.620513845	3.98E-17				ATCG44500.1		O-fucosyltransferase family protein
Sapur.010G156700.1	4.015667033	2.248025521	0.180012739	-12.4881	8.66E-36	3.68E-35	cpm	-0.673472007	5.21E-22				ATCG37740.1	ATZIP10,ZIP10	zinc-finger protein 10
Sapur.010G047700.1	380.3951732	0.529802293	0.042432514	-12.4843	9.10E-36	3.86E-35	cpm	-0.753052651	9.70E-30	GO:0045941;GO:0005742			ATCG27980.1	TONSD-2	translocase outer membrane 20-2
Sapur.010G235200.1	54.03997839	-0.575318898	0.046332992	-12.4821	9.35E-36	3.97E-35	cpm	-0.736321204	4.35E-28	GO:0005524			ATCG37120.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.005G095400.1	486.6602348	-0.279388934	0.02238387	-12.4817	9.39E-36	3.99E-35	cpm	-0.72145923	1.27E-25				ATCG75430.1		UDP-Glycosyltransferase superfamily protein
Sapur.008G135000.1	22.29668509	0.7	0.056112294	12.4769	9.71E-36	4.12E-35	cpm	-0.644204306	2.38E-20				ATPPCK1,PPCK1	ATPPCK1,PPCK1	phosphoenolpyruvate carboxylase kinase
Sapur.T097600.1	6.246540791	1.510222707	0.121031729	12.47791	9.85E-36	4.18E-35	cpm	0.742434566	8.92E-32				ATFIM1,FIM1	ATFIM1,FIM1	fimbrin 1
Sapur.T104800.1	171.5140209	0.7	0.058652823	12.4726	1.02E-35	4.32E-35	cpm	0.667866154	2.04E-23						nucleic acid binding;ATP-dependent helicase;ATP-binding;helicase;ATP-dependent helicases
Sapur.006G029100.1	20.4937341	0.962611752	0.079172459	12.47431	1.03E-35	4.37E-35	cpm	0.712645892	1.28E-25	GO:0009052;GO:0004751			ATCG04790.1		Ribose 5-phosphate isomerase, type A protein
Sapur.017G089300.1	31.73625542	0.612629999	0.081216253	-12.4712	1.07E-35	4.56E-35	cpm	-0.727813939	3.56E-27						
Sapur.003G142500.1	176.9418912	-0.98451646	0.07897829	-12.4667	1.11E-35	4.87E-35	cpm	-0.679145707	4.12E-22				ATMYB5,MYB5	ATMYB5,MYB5	myb domain protein 5
Sapur.016G141000.1	13.31216646	0.829013584	0.06069505	12.4654	1.15E-35	5.05E-35	cpm	-0.674145215	4.46E-25				ATCG10960.2		Heavy metal transport/detoxification superfamily protein
Sapur.014G055800.1	25.48554031	1.144139116	0.09178642	12.46523	1.16E-35	4.89E-35	cpm	0.662103056	3.66E-21				ATCG45480.1	ATSAP18,SAP18	SIN3 associated polypeptide P18
Sapur.010G199500.1	39.06441775	-1.951363929	0.157134489	-12.4623	1.20E-35	5.07E-35	cpm	-0.70890766	1.62E-24	GO:0005515;GO:0006468;GO:0005524;GO:0004672			ATCG25681.1	NK2	NSP-interacting kinase 2
Sapur.010G199900.1	6.731659997	-0.567192756	0.123717303	-12.4622	1.20E-35	5.08E-35	cpm	-0.72052602	2.00E-26	GO:0006260;GO:0005634			ATCG12530.1	PSF2	DNA replication complex GINS protein psf2
Sapur.003G140500.1	292.0529003	0.557780295	0.0447198	12.4616	1.21E-35	5.12E-35	cpm	0.673437858	5.26E-22				ATCG24100.1		hypothetical protein
Sapur.020G151500.1	420.4247078	0.625862216	0.053638168	-12.458	1.26E-35	5.28E-35	cpm	-0.712364525	1.35E-25	GO:0016810;GO:0006807			ATNLP1,CFA,NLP1	ATNLP1,CFA,NLP1	nitrilase-like protein 1
Sapur.004G166000.1	30.58262621	-0.387482631	0.111436119	-12.4509	1.38E-35	5.84E-35	cpm	-0.698451893	2.74E-24				ATCG01750.2		Protein of unknown function (DUF567)
Sapur.012G208700.1	521.8816643	0.564887117	0.051888181	12.44952	1.41E-35	5.95E-35	cpm	-0.690442441	1.47E-23	GO:0016020			ATCG51570.1		SPIN/Band 7/Mec2 family protein membrane-associated protein family
Sapur.013G013200.1	6.28807362	2.141755852	0.172046859	-12.4487	1.42E-35	6.01E-35	cpm	-0.678937074	1.66E-22	GO:0016020;GO:0006810;GO:0005215			ATCG25540.1		Major facilitator superfamily protein
Sapur.008G127800.1	138.3625777	0.533261104	0.120906896	12.44591	1.47E-35	6.22E-35	cpm	0.645894636	3.60E-20						
Sapur.006G127800.1	202.8413635	0.605631265	0.032615342	12.44587	1.47E-35	6.22E-35	cpm	0.684511224	4.90E-23				ATCG21200.1		sequence-specific DNA binding transcription factors
Sapur.006G020400.1	418.5387732	-0.687774246	0.055261806	-12.4457	1.48E-35	6.26E-35	cpm	-0.753885579	3.12E-28				ATCG01255.1		
Sapur.T034800.1	9.325568994	1.66080823	0.133448009	12.44536	1.48E-35	6.26E-35	cpm	0.6869498	3.00E-23						hypothetical protein
Sapur.017G085100.1	7.980881212	1.773804555	0.142666235	12.43324	1.73E-35	7.28E-35	cpm	0.688287745	5.13E-23	GO:0007165;GO:0005515;GO:0043531			ATCG37680.1		disease resistance protein (TIR-NBS-LRR class), putative
Sapur.010G206700.1	2076.733862	0.619366615	0.049822666	12.43142	1.76E-35	7.45E-35	cpm	0.664293797	2.44E-21				ATCG33600.1		hypothetical protein
Sapur.010G107300.1	14.895708	1.585349495	0.127579285	-12.4312	1.77E-35	7.47E-35	cpm	-0.658947081	2.76E-20				ATCG75691.1		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.011G044000.1	179.8895747	0.973222327	0.078152713	-12.457	1.80E-35	7.58E-35	cpm	-0.669714094	2.24E-22	GO:0016788			ATCG45020.1		SGNH hydrolase-type esterase superfamily protein
Sapur.004G170500.1	25.81916194	0.758389488	0.061018864	-12.4288	1.82E-35	7.66E-35	cpm	-0.704327084	7.74E-25				ATCG26681.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.T037700.1	37.13777904	1.149897286	0.092546371	12.4262	1.88E-35	7.91E-35	cpm	0.674252424	3.70E-22						hypothetical protein
Sapur.007G018500.1	1391.611399	0.070037391	0.16679564	12.41225	2.24E-35	9.44E-35	cpm	0.584988461	8.62E-16	GO:0008168			ATCG11480.1	ATBSMT1,BSMT1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.005G047600.1	55.11906988	1.822207806	0.146887019	12.40968	2.43E-35	1.02E-34	cpm	0.594132628	2.31E-16	GO:0016747;GO:0008610;GO:0016020;GO:0006633			ATCG46640.1	KCS10	3-ketoacyl-CoA synthase 10
Sapur.T134700.1	6.280606021	1.927819714	0.155465159	12.40033	2.60E-35	1.09E-34	cpm	0.604739314	4.94E-17				ATCG10820.2		Transcription elongation factor (TFIIS) family protein
Sapur.017G128200.1	364.0515645	-0.45364134	0.036020492	-12.3941	2.81E-35	1.18E-34	cpm	-0.739151442	2.16E-28	GO:0016592;GO:0006357;GO:0001104			ATCG21910.1	MED6	RNA polymerase transcriptional regulation mediator-related
Sapur.013G020200.1	86.85315645	-0.956560222	0.08009272	-12.3939	2.82E-35	1.18E-34	cpm	-0.691911846	1.30E-23				ATCG12700.1		ATP binding;nucleic acid binding;helicases
Sapur.010G124300.1	1920.816799	-0.307097976	0.07420517	-12.3904	2.95E-35	1.24E-34	cpm	-0.672488893	1.22E-26				ATCG04480.1	ATNRP1,NRP1	nodulin-related protein 1
Sapur.008G208700.1	281.3612245	0.740793297	0.05981267	-12.3851	3.15E-35	1.32E-34	cpm	-0.70780035	3.61E-25				ATCG12451.1		PEBP-type phosphatidyl-cis-trans isomerase, putative
Sapur.006G077000.1	168.6548017	0.998667942	0.08062973	-12.3834	3.22E-35	1.35E-34	cpm	-0.720711992	1.92E-26	GO:0006468;GO:0006672			ATCG54530.1		Protein kinase protein with tetratricopeptide repeat domain
Sapur.005G190400.1	5.715455843	1.888846419	0.153577969	12.3795	3.37E-35	1.42E-34	cpm	-0.652384188	1.32E-20				ATCG59502.2	ATOST1,OST1,P44,SNR62-6	Ribophorin I family protein
Sapur.013G121800.1	31.56227737	-0.89419887	0.072248861	-12.3773	3.47E-35	1.45E-34	cpm	-0.714828291	8.16E-26				ATCG62730.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.016G134400.1	839.3398212	0.772279122	0.062402076	12.37586	3.53E-35	1.48E-34	cpm	0.668381076	2.66E-21				ATCG44360.1		hypothetical protein
Sapur.002G007200.1	276.6100299	-0.763217332	0.061678229	-12.3742	3.61E-35	1.51E-34	cpm	-0.681111175	9.67E-23				ATCG42310.1		Pentatricopeptide repeat (PPR-like) superfamily protein
Sapur.010G051200.1	19.79073573	1.039971862	0.087202794	-12.3732	3.63E-35	1.52E-34	cpm	-0.695236689	5.38E-24				ATCG05260.1		
Sapur.019G071000.1	27.87554676	0.974164516	0.07851859	-12.372	3.70E-35	1.55E-34	cpm	0.665413982	1.98E-21	GO:0006468;GO:0005524;GO:0004672			ATCG75130.1		hypothetical protein
Sapur.009G284800.1	36.57336351	1.622092805	0.13113137	-12.37	3.80E-35	1.59E-34	cpm	-0.679291883	7.91E-22						Protein kinase family protein
Sapur.T151700.1	2.16605943	3.220871357	0.260439389	12.36753	3.93E-35	1.64E-34	cpm	0.674497906	2.26E-22	GO:0005681;GO:0000398;GO:0000387			ATCG54385.1		transmembrane protein, putative
Sapur.003G154800.1	136.6478339	-1.189387228	0.096208042	-12.3626	4.17E-35	1.74E-34	cpm	-0.625388592	2.03E-18	GO:0005515			ATCG02930.1	ATGGT3,GST16,GGT3	ARM repeat superfamily protein
Sapur.008G120500.1	181.6512384	-0.703487929	0.056909454	-12.3605	4.17E-35	1.74E-34	cpm	-0.723363125	1.21E-26	GO:0005622;GO:0005524			ATCG03670.1	CDC48B	glutathione S-transferase F3
Sapur.010G051000.1	90.49663556	-0.671337263	0.054232732	-12.3567	4.48E-35	1.87E-34	cpm	-0.718601518	1.13E-26	GO:0006468;GO:0005524;GO:0004672			ATCG10080.1		cell division cycle 48
Sapur.004G271100.1	10.28421839	-0.804074219	0.061887568	-12.3103	4.67E-35	1.95E-34	cpm	-0.691938224	1.88E-22	GO:0003729;GO:0032147;GO:0005819			ATCG15110.1		AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein
Sapur.019G051000.1	248.0912393	0.372658109	0.030170464	12.35291	4.70E-35	1.96E-34	cpm	0.699888313	2.02E-24	GO:0005515			ATCG03260.1		TPX2 (targeting protein for Xklp2) family protein
Sapur.015G000300.1	438.0418261	-0.60547348	0.049016818	-12.3524	4.73E-35	1.98E-34	cpm	-0.737908242	2.87E-28	GO:0015126;GO:0009451;GO:0008324;GO:0051536			ATCG01300.1		Transducin/WD40 repeat-like superfamily protein
Sapur.012G029900.1	50.86675179	0.864576614	0.069995623	-12.3519	4.76E-35	1.99E-34	cpm	-0.698327653	3.76E-24	GO:0016758;GO:0008152			ATCG36730.1		Methyltransferase family protein
Sapur.012G061600.1	27.40718202	0.719461931	0.05827147	12.34673	5.07E-35	2.12E-34	cpm	0.687388789	1.44E-24				ATCG42670.1		UDP-Glycosyltransferase superfamily protein
Sapur.013G160000.2	418.4961137	0.878424118	0.071163487	12.34375	5.26E-35	2.20E-34	cpm	0.640247218	6.45E-20				ATCG04020.1		DC1 domain-containing protein
Sapur.001G071900.1	45.64318995	1.634806204	0.132539905	12.32882	6.34E-35	2.64E-34	cpm	0.703752436	8.77E-25	GO:0005515			ATCG24020.1	NLP7	NLN-like protein 7
Sapur.005G168200.1	156.6948261	-0.751252833	0.060936953	-12.3284	6.37E-35	2.66E-34	cpm	-0.742641125	2.78E-29				ATCG22481.1		DNAse I-like superfamily protein
Sapur.T086900.1	19.15802242	1.521849887	0.123462538	12.32516	6.63E-35	2.76E-34	cpm	0.679278924	1.26E-22				ATCG19820.1	emb3734	ARM repeat superfamily protein
Sapur.002G073000.1	540.5663938	1.023517882	0.083074861	12.32043	7.03E-35	2.93E-34	cpm	0.643470515	1.50E-19	GO:0043565;GO:0006355;GO:0003700;GO:0006351			ATCG79520.1		bZIP transcription factor family protein
Sapur.005G078800.1	4.219881662	-2.427707794	0.197076116	12.31884	7.16E-35	2.98E-34	cpm	0.612258835	1.60E-17	GO:0005085;GO:0016021			ATCG17500.2		Auxin efflux carrier family protein
Sapur.016G042600.1	249.7521526	-0.38860419	0.031586622	12.31869	7.16E-35	2.98E-34	cpm	0.724499107	7.84E-27				ATCG60050.1	RIP1	FRIGIDA-interacting protein 1
Sapur.008G079500.1	2645.647759	0.354297802	0.028744323	12.31736	7.30E-35	3.04E-34	cpm	0.679387388	7.27E-22	GO:0005660;GO:0008033;GO:0015134;GO:0016491;GO:0045454			ATCG48030.1	mtLPD1	mitochondrial lipoamide dehydrogenase 1
Sapur.005G054500.1	68.57354435	1.442547523	0.117121187	12.3047	7.36E-35	3.07E-34	cpm	0.555560021	1.08E-14				ATCG05810.1		hypothetical protein
Sapur.004G114500.1	1.4362665	1.896387724	0.31615916	12.31566	7.46E-35	3.10E-34	cpm	0.589917674	4.31E-16				ATCG49330.1		hydroxyproline-rich glycoprotein family protein
Sapur.010G030400.1	148.1453222	0.896936576	0.068187873	12.31358	7.68E-35	3.19E-34	cpm	0.524805519	1.70E-12	GO:0009982			ATCG55420.1	ACBP4	acyl-CoA binding protein 4
Sapur.008G179500.1	292.9805240	0.610516235	0.05261839	12.31251	7.70E-35	3.20E-34	cpm	-0.7615895	1.51E-31	GO:0008173;GO:0006396;GO:0003723			ATCG15120.1		tRNA/rRNA methyltransferase (Spo11 family) protein
Sapur.002G161300.1	704.6924882	0.90068299	0.073881441	12.31274	7.74E-35	3.22E-34	cpm	0.649520282	3.52E-20				ATCG47481.1		hypothetical protein
Sapur.006G288500.4	24.10666425	0.525466407	0.0384631	-12.3122	7.78E-35	3.24E-34	cpm	-0.711122199	1.72E-25				ATCG42410.1	AtCESA1,CESA1,RSW1	cellulose synthase 1
Sapur.008G073900.1	11.15166107	2.950960217	0.183619861	12.30821	8.18E-35	3.40E-34	cpm	0.674660312	4.10E-22				ATCG26600.1	CLE9	CLAVATA3/ESR-RELATED 9
Sapur.006G142400.1	2.831842836	3.708427422	0.301307923	12.3078	8.22E-35	3.42E-34	cpm	-0.7615895	1.51E-31	GO:0055114;GO:0016491			ATCG28220.1		2-oxoglutarate (FeII)-dependent oxygenase superfamily protein
Sapur.T028100.1	15.71953468	1.568704026	0.127471298	12.30633	8.37E-35	3.48E-34	cpm	0.689202582	3.52E-20				ATCG48180.1	emb3734	ARM repeat superfamily protein
Sapur.002G042200.1	6163.146993	0.518147224	0.042144708	12.3056	8.45E-35	3.51E-34	cpm	0.668865653	1.20E-21	GO:0019888;GO:0015079;GO:0009654;GO:0009653;GO:0005509			ATCG26140.1	OE23L,OE23L2,PSBP-1,PSB-P	oxygen-evolving enhancer protein
Sapur.007G116000.1	148.4364946	0.567210548	0.046095946	12.305	8.51E-35	3.54E-34	cpm	0.680501562	1.08E-22	GO:0006810;GO:0005215			ATCG00130.1	ATRBL13,RBL13	rhomboid family protein 13
Sapur.004G188000.1	11.15665004	1.622487146	0.135178829	12.3024	8.80E-35	3.66E-34	cpm	-0.677553114	4.96E-22	GO:0055114;GO:0046983;GO:0016620;GO:0008653;GO:0005737;GO:0003942;GO:0051128			ATCG00340.1		oxidoreductase, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;copper ion binding
Sapur.003G109500.1	2592.72624	0.482799464	0.039258027	12.2978	9.31E-35	3.86E-34	cpm	0.674384728	3.75E-22	GO:0019236;GO:0007186;GO:0016021			ATCG42090.1		Lung seven transmembrane receptor family protein
Sapur.010G086200.1	68.55385624	-0.196823681	0.092456867	-12.2965	9.45E-35	3.92E-34	cpm	-0.704682005	7.62E-25				ATCG58100.1		TCP family transcription factor
Sapur.001G313000.1	422.6168894	0.579081981	0.047028118	-12.2927	9.92E-35	4.12E-34	cpm	-0.695734677	4.88E-24	GO:0055114;GO:0016491;GO:0008270			ATCG27401.1		Oxidoreductase, zinc-binding dehydrogenase family protein
Sapur.T096500.1	38.7695028	0.623731305	0.052743743	-12.2914	1.01E-34	4.18E-34	cpm	-0.69439415	6.46E-24				ATCG30700.1		NA
Sapur.004G160300.1	209.9488077	1.124169415	0.09173246	12.29179	1.02E-34	4.22E-34	cpm	0.514404546	5.56E-12	GO:0016757;GO:0047262			ATCG14540.1	GAUT14	galacturonosyltransferase 14
Sapur.003G117800.1	1164.120787	0.526481992	0.043844224	12.28828	1.05E-34	4.34E-34	cpm	0.668793933	2.05E-21	GO:0005737;GO:0000045			ATCG16520.1	ATG8F	Ubiquitin-like superfamily protein
Sapur.003G020600.1	49.2752261	-1.227826	0.099943737	-12.2866	1.06E-34	4.36E-34	cpm	-0.701181181	1.54E-26	GO:0016788;GO:0005777			ATCG01680.1		putative esterase/lipase/thioesterase family protein with C2H2-type zinc finger domain
Sapur.013G131100.1	606.9060247	0.569563232	0.046380152	-12.2803	1.16E-34	4.79E-34	cpm	-0.702492924	1.15E-24				ATCG28230.1	emb1923	embryo defective 1923
Sapur.018G000100.1	455.4661884	0.678618162	0.05240663	-12.2779	1.18E-34	4.87E-34	cpm	-0.715757122	2.08E-26	GO:0003674			ATCG

Sapur.010G062900.1	68.52249545	0.890576886	0.074298698	11.98644	4.19E-33	1.69E-32	cyan	0.652533853	2.07E-20	GO:0008080	AT3G22560.1		Acyl-CoA N-acyltransferases (NAT) superfamily protein	acetyltransferase (GNAT) domain protein
Sapur.019G082700.1	57.99547686	-0.780374857	0.065113609	-11.9848	4.27E-33	1.72E-32	cyan	-0.698887881	2.50E-24		AT1G34370.1	STOP1	C2H2 and C2HC zinc fingers superfamily protein	zinc finger, C2H2 type protein
Sapur.006G081300.1	4809.356152	-0.750560369	0.062635004	-11.9831	4.36E-33	1.75E-32	cyan	-0.689797088	1.68E-23	GO:0016020,GO:0009765	AT3G08940.2	LHCB4.2	light harvesting complex photosystem II	light-harvesting complex I chlorophyll A/B-binding protein
Sapur.003G056600.2	4.837833003	2.121978265	0.177095808	11.98209	4.41E-33	1.78E-32	cyan	0.666692248	1.56E-21	GO:0030955,GO:0006096,GO:0004743,GO:0000287	AT1G32440.1	PKp3	plastidial pyruvate kinase 3	pyruvate kinase
Sapur.006G229300.1	24.57901821	-0.940894223	0.07853713	-11.9802	4.51E-33	1.82E-32	cyan	-0.675462483	2.93E-22		AT2G24395.1		chaperone protein dnaJ-related	NA
Sapur.15WG083400.1	41.24898623	0.545601649	0.045544386	11.97956	4.55E-33	1.83E-32	cyan	0.724222477	8.38E-27	GO:0005515	AT5G38390.1		F-box/RNI-like superfamily protein	NA
Sapur.016G226200.1	7.769009419	-1.514714796	0.12650814	-11.9733	4.91E-33	1.97E-32	cyan	-0.676600875	2.35E-22		AT5G46460.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.013G006400.1	23.90991115	-1.410955705	0.117888798	-11.9685	5.19E-33	2.09E-32	cyan	-0.694952573	5.75E-24					NA
Sapur.005G207800.1	53.209665	1.170012711	0.097764543	11.96766	5.25E-33	2.11E-32	cyan	0.656165709	1.08E-20		AT1G21010.1			mRNA, 952 bp sequence protein, putative
Sapur.005G156200.1	650.7516397	0.41441667	0.034655877	11.95805	5.89E-33	2.37E-32	cyan	0.686813349	3.08E-23	GO:0005525	AT4G09720.1	ATRABG3A,RABG3A	RAB GTPase homolog G3A	Rab-related GTPase family protein
Sapur.004G007400.1	600.382274	-0.792332499	0.066262411	-11.9575	5.93E-33	2.38E-32	cyan	-0.670937725	6.99E-22		AT1G11840.6	ATGLX1,GLX1	glyoxalase I homolog	lactoylglutathione lyase
Sapur.010G196400.1	29.3195425	-0.937580159	0.078444161	-11.9522	6.32E-33	2.54E-32	cyan	-0.698741673	2.58E-24		AT5G04840.1		bZIP protein	BZIP protein
Sapur.018G057400.1	6.932829887	-1.596501382	0.133625441	-11.9476	6.68E-33	2.68E-32	cyan	-0.670497702	7.60E-22	GO:0005515	AT1G60770.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.004G083100.1	6845.773659	0.336482897	0.028164571	11.94703	6.73E-33	2.70E-32	cyan	0.675046749	3.17E-22	GO:0019904	AT3G02520.1	GF14 NU,GRF7	general regulatory factor 7	14-3-like protein GF14 protein
Sapur.007G027600.1	914.1881341	-0.470957831	0.039426712	-11.9451	6.88E-33	2.76E-32	cyan	-0.705227447	6.36E-25		AT1G75080.1	BZR1	Brassinosteroid signalling positive regulator (BZR1) family protein	brassinazole-resistant 1 protein, putative
Sapur.010G149400.1	302.2015579	-0.739527928	0.061934904	-11.9404	7.29E-33	2.92E-32	cyan	-0.726981643	4.33E-27		AT2G40070.1			proteophosphoglycan protein, putative
Sapur.010G146100.1	1.555028808	3.902112254	0.32708694	11.92989	8.27E-33	3.31E-32	cyan	0.571278332	5.58E-15	GO:0006355,GO:0003700	AT2G40220.1	ABI4.ATABI4.GIN6.ISI3.SAN	Integrase-type DNA-binding superfamily protein	NA
Sapur.013G122700.1	51.70186634	-1.336793999	0.112059699	-11.9293	8.33E-33	3.34E-32	cyan	-0.663423752	2.87E-21	GO:0005515	AT2G20710.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.15WG043700.1	1.908740154	3.313455281	0.27780257	11.92737	8.52E-33	3.41E-32	cyan	0.656029031	1.11E-20	GO:0008270,GO:0005515	AT1G73760.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein, putative
Sapur.014G128800.1	157.3062761	-0.547804642	0.045935726	-11.9255	8.72E-33	3.49E-32	cyan	-0.722463876	1.27E-26	GO:0055085,GO:0016020,GO:0006810,GO:0005215	AT2G05760.1		Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.004G152400.1	13.02382352	-1.30946939	0.109862611	-11.9192	9.41E-33	3.77E-32	cyan	-0.687266123	2.81E-23		AT1G08360.1		Ribosomal protein L1p/L10e family	60S ribosomal protein L10a-1
Sapur.008G104200.2	33.89907693	-0.956514865	0.080271098	-11.9161	9.76E-33	3.91E-32	cyan	-0.680222332	1.15E-22	GO:0055085,GO:0016021	AT1G70940.1	ATPIN3,PIN3	Auxin efflux carrier family protein	auxin efflux carrier protein
Sapur.005G096000.1	9.571332997	1.692673984	0.14205294	11.9158	9.79E-33	3.92E-32	cyan	0.6621987	3.60E-21	GO:0006468,GO:0005524,GO:0004672	AT2G18170.1	ATMPK7,MPK7	MAP kinase 7	MAP kinase
Sapur.004G092400.1	1.27417736	3.135252173	0.263133189	11.91508	9.88E-33	3.95E-32	cyan	0.713448248	1.02E-25	GO:0005681,GO:0000398,GO:0000387	AT1G54385.1		ARM repeat superfamily protein	NA
Sapur.009G112300.1	51.69136872	1.547336438	0.129882665	11.91334	1.01E-32	4.03E-32	cyan	0.653530048	1.73E-20	GO:0009733	AT1G29450.1		SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.014G005800.1	208.4926294	-0.881971984	0.074042431	-11.9117	1.03E-32	4.11E-32	cyan	-0.694014487	6.99E-24	GO:0016567,GO:0004842	AT5G65920.1		ARM repeat superfamily protein	E3 ubiquitin ligase PUB14, putative
Sapur.008G108000.1	21.59269834	-1.2927056	0.108531474	-11.9109	1.04E-32	4.15E-32	cyan	-0.684183829	5.24E-23	GO:0007017,GO:0005875	AT1G23220.1		Dynein light chain type 1 family protein	dynein light chain type 1 family protein
Sapur.013G006800.1	127.0494166	-0.738418633	0.061997539	-11.9105	1.04E-32	4.17E-32	cyan	-0.730134339	2.02E-27	GO:0030145,GO:0004177	AT1G09300.1		Metallopeptidase M24 family protein	metallopeptidase family M24 containing protein
Sapur.009G076800.1	161.8485585	1.442224455	0.121107258	11.90865	1.07E-32	4.26E-32	cyan	0.631173304	7.93E-19	GO:0016758,GO:0008152	AT2G15490.1	UGT73B4	UDP-glycosyltransferase 73B4	UDP-glucose:glucosyltransferase
Sapur.005G183000.1	757.9820518	0.564779285	0.047429093	11.90787	1.08E-32	4.30E-32	cyan	0.678929764	1.49E-22	GO:0016021	AT2G21600.1	ATRER1B,RER1B	endoplasmatic reticulum retrieval protein 1B	RER1A protein
Sapur.014G023100.1	184.7895785	-1.313594547	0.110337797	-11.9052	1.11E-32	4.44E-32	cyan	-0.635463566	3.90E-19		AT1G47480.1		alpha/beta-Hydrolases superfamily protein	gibberellin receptor GID1, putative
Sapur.006G149700.1	88.81438597	-0.721578242	0.060671301	-11.8932	1.28E-32	5.12E-32	cyan	-0.655871905	1.14E-20	GO:0016021	AT4G28088.1		Low temperature and salt responsive protein family	proteolipid membrane modulator, putative
Sapur.007G091400.1	211.3374224	0.558466438	0.046958496	11.89277	1.29E-32	5.15E-32	cyan	0.678408903	1.65E-22		AT2G31305.1	INH3	inhibitor-3	protein phosphatase inhibitor protein
Sapur.T040400.1	2.284127642	-2.208823903	0.185778233	-11.8896	1.34E-32	5.35E-32	cyan	-0.812296293	4.00E-38		AT3G28455.1	CLE25	CLAVATA3/ESR-RELATED 25	NA
Sapur.010G162200.1	1635.221435	0.443313915	0.037291115	11.88792	1.37E-32	5.46E-32	cyan	0.664044485	2.56E-21		AT3G12570.4	FYD	FYD	sodium- and lithium-tolerant protein
Sapur.002G057700.1	1.47008776	3.905237533	0.328584914	11.88502	1.42E-32	5.65E-32	cyan	0.581176994	1.46E-15		AT1G17950.1	ATMYB52,BW52,MYB52	myb domain protein 52	R2R3-MYB transcription factor, putative
Sapur.005G081400.1	147.0779422	-0.674299587	0.056737034	-11.8846	1.42E-32	5.67E-32	cyan	-0.722285404	1.32E-26	GO:0030983,GO:0006298,GO:0005524,GO:0032300,GO:0007131	AT4G35520.1	ATMLH3,MLH3	MUTL protein homolog 3	NA
Sapur.T181600.1	1.537783058	3.168392607	0.266611854	11.88391	1.43E-32	5.72E-32	cyan	0.656003859	1.11E-20	GO:0005681,GO:0000398,GO:0000387	AT1G54385.1		ARM repeat superfamily protein	NA
Sapur.002G141800.1	116.8565344	-1.032089823	0.086852122	-11.8833	1.45E-32	5.76E-32	cyan	-0.737382492	3.35E-28	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G46660.1	CYP78A6	cytochrome P450, family 78, subfamily A, polypeptide 6	cytochrome P450 family 78 protein
Sapur.15WG075400.1	11.12862264	-1.869003526	0.157294072	-11.8822	1.46E-32	5.83E-32	cyan	-0.679370264	1.36E-22	GO:0055114,GO:0016655	AT4G37925.1	NDH-M	subunit NDH-M of NAD(P)H:plastoquinone dehydrogenase complex	NA
Sapur.010G031200.1	456.959749	0.778185749	0.065492983	11.88197	1.47E-32	5.85E-32	cyan	0.670121984	8.17E-22	GO:0016757	AT1G70090.1	GATL9,LGT8	glucosyl transferase family 8	CAZy family GT8 glycosyltransferase
Sapur.006G001400.1	167.0429719	-0.574069272	0.048321244	-11.8803	1.50E-32	5.97E-32	cyan	-0.698950136	2.47E-24	GO:0005975,GO:0004553	AT4G17180.1		O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase
Sapur.T177400.1	3.090741405	2.519677177	0.212102134	11.87955	1.51E-32	6.02E-32	cyan	0.679395922	1.36E-22	GO:0005681,GO:0000398,GO:0000387	AT1G54385.1		ARM repeat superfamily protein	NA
Sapur.T024700.1	42.29554512	1.254104441	0.105626147	11.87305	1.63E-32	6.51E-32	cyan	0.60788984	3.10E-17		AT1G50140.2		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.005G203500.1	634.7203392	0.304786954	0.025674645	11.87113	1.67E-32	6.66E-32	cyan	0.716798941	4.74E-26	GO:0006468,GO:0004672,GO:0006397,GO:0004540	AT5G24360.1	ATIRE1-1,IRE1-1	inositol requiring 1-1	Serine/Threonine kinase/endoribonuclease Ire1, putative
Sapur.011G021000.1	17.93990803	2.314561916	0.19498171	11.87066	1.68E-32	6.69E-32	cyan	0.605135044	4.69E-17	GO:0048544,GO:0006468,GO:0004672	AT1G11340.1		S-locus lectin protein kinase family protein	Serine/Threonine-kinase
Sapur.T134100.1	1.566106534	3.602489307	0.303560584	11.86745	1.75E-32	6.95E-32	cyan	0.604331532	5.29E-17					NA
Sapur.010G148000.1	1390.673404	-0.601119889	0.050663498	-11.865	1.80E-32	7.16E-32	cyan	-0.683906936	5.54E-23	GO:0005515,GO:0035556,GO:0007165,GO:0006629,GO:0004435	AT3G08510.1	ATPLC2,PLC2	phospholipase C 2	NA
Sapur.002G181600.1	403.4223117	0.441323504	0.03720109	11.86319	1.84E-32	7.31E-32	cyan	0.695709283	4.90E-24		AT1G14780.1		MAC/Perforin domain-containing protein	MAC/perforin domain protein
Sapur.018G090900.1	11.38920199	2.296829021	0.193673018	11.85931	1.93E-32	7.66E-32	cyan	0.499319796	2.80E-11		AT2G12550.1		ubiquitin-associated (UBA)/TS-N domain-containing protein	NA
Sapur.018G009800.1	4735.252587	-0.410909378	0.034650521	-11.8587	1.94E-32	7.71E-32	cyan	-0.684141309	5.28E-23	GO:0008270,GO:0005622,GO:0005515	AT5G24930.1	ATCOL4,COL4	CONSTANS-like 4	constans-like zinc finger protein
Sapur.008G013500.1	3769.437068	0.556708331	0.046949647	11.85756	1.97E-32	7.81E-32	cyan	0.665282411	2.03E-21	GO:0051536,GO:0009055	AT2G27510.1	ATFD3,FD3	ferredoxin 3	ferredoxin-3 protein
Sapur.011G099200.2	155.3903389	1.267362786	0.106905567	11.85497	2.03E-32	8.06E-32	cyan	0.652499592	2.08E-20		AT4G05320.2	UBQ10	polyubiquitin 10	NA
Sapur.T151400.1	5.670665566	1.529621032	0.129059358	11.85207	2.10E-32	8.33E-32	cyan	0.694836802	5.89E-24		AT5G35700.1	FIM2	fimbrin-like protein 2	NA
Sapur.019G054400.1	93.68323366	-0.631610015	0.05330304	-11.8494	2.17E-32	8.60E-32	cyan	-0.662737301	3.26E-21		AT3G56250.1			hypothetical protein
Sapur.009G081100.1	238.8971918	0.422335136	0.03565185	11.84609	2.25E-32	8.94E-32	cyan	0.681137678	9.62E-23		AT2G15695.1		Protein of unknown function DUF829, transmembrane 53	DUF829 domain protein
Sapur.005G180900.1	814.0568847	1.132037711	0.095588593	11.84281	2.34E-32	9.30E-32	cyan	0.675337156	3.00E-22	GO:0016887,GO:0005524	AT1G03905.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	ABC transporter I family protein
Sapur.001G058600.1	4.870762806	2.269109312	0.19160348	11.84274	2.35E-32	9.31E-32	cyan	0.619874624	4.88E-18	GO:0051716,GO:0046658	AT4G20260.2	ATPCAP1,PCAP1	plasma-membrane associated cation-binding protein 1	DREPP plasma membrane protein
Sapur.001G080800.1	5683.265048	0.865209399	0.073062791	11.842	2.37E-32	9.39E-32	cyan	0.620929213	4.13E-18	GO:0005975,GO:0004553	AT4G23560.1	AtGH9B15,GH9B15	glycosyl hydrolase 9B15	endo-1%2C4-beta-glucanase
Sapur.002G127000.1	432.1071787	0.60869292	0.051406285	11.84083	2.40E-32	9.52E-32	cyan	0.660738656	4.70E-21		AT3G61200.1		Thioesterase superfamily protein	acyl-CoA thioesterase, putative
Sapur.012G079400.1	398.1167947	-0.486119122	0.041061042	-11.8389	2.46E-32	9.73E-32	cyan	-0.718972	2.87E-26	GO:0005515	AT5G50900.1		ARM repeat superfamily protein	armadillo protein
Sapur.002G172500.1	34.89955779	-1.146409821	0.096847009	-11.8373	2.50E-32	9.92E-32	cyan	-0.658659651	6.87E-21					NA
Sapur.009G105900.1	134.3008088	-1.351924555	0.114247057	-11.8333	2.62E-32	1.04E-31	cyan	-0.687101342	2.91E-23	GO:0005622,GO:0003779,GO:0030042,GO:0015629	AT2G16700.1	ADF5,ATADF5	actin depolymerizing factor 5	actin-depolymerizing factor 5
Sapur.010G073700.1	1303.395778	0.409846203	0.034638048	11.83225	2.66E-32	1.05E-31	cyan	0.658531023	7.03E-21	GO:0008137,GO:0005739,GO:0003954	AT2G02050.1		NADH-ubiquinone oxidoreductase B18 subunit, putative	NADH-ubiquinone oxidoreductase B18 subunit
Sapur.005G076200.1	15.78166164	-1.324835061	0.111995595	-11.8293	2.75E-32	1.09E-31	cyan	-0.719443841	2.57E-26	GO:0009733	AT3G12830.1		SAUR-like auxin-responsive protein family	auxin-responsive family protein
Sapur.011G107300.1	16.60183824	1.267386317	0.107173576	11.82555	2.88E-32	1.14E-31	cyan	0.647753017	4.79E-20					hypothetical protein
Sapur.010G189000.1	6.119562559	2.150604921	0.181882261	11.82416	2.93E-32	1.16E-31	cyan	0.585008223	8.60E-16	GO:0006468,GO:0004672,GO:0005524	AT3G44610.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.014G120500.1	426.8940827	0.558733075	0.047254931	11.8238	2.94E-32	1.16E-31	cyan	0.680875117	1.01E-22		AT3G25400.1			nucleoside triphosphate pyrophosphohydrolase
Sapur.002G192600.1	188.4732571	-0.425291354	0.035973082	-11.8225	2.99E-32	1.18E-31	cyan	-0.707650212	3.73E-25		AT3G25210.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.013G087000.1	4.600989037	2.422817354	0.204984789	11.8195	3.10E-32	1.22E-31	cyan	0.618024969	6.53E-18					NA
Sapur.001G041500.1	4459.416774	-1.260774871	0.106681749	-11.8181	3.15E-32	1.24E-31	cyan	-0.621545554	3.75E-18	GO:0016747,GO:0008610	AT5G13930.1	ATCHS,CHS,TT4	Chalcone and stilbene synthase family protein	chalcone synthase
Sapur.005G009300.1	11.20297786	1.776868887	0.150381803	11.81572	3.24E-32	1.28E-31	cyan	0.5691578	7.40E-15		AT1G18610.1		Galactose oxidase/kelch repeat superfamily protein	kelch motif protein
Sapur.001G093700.1	415.4374861	-0.671650902	0.056856017	-11.8132	3.34E-32	1.32E-31	cyan	-0.705814086	5.59E-25	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT1G12460.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.008G018400.1	1233.222863	0.543240041	0.045998403	11.80998	3.47E-32	1.37E-31	cyan	0.670108488	8.19E-22	GO:0030955,GO:0006096,GO:0004743,GO:0000287	AT3G52990.1		Pyruvate kinase family protein	pyruvate kinase
Sapur.004G010400.1	1516.418295	-0.39414529	0.03337844	-11.8084	3.53E-32	1.40E-31	cyan	-0.687491223	2.68E-23	GO:0003676	AT1G11650.2	ATRBP45B,RBP45B	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in RNA-binding protein 28 (RBM28)-like protein
Sapur.008G071800.2	24.65835952	-0.902732895	0.076451229	-11.808	3.55E-32	1.40E-31	cyan	-0.669018105	1.01E-21	GO:0016020	AT1G69450.1		Early-responsive to dehydration stress protein (ERD4)	early-responsive to dehydration stress protein (ERD4), putative
Sapur.011G060400.3	3.722207937	-2.090008737	0.177003922	-11.8077	3.56E-32	1.41E-31	cyan	-0.689284399	1.86E-23	GO:0006355,GO:0005739,GO:0003690	AT5G55580.1		Mitochondrial transcription termination factor family protein	transcription termination factor family protein
Sapur.004G138700.1	204.7626466	-0.515278113	0.043663231	-11.8012	3.85E-32	1.52E-31	cyan	-0.695737867	4.87E-24		AT2G27590.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	hypothetical protein
Sapur.007G129200.1	481.0787297	0.73258943	0.06208054	11.80063	3.87E-32	1.53E-31	cyan	0.656773304	9.67E-21		AT2G31820.1		Ankyrin repeat family protein	ankyrin-like protein
Sapur.002G059400.1	49.36714069	2.032913599	0.172280337	11.80003	3.90E-32	1.54E-31	cyan	0.583433141	1.07E-15	GO:0030247,GO:0006468,GO:0005524,GO:0004672	AT1G21270.1	WAK2	wall-associated kinase 2	tyrosine kinase domain protein
Sapur.014G131200.1	2299.085095	0.56113942	0.047557922	11.79907	3.95E-32	1.56E-31	cyan	0.653618125	1.70E-20	GO:0006413,GO:0003743,GO:0003723	AT2G04520.1		Nucleic acid-binding, OB-fold-like protein	eukaryotic translation initiation factor 1A
Sapur.012G100600.1	2140.871467	-0.609782406	0.051708259	-11.7927	4.25E-32	1.68E-31	cyan	-0.706009417	5.36E-25	GO:0005634,GO:0005524,GO:0004386,GO:0003723,GO:0003676	AT5G62190.1	PRH75	DEAD box RNA helicase (PRH75)	DEAD-box ATP-dependent RNA helicase
Sapur.010G103000.1	180.9188791	-0.537029286	0.045557328	-11.788	4.50E-32	1.77E-31	cyan	-0.703868801	8.55E-25	GO:0008270	AT1G68730.1		Zim17-type zinc finger protein	DNL zinc finger protein
Sapur.013G027900.1	600.493681	-0.398641384	0.03381884	-11.7876	4.52E-32	1.78E-31	cyan	-0.697153265	3.61E-24	GO:0055085,GO:0016021	AT1G54730.2		Major facilitator superfamily protein	sugar transporter ERD6-like protein
Sapur.001G190400.1	2.238456543	3.19540896	0.271095518	11.78702	4.55E-32	1.79E-31	cyan	0.655135262	1.30E-20	GO:0006468,GO:0004672	AT1G79620.1		Leucine-rich repeat protein kinase family protein	somatic embryogenesis receptor-like kinase
Sapur.006G149500.1	17.58849161	1.14985951	0.09757446	11.78443	4.70E-32	1.85E-31	cyan	0.610775855	2.00E-17		AT3G23580.1	RNR2,RNR2A	ribonucleotide reductase 2A	NA
Sapur.001G076800.1	253.0894319	-0.378862205	0.032151636	-11.7836	4.74E-32	1.87E-31	cyan	-0.72217375	1.36E-26		AT4G11090.1	TBL23	TRICHOME BIREFRINGENCE-LIKE 23	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.001G172400.1	1154.175619	-0.566403211	0.048067619	-11.7835	4.75E-32	1.87E-31	cyan	-0.676156687	2.56E-22		AT1G15200.1		protein-protein interaction regulator family protein	pinin/SDK/memA/motif protein
Sapur.014G028400.1	56.42666877	1.741128328	0.147767111	11.78292	4.78E-32	1.88E-31	cyan	0.538442389	3.51E-13	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G31940.1	CYP82C4	cytochrome P450, family 82, subfamily C, polypeptide 4	cytochrome P450 family protein
Sapur.003G121500.3	4.408931324	-1.572121486	0.133439077	-11.7816	4.86E-32	1.91E-31	cyan	-0.624664825	2.28E-18		AT5G13260.1			ripening-regulated protein
Sapur.013G094000.2	3.548361718	-2.076434897	0.176253045	-11.781	4.89E-32	1.93E-31	cyan	-0.662583104	3.35E-21	GO:0016597,GO:0008152,GO:0055114,GO:0006520,GO:0050661,GO:0016491	AT4G19710.2	AK-HSDH,AK-HSDH II	aspartate kinase-homoserine dehydrogenase ii	aspartokinase/homoserine dehydrogenase
Sapur.012G096600.1	843.5094391	1.140961715	0.096859194	11.77959	4.97E-32	1.96E-31	cyan	0.663046907	3.07E-21		AT3G12800.1	DECR,SDRB	short-chain dehydrogenase-reductase B	peroxisomal 2%2C4-dienoyl-CoA reductase
Sapur.002G128100.1	258.7176048	-0.705802144	0.059938074	-11.7755	5.22E-32	2.05E-31	cyan	-0.729620703	2.29E-27	GO:0055114,GO:0009396,GO:0004488,GO:0003824	AT4G00620.1		Amino acid dehydrogenase family protein	tetrahydrofolate dehydrogenase/cyclohydrolase, putative
Sapur.005G064000.1	107.2046167	-0.683297582	0.0580312	-11.7747	5.27E-32	2.07E-31	cyan	-0.675247099	3.05E-22					hypothetical protein
Sapur.001G145700.1	3.628904088	-1.852086782	0.157306952	-11.7737	5.33E-32	2.10E-31	cyan	-0.691243615	1.24E-23		AT3G49890.1			hypothetical protein
Sapur.010G147700.1	707.5276943	0.434243829	0.036884705	11.77301	5.38E-32	2.11E-31	cyan	0.643647612	9.76E-20		AT3G55960.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	NLI interacting factor-like phosphatase
Sapur.013G015400.1	61.26470406	-0.789033869	0.0670406	-11.7695	5.61E-32	2.20E-31	cyan	-0.693806199	7.30E-24	GO:0005515	AT4G26090.1	RPS2	NB-ARC domain-containing disease resistance protein	NA
Sapur.005G081300.1	258.8340856	-0.50564245	0.042999343	-11.7593	6.33E-32	2.48E-31	cyan	-0.705787896	5.62E-25	GO:0003677	AT4G35550.1	ATWOX13,HB-4,WOX13	WUSCHEL related homeobox 13	HB1 homeodomain protein
Sapur.010G056000.1	59.24918169	-0.504453268	0.042906789	-11.757	6.50E-32	2.55E-31	cyan	-0.693958688	7.08E-24		AT3G04130.1		Tetratricopeptide repeat (TPR)-like superfamily protein	pentatricopeptide (PPR) repeat protein, putative
Sapur.003G146200.1	243.9425596	0.711707776	0.060566319	11.75088	6.99E-32	2.74E-31	cyan	0.652302703	2.15E-20	GO:0015031,GO:0006464	AT3G12400.1	ATELC,ELC	Ubiquitin-conjugating enzyme/RWD-like protein	tumor susceptibility protein
Sapur.15WG099100.1	323.7626665	0.485953988	0.041361205	11.74903	7.14E-32	2.80E-31	cyan	0.660786516	4.66E-21		AT5G63060.1		Sec14p-like phosphatidylinositol transfer family protein	CRAL/TRIO domain protein
Sapur.012G100700.1	317.0532756	0.352527853	0.030019645	11.74324	7.65E-32	3.00E-31	cyan	0.692340328	9.91E-24	GO:0006508,GO:0004222	AT5G51740.1		Peptidase family M48 family protein	M48 family peptidase
Sapur.007G088800.1	106.8245735	0.470040165	0.040035304	11.74064	7.89E-32	3.09E-31	cyan	0.683894705	5.55E-23		AT3G19640.1	MGT4,MRS2-3	magnesium transporter 4	NA
Sapur.008G117400.1	844.4861865	-0.684787246	0.058327174	-11.7404	7.91E-32	3.10E-31	cyan	-0.670791184	7.19E-22	GO:0030163	AT1G68660.1		Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein	ATP-dependent Clp protease adapter protein ClpS
Sapur.007G086500.1	423.6909283	-0.90586388	0.077173204	-11.7381	8.13E-32	3.19E-31	cyan	-0.649747442	3.38E-20	GO:0009073,GO:0003849	AT4G39980.1	DHS1	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase
Sapur.001G075300.1	474.9489139	-0.58125601	0.049525707	-11.7365	8.29E-32	3.25E-31	cyan	-0.699683913	2.11E-24	GO:0051205,GO:0016021	AT5G62050.1	ATOXA1,OXA1,OXA1AT	homolog of yeast oxidase assembly 1 (OXA1)	inner membrane protein
Sapur.019G062700.1	194.7059596	-0.571091867	0.048683926	-11.7306	8.88E-32	3.48E-31	cyan	-0.699598407	2.15E-24		AT2G40760.1		Rhodanese/Cell cycle control phosphatase superfamily protein	photosystem I P700 chlorophyll A apoprotein, putative
Sapur.019G082900.1	13.70299437	-1.359901439	0.116062166	-11.717	1.04E-31	4.08E-31	cyan	-0.584570592	9.14E-16		AT1G22710.1	ATSUC2,SUC2,SUT1	sucrose-proton symporter 2	sucrose transporter
Sapur.008G021200.1	190.1812413	-0.842655501	0.071922598	-11.7161	1.05E-31	4.12E-31	cyan	-0.667177389	1.42E-21		AT3G52790.1		peptidoglycan-binding LysM domain-containing protein	carbohydrate-binding module family 50 protein
Sapur.001G092800.2	23.42602559	-0.872458268	0.074467665	-11.7159	1.06E-31	4.13E-31	cyan	-0.67556081	2.87E-22		AT4G11970.2		YTH family protein	splicing factor YT521-B, putative
Sapur.006G099600.1	504.8568363	-0.358836823	0.03062844	-11.7158	1.06E-31	4.14E-31	cyan	-0.661249958	4.28E-21		AT2G32600.1		hydroxyproline-rich glycoprotein family protein	splicing factor 3A subunit 2, putative
Sapur.019G086500.1	14.6590842	-1.156225841	0.098709483	-11.7134	1.09E-31	4.25E-31	cyan	-0.690436975	1.47E-23		AT3G58590.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.011G085900.1	1.539826667	3.044924889	0.259987133	11.71183	1.11E-31	4.33E-31	cyan	0.726928424	4.39E-27	GO:0006355,GO:0003677	AT4G01540.1	ANAC068,NTM1	NAC with transmembrane motif1	No apical meristem (NAM) protein
Sapur.012G046100.1	34.16803737	1.424337519	0.121627602	11.71064	1.12E-31	4.39E-31	cyan	0.64820375	4.43E-20					NA
Sapur.007G056100.1	2.769218983	-2.041808614	0.17436661	-11.7099	1.13E-31	4.43E-31	cyan	-0.695314583	5.33E-24		AT4G35730.1		Regulator of Vps4 activity in the MVB pathway protein	NA
Sapur.005G004600.1	750.6754479	-0.662935168	0.056615801	-11.7094	1.14E-31	4.46E-31	cyan	-0.698688275	2.61E-24	GO:0016788	AT1G09390.1		GDSL-like Lipase/Acylhydrolase superfamily protein	NA
Sapur.001G040900.1	20.24386736	1.472011296	0.12573177	11.70755	1.17E-31	4.55E-31	cyan	0.644657606	8.20E-20	GO:0000160	AT2G26594.1	ARR24,RR24	response regulator 24	extra response regulator
Sapur.001G077300.1	7.443664342	1.597641328	0.136519547	11.70266	1.24E-31	4.82E-31	cyan	0.640577452	1.65E-19		AT1G64320.1		myosin heavy chain-related	NA
Sapur.010G090900.1	296.1649952	1.60293097	0.137020568	11.69847	1.30E-31	5.07E-31	cyan	0.606062079	4.08E-17	GO:0055085,GO:0016020,GO:0006810,GO:0015171,GO:0003333	AT2G01170.1	BAT1	bidirectional amino acid transporter 1	amino acid permease
Sapur.018G118900.1	524.1707257	-0.494914974	0.042314087	-11.6962	1.33E-31	5.20E-31	cyan	-0.679615001	3.28E-24		AT5G58130.1	ROS3	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif protein
Sapur.013G008700.1	33.67142502	-0.890562118	0.076145989	-11.6955	1.34E-31	5.24E-31	cyan	-0.664230685	2.47E-21	GO:0009982,GO:0009451,GO:0003723,GO:0001522	AT1G56345.1		Pseudouridine synthase family protein	RNA pseudouridine synthase
Sapur.006G199700.5	31.63003101	-1.203877976	0.102941251	-11.6948	1.35E-31	5.28E-31	cyan	-0.674914683	3.26E-22		AT2G20740.1		Tetraspanin family protein	transmembrane protein, putative
Sapur.008G040200.1	3.633145183	2.534089884	0.216697121	11.69416	1.37E-31	5.32E-31	cyan	0.644980167	7.76E-20					hypothetical protein
Sapur.010G070700.1	78.58157644	0.881521598	0.075382152	11.69404	1.37E-31	5.33E-31	cyan	0.671447065	6.34E-22	GO:0048544,GO:0006468,GO:0005524,GO:0004672	AT2G19130.1		S-locus lectin protein kinase family protein	Serine/Threonine kinase domain protein
Sapur.009G008400.4	44.7380026	1.372186594	0.117365718	11.69155	1.41E-31	5.49E-31	cyan	0.610323686	2.14E-17	GO:0055114,GO:0046429,GO:0016114	AT5G60600.1	CLB4,CSB3,GCPE,HDS,ISPG	4-hydroxy-3-methylbut-2-enyl diphosphate synthase	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
Sapur.15WG129500.1	337.9011409	-0.394605444	0.033752942	-11.691	1.42E-31	5.52E-31	cyan	-0.676824324	2.25E-22		AT5G45170.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	2-deoxyglucose-6-phosphate phosphatase, putative
Sapur.007G063000.1	32.89101281	1.140119454	0.097527141	11.69028	1.43E-31	5.57E-31	cyan	0.64234394	1.22E-19					NA
Sapur.004G176500.1	3.368594112	-1.794403658	0.153531695	-11.6875	1.48E-31	5.75E-31	cyan	-0.715237642	6.79E-26					hypothetical protein
Sapur.009G058000.1	668.0535949	1.174237306	0.100486125	11.68557	1.51E-31	5.88E-31	cyan	0.673624857	4.18E-22	GO:0008080	AT2G30090.1		Acyl-CoA N-acyltransferases (NAT) superfamily protein	N-acetyltransferase, putative
Sapur.013G139300.1	38.81396676	-1.25275058	0.1072225	-11.6837	1.55E-31	6.02E-31	cyan	-0.785705866	3.78E-34	GO:0003677	AT1G06920.1	ATOFP4,OFP4	ovate family protein 4	ovate transcriptional repressor
Sapur.016G140300.1	8.030215421	3.117008871	0.266840669	11.68116	1.59E-31	6.19E-31	cyan	0.504527306	1.61E-11		AT5G58850.1	ATMYB119,MYB119	myb domain protein 119	Myb-like DNA-binding domain protein
Sapur.019G054800.1	335.3118862	-0.42778768	0.036626783	-11.6796	1.62E-31	6.31E-31	cyan	-0.672054197	5.65E-22	GO:0032259,GO:0008168,GO:0001510	AT5G01230.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ribosomal RNA methyltransferase, putative
Sapur.017G117600.1	9.886671687	3.977578439	0.340632106	11.67705	1.67E-31	6.50E-31	cyan	0.497639192	3.34E-11	GO:0006468,GO:0005524,GO:0004672	AT3G47570.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.006G136400.1	2.625494065	3.048279348	0.261050042	11.67699	1.67E-31	6.50E-31	cyan	0.657547203	8.41E-21					NA
Sapur.018G007600.1	244.0389605	0.673847469	0.057717417	11.67494	1.71E-31	6.66E-31	cyan	0.701761555	1.35E-24	GO:0055085,GO:0016020,GO:0006811,GO:0005216	AT2G24610.1	ATCNGC14,CNGC14	cyclic nucleotide-gated channel 14	cyclic nucleotide-gated ion channel protein, putative
Sapur.005G133000.1	389.1829306	-0.594081138	0.050887456	-11.6744	1.72E-31	6.70E-31	cyan	-0.718202488	3.43E-26		AT1G36320.1			plant/F7F23-4 protein
Sapur.016G129800.1	28.31508456	1.409223929	0.120711088	11.67435	1.72E-31	6.70E-31	cyan	0.564128525	1.43E-14	GO:0003676	AT4G13850.1	ATGRP2,GR-RBP2,GRP2	glycine-rich RNA-binding protein 2	RNA recognition motif 2 in RNA-binding protein 28 (RBM28)-like protein
Sapur.011G065500.1	50.2436077	-1.592225758	0.136407522	-11.6726	1.76E-31	6.85E-31	cyan	-0.775133609	1.01E-32	GO:0005515	AT3G14740.2		RING/FYVE/PHD zinc finger superfamily protein	PHD zinc finger protein
Sapur.011G022500.1	5.53001665	1.570967862	0.134603608	11.67107	1.79E-31	6.96E-31	cyan	0.629556053	1.03E-18	GO:0048544,GO:0006468,GO:0004672	AT4G21380.1	ARK3,RK3	receptor kinase 3	Serine/Threonine kinase domain protein
Sapur.011G163800.1	1525.944448	0.485006607	0.041556665	11.67097	1.79E-31	6.97E-31	cyan	0.69382701	7.27E-24		AT3G16270.1		ENTH/VHS family protein	VHS domain plant protein
Sapur.010G066100.1	1691.947943	0.507246405	0.043465832	11.67	1.81E-31	7.05E-31	cyan	0.677197718	2.09E-22	GO:0016021,GO:0006810	AT3G22845.1		emp24/gp25L/p24 family/GOLD family protein	transmembrane emp24 domain protein
Sapur.004G040800.3	2.462890942	-2.584281696	0.221448715	-11.6699	1.82E-31	7.06E-31	cyan	-0.653867777	1.63E-20	GO:0055085,GO:0016020,GO:0006810,GO:0005215	AT2G34190.1		Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.006G087700.1	147.776058	-0.881138933	0.075548435	-11.6632	1.96E-31	7.61E-31	cyan	-0.656355363	1.04E-20		AT2G40475.1			hypothetical protein
Sapur.016G083400.1	1256.390991	0.317525862	0.02722929	11.66119	2.01E-31	7.81E-31	cyan	0.698863901	2.51E-24	GO:0005515	AT3G09740.1	ATSYP71,SYP71	syntaxin of plants 71	syntaxin-71 protein
Sapur.006G150400.1	320.7670929	-0.64441719	0.055265095	-11.6605	2.03E-31	7.88E-31	cyan	-0.677203427	2.09E-22	GO:0003723	AT5G57930.2	APO2,emb1629	Arabidopsis thaliana protein of unknown function (DUF794)	APO RNA-binding protein
Sapur.003G099000.1	37.40062915	-0.903162396	0.077467597	-11.6586	2.07E-31	8.05E-31	cyan	-0.718736359	3.03E-26		AT5G41650.1		Lactoylglutathione lyase / glyoxalase I family protein	lactoylglutathione lyase family protein
Sapur.011G020100.1	1056.164931	0.500364482	0.042920898	11.65783	2.09E-31	8.12E-31	cyan	0.6633856	2.89E-21		AT1G11440.1			NA
Sapur.019G052800.1	660.4681702	0.848638451	0.072797175	11.65757	2.10E-31	8.14E-31	cyan	0.658409481	7.19E-21	GO:0006508,GO:0004185	AT4G12910.1	scpl20	serine carboxypeptidase-like 20	serine carboxypeptidase
Sapur.014G087000.1	127.0002907	-0.422440463	0.036241985	-11.6561	2.14E-31	8.29E-31	cyan	-0.70259079	1.13E-24	GO:0031011	AT1G02290.1			hypothetical protein
Sapur.15WG026700.1	80.58815268	-0.787072909	0.067533989	-11.6545	2.18E-31	8.44E-31	cyan	-0.667075431	1.45E-21	GO:0055085,GO:0016020,GO:0006811,GO:0005216	AT3G17700.1	ATCNGC20.CNBT1.CNGC20	cyclic nucleotide-binding transporter 1	NA
Sapur.003G074500.1	13.28653872	-1.317673738	0.113065492	-11.6541	2.19E-31	8.48E-31	cyan	-0.687238173	2.83E-23	GO:0016559,GO:0005779	AT3G47430.1	PEX11B	peroxin 11B	peroxisomal biogenesis factor 11
Sapur.017G081400.1	323.6386345	-0.685681986	0.058847735	-11.6518	2.25E-31	8.71E-31	cyan	-0.722681099	1.21E-26		AT1G15802.1			hypothetical protein
Sapur.011G076600.1	33.80202915	-0.874409104	0.075064607	-11.6488	2.33E-31	9.02E-31	cyan	-0.678408352	1.65E-22		AT1G78700.1	BEH4	BES1/BZR1 homolog 4	brassinosteroid signaling positive regulator-like protein
Sapur.016G018000.1	917.0617402	1.0720323	0.092044906	11.64684	2.38E-31	9.22E-31	cyan	0.621981855	3.50E-18	GO:0020037,GO:0009055	AT1G22840.1	ATCYTC-A,CYTC-1	CYTOCHROME C-1	cytochrome protein C
Sapur.15WG038300.1	22.80770372	1.216043705	0.104423806	11.64527	2.43E-31	9.39E-31	cyan	0.692206069	1.02E-23					hypothetical protein
Sapur.005G125500.1	100.6266028	0.932123802	0.080074936	11.64064	2.56E-31	9.91E-31	cyan	0.656909389	9.44E-21		AT4G33985.1		Protein of unknown function (DUF1685)	DUF1685 family protein
Sapur.001G148800.1	4.455875343	-2.224734484	0.191158072	-11.6382	2.64E-31	1.02E-30	cyan	-0.711166599	1.71E-25					hypothetical protein
Sapur.002G201900.1	19.6214012	-0.953530161	0.081954544	-11.6349	2.74E-31	1.06E-30	cyan	-0.678224472	1.71E-22	GO:0016020,GO:0006810,GO:0005215	AT5G46050.1	ATPTR3,PTR3	peptide transporter 3	NA
Sapur.T060100.1	14.89200258	1.47538455	0.126808884	11.63471	2.75E-31	1.06E-30	cyan	0.664842443	2.20E-21		AT5G19820.1	emb2734	ARM repeat superfamily protein	NA
Sapur.002G145800.1	36.46188548	-1.183215542	0.101736282	-11.6302	2.89E-31	1.12E-30	cyan	-0.690282613	1.52E-23	GO:0003677,GO:0000786	AT1G01370.1	CENH3,HTR12	Histone superfamily protein	centromeric histone H3
Sapur.005G201500.1	472.8803776	0.48682929	0.041862621	11.62921	2.93E-31	1.13E-30	cyan	0.657087218	9.14E-21		AT1G12680.1	PEPKR2	phosphoenolpyruvate carboxylase-related kinase 2	Serine/Threonine kinase domain protein
Sapur.006G192000.1	1643.673901	-0.441688463	0.03799828	-11.6239	3.12E-31	1.20E-30	cyan	-0.681654575	8.68E-23	GO:0016740	AT4G32520.2	AtSHMT3,SHM3	serine hydroxymethyltransferase 3	serine hydroxymethyltransferase
Sapur.011G122100.1	29.49300343	-0.936784606	0.080631644	-11.6181	3.34E-31	1.29E-30	cyan	-0.691548076	1.17E-23	GO:0005515,GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT3G44730.1	ATKP1,KP1	kinesin-like protein 1	kinesin heavy chain, putative
Sapur.012G046400.1	21.45577477	1.457825036	0.125536783	11.61273	3.55E-31	1.37E-30	cyan	0.668440805	1.12E-21					NA
Sapur.006G115800.1	901.3015151	0.442249019	0.038098988	11.60789	3.76E-31	1.45E-30	cyan	0.670389584	7.76E-22	GO:0019773,GO:0006511,GO:0004175,GO:0051603,GO:0005839,GO:0004298	AT2G05840.1	PAA2	20S proteasome subunit PAA2	proteasome subunit alpha type-6 protein
Sapur.012G016300.1	114.8797915	-0.621496347	0.053541085	-11.6078	3.76E-31	1.45E-30	cyan	-0.701291413	1.49E-24		AT5G06160.1	ATO	splicing factor-related	splicing factor 3a subunit 3, putative
Sapur.006G113100.1	1.290838077	3.387357345	0.291834228	11.60713	3.79E-31	1.46E-30	cyan	0.781654907	1.36E-33	GO:0009733	AT5G20810.1		SAUR-like auxin-responsive protein family	SAUR-like auxin-responsive protein
Sapur.017G075500.2	86.94125209	0.646409487	0.055709653	11.60319	3.97E-31	1.53E-30	cyan	0.702549861	1.14E-24		AT1G26580.1			ATP-binding protein, putative
Sapur.016G145700.1	89.72281156	1.380702556	0.118994288	11.6031	3.97E-31	1.53E-30	cyan	0.604827506	4.91E-17					hypothetical protein
Sapur.009G132300.1	647.3134011	0.851499207	0.073395049	11.60159	4.04E-31	1.56E-30	cyan	0.684360828	5.05E-23		AT4G35360.1		Uncharacterised conserved protein (UCP030210)	pantothenate kinase
Sapur.013G110400.1	49.10863692	-0.985771969	0.084973568	-11.6009	4.08E-31	1.57E-30	cyan	-0.686398552	3.35E-23		AT3G58100.1	PDCB5	plasmodesmata callose-binding protein 5	carbohydrate-binding module family 43 protein
Sapur.T079200.1	3.42556583	4.665551091	0.402361386	11.59542	4.35E-31	1.67E-30	cyan	0.548746766	1.00E-13					hypothetical protein
Sapur.012G083200.1	113.7689626	-1.202867361	0.103762042	-11.5926	4.50E-31	1.73E-30	cyan	-0.730114062	2.03E-27					NA
Sapur.018G108400.1	121.4858937	1.42966995	0.12330497	11.59219	4.51E-31	1.74E-30	cyan	0.602647545	6.80E-17	GO:0046983	AT5G57150.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH protein
Sapur.016G010300.1	1464.79251	0.512685695	0.044227431	11.59203	4.52E-31	1.74E-30	cyan	0.689007756	1.97E-23	GO:0005515	AT4G12560.2	CPR30	F-box and associated interaction domains-containing protein	F-box protein interaction domain protein
Sapur.005G133700.1	7.358818061	-1.609975647	0.138914808	-11.5897	4.65E-31	1.79E-30	cyan	-0.670170962	8.09E-22		AT1G36940.1			hypothetical protein
Sapur.013G090800.1	525.8874702	-0.576789507	0.049784537	-11.5857	4.87E-31	1.87E-30	cyan	-0.669734808	8.79E-22		AT4G10300.1		RmlC-like cupins superfamily protein	enzyme of the cupin superfamily protein
Sapur.004G094800.1	1.051069674	3.189439165	0.275292851	11.58562	4.87E-31	1.88E-30	cyan	0.672538724	5.15E-22	GO:0005681,GO:0000398,GO:0000387	AT1G54385.1		ARM repeat superfamily protein	NA
Sapur.011G000100.1	191.1549342	-0.547561323	0.047262929	-11.5854	4.89E-31	1.88E-30	cyan	-0.688909395	2.01E-23		AT1G61870.1	PPR336	pentatricopeptide repeat 336	membrane-associated salt-inducible protein, putative
Sapur.011G085200.1	1.685087038	3.112116782	0.268689186	11.58259	5.05E-31	1.94E-30	cyan	0.644366763	8.62E-20	GO:0006355,GO:0003677	AT4G01540.1	ANAC068,NTM1	NAC with transmembrane motif1	NA
Sapur.006G088400.1	51.16926702	-0.852133621	0.073572055	-11.5823	5.07E-31	1.95E-30	cyan	-0.685805587	3.78E-23	GO:0003677	AT2G30400.1	ATOFP2,OFP2	ovate family protein 2	NA
Sapur.012G076600.1	43.65179613	-1.360850301	0.117529733	-11.5788	5.28E-31	2.03E-30	cyan	-0.642712348	1.15E-19		AT5G13090.1			NA
Sapur.016G073700.1	5.062401402	3.274794567	0.282836185	11.57841	5.30E-31	2.04E-30	cyan	0.567534092	9.16E-15		AT5G42450.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing protein, putative
Sapur.006G061200.1	580.9160421	0.333694142	0.028822886	11.5774	5.36E-31	2.06E-30	cyan	0.664630522	2.29E-21		AT4G29960.1			transmembrane protein, putative
Sapur.006G024000.1	14.76415078	1.146329314	0.099017374	11.57705	5.39E-31	2.07E-30	cyan	0.643552091	9.92E-20	GO:0006904,GO:0000145	AT3G56640.1	SEC15A	exocyst complex component sec15A	exocyst complex component Sec15, putative
Sapur.014G143700.1	759.0913026	-0.500365934	0.043226086	-11.5756	5.48E-31	2.11E-30	cyan	-0.682194391	7.80E-23		AT2G43800.1		Actin-binding FH2 (formin homology 2) family protein	formin-like 2 domain protein
Sapur.016G126100.1	15.86704236	-1.339202832	0.115697072	-11.5751	5.51E-31	2.12E-30	cyan	-0.7071887	4.13E-25	GO:0005975,GO:0004553	AT1G05590.1	ATHEX3,HEXO2	beta-hexosaminidase 2	beta-hexosaminidase
Sapur.010G169600.1	363.2075648	-0.386650181	0.033445121	-11.5607	6.51E-31	2.50E-30	cyan	-0.67379783	4.04E-22	GO:0046540,GO:0000398	AT1G28060.1		Pre-mRNA-splicing factor 3	U4/U6 small nuclear ribonucleoprotein PRP3, putative
Sapur.006G223200.1	183.5581653	1.291288447	0.111753513	11.55479	6.98E-31	2.68E-30	cyan	0.6256765	1.94E-18	GO:0016758,GO:0008152	AT2G15480.1	UGT73B5	UDP-glucosyl transferase 73B5	UDP-glycosyltransferase, putative
Sapur.011G086200.1	1.516333938	3.174810518	0.274926938	11.54783	7.57E-31	2.90E-30	cyan	0.650469895	2.98E-20	GO:0006355,GO:0003677	AT4G01540.1	ANAC068,NTM1	NAC with transmembrane motif1	NA
Sapur.008G044500.1	9.047179509	1.390824346	0.12048118	11.54391	7.92E-31	3.04E-30	cyan	0.642097746	1.27E-19	GO:0031047	AT3G48670.1	IDN2,RDM12	XH/XS domain-containing protein	transcription factor X1-like protein
Sapur.008G130100.1	44.75884289	0.775687207	0.067199868	11.54299	8.01E-31	3.07E-30	cyan	0.655503515	1.22E-20	GO:0007165	AT4G14580.1	CIPK4,SnRK3.3	CBL-interacting protein kinase 4	CBL-interacting kinase
Sapur.016G031700.1	436.3655746	0.340260436	0.029478135	11.54281	8.03E-31	3.08E-30	cyan	0.703378747	9.51E-25		AT3G56740.1		Ubiquitin-associated (UBA) protein	ubiquitin-associated/TS-N domain protein
Sapur.001G120000.1	15.73565046	1.132171518	0.098093503	11.54176	8.12E-31	3.11E-30	cyan	0.587277019	6.26E-16					hypothetical protein
Sapur.011G070500.2	2.460674669	2.711913543	0.234969524	11.54155	8.14E-31	3.12E-30	cyan	0.670159688	8.11E-22	GO:0003676	AT1G53650.2	CID8	CTC-interacting domain 8	RNA recognition motif 2 in plant thaliana CTC-interacting domain protein CID8
Sapur.004G007600.1	166.5675873	-0.885548402	0.076755551	-11.5373	8.56E-31	3.28E-30	cyan	-0.71687352	4.66E-26	GO:0009094,GO:0004664	AT1G11790.1	ADT1	arogenate dehydratase 1	arogenate dehydratase/prephenate dehydratase
Sapur.006G002900.2	64.35918699	1.078979529	0.093533557	11.53575	8.71E-31	3.33E-30	cyan	0.66097195	4.51E-21		AT5G47730.1		Sec14p-like phosphatidylinositol transfer family protein	SEC14 cytosolic factor, putative
Sapur.013G072200.1	273.0780892	-0.935554377	0.081108318	-11.5346	8.83E-31	3.38E-30	cyan	-0.664771144	2.23E-21	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	AT3G03620.1		MATE efflux family protein	NA
Sapur.006G181600.1	411.7084611	-0.604272737	0.052389388	-11.5343	8.86E-31	3.39E-30	cyan	-0.713641366	9.76E-26		AT1G02180.1		ferredoxin-related	ferredoxin-like protein
Sapur.016G226100.1	8.850661162	-1.357333198	0.117692168	-11.5329	9.00E-31	3.44E-30	cyan	-0.651524969	2.47E-20	GO:0005975,GO:0004553	AT3G19620.1		Glycosyl hydrolase family protein	NA
Sapur.003G126100.4	3.203650864	-2.841453868	0.246445302	-11.5298	9.34E-31	3.57E-30	cyan	-0.631914334	7.02E-19	GO:0006269,GO:0003896	AT1G67320.2		DNA primase, large subunit family	DNA primase large subunit, putative
Sapur.005G004900.1	1.913237798	3.609353208	0.313077803	11.52861	9.47E-31	3.62E-30	cyan	0.563624321	1.53E-14					NA
Sapur.008G166400.1	27.44302817	-1.109305801	0.09623154	-11.5275	9.59E-31	3.67E-30	cyan	-0.698812607	2.54E-24	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT3G28740.1	CYP81D1	Cytochrome P450 superfamily protein	NA
Sapur.008G040700.1	188.2203996	0.619981122	0.053786732	11.52666	9.68E-31	3.70E-30	cyan	0.635600542	3.81E-19	GO:0008152,GO:0003824	AT1G65520.1	ATECI1,ECHIC,ECI1,PEC11	delta(3), delta(2)-enoyl CoA isomerase 1	enoyl-CoA hydratase/isomerase, putative
Sapur.001G119900.2	2.455903873	-2.914106331	0.252861176	-11.5245	9.93E-31	3.79E-30	cyan	-0.672775729	4.92E-22		AT1G32470.1		Single hybrid motif superfamily protein	glycine cleavage system H protein
Sapur.010G079700.1	959.2345289	0.475257407	0.041250988	11.52112	1.03E-30	3.94E-30	cyan	0.676594864	2.35E-22	GO:0031625,GO:0006511	AT1G26830.1	ATCUL3.ATCUL3A.CUL3.CU	cullin 3	cullin protein
Sapur.010G180100.1	456.5930509	0.558810461	0.048505222	11.52062	1.04E-30	3.96E-30	cyan	0.672482187	5.20E-22	GO:0016887,GO:0005524	AT3G10350.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	anion-transporting ATPase
Sapur.012G030700.1	680.5663635	-0.628622675	0.054573507	-11.5188	1.06E-30	4.05E-30	cyan	-0.689133101	1.92E-23	GO:0005524,GO:0003676	AT2G33730.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.005G077400.1	2.14400575	3.986396873	0.34614327	11.51661	1.09E-30	4.15E-30	cyan	0.551696987	6.96E-14	GO:0006355,GO:0003677	AT2G43000.1	anac042,NAC042	NAC domain containing protein 42	NAC transcription factor 030
Sapur.018G029600.1	21.29911217	-1.071100697	0.093022492	-11.5144	1.12E-30	4.26E-30	cyan	-0.666372948	1.66E-21	GO:0005634	AT1G61470.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	CAF1 family ribonuclease
Sapur.013G081700.1	212.4645366	-1.042580736	0.090557036	-11.513	1.13E-30	4.33E-30	cyan	-0.688527875	2.17E-23	GO:0016747	AT5G17540.1		HXXXD-type acyl-transferase family protein	NA
Sapur.017G080600.1	561.6743506	0.503098797	0.043733292	11.50379	1.26E-30	4.81E-30	cyan	0.666510372	1.61E-21		AT5G15640.1		Mitochondrial substrate carrier family protein	substrate carrier family protein
Sapur.004G043900.1	104.7705668	0.786072407	0.068349348	11.5008	1.31E-30	4.98E-30	cyan	0.640367691	1.71E-19					NA
Sapur.013G062200.1	2.732324552	2.343679743	0.203834628	11.49795	1.35E-30	5.15E-30	cyan	0.70796604	3.48E-25					NA
Sapur.006G034100.1	379.5358628	-0.315378381	0.027429128	-11.4979	1.35E-30	5.15E-30	cyan	-0.702130364	1.25E-24		AT2G41350.1			HAUS augmin-like complex subunit
Sapur.001G028600.1	176.6261857	-0.289210632	0.02516593	-11.4921	1.44E-30	5.50E-30	cyan	-0.680784186	1.03E-22		AT3G54380.1		SAC3/GANP/Nin1/mts3/eIF-3 p25 family	SAC3/GANP family protein
Sapur.011G039500.1	951.0085648	0.731568828	0.063662517	11.49136	1.46E-30	5.55E-30	cyan	0.680042152	1.20E-22		AT3G05700.1		Drought-responsive family protein	stress-induced protein Di19, carboxy-terminal protein
Sapur.001G102500.1	634.6422117	-0.407100468	0.035436451	-11.4882	1.51E-30	5.76E-30	cyan	-0.671791449	5.94E-22	GO:0006376,GO:0005685,GO:0003729	AT5G51410.2		LUC7 N_terminus domain-containing protein	LUC7 amino-terminal protein
Sapur.019G109900.1	10.43428179	-2.178341102	0.189644923	-11.4864	1.54E-30	5.87E-30	cyan	-0.681467578	9.01E-23		AT2G40435.1			transcription factor bHLH93
Sapur.013G020700.1	68.54930019	1.480976626	0.129034015	11.47741	1.71E-30	6.51E-30	cyan	0.632906947	5.96E-19	GO:0006468,GO:0004672	AT3G57710.1		Protein kinase superfamily protein	kinase family protein
Sapur.003G108500.1	189.7529979	-0.547087196	0.04766914	-11.4768	1.73E-30	6.56E-30	cyan	-0.698260554	2.86E-24		AT5G41960.1			NA
Sapur.016G143300.2	8.788478458	-1.231886349	0.107384796	-11.4717	1.83E-30	6.95E-30	cyan	-0.662520602	3.39E-21	GO:0055114,GO:0050897,GO:0016636,GO:0010024	AT3G09150.2	ATHY2,GUN3,HY2	phytochromobilin:ferredoxin oxidoreductase, chloroplast / phytochromobilin synthase (HY2)	heme oxygenase 2 protein, putative
Sapur.005G085000.1	232.8704016	-0.647164483	0.056429058	-11.4686	1.90E-30	7.20E-30	cyan	-0.656887712	9.47E-21		AT4G35740.2	ATRECQ3,RecQl3	DEAD/DEAH box RNA helicase family protein	NA
Sapur.T075000.1	97.14148229	-0.644068454	0.056167386	-11.4669	1.93E-30	7.34E-30	cyan	-0.68248859	7.35E-23	GO:0005524,GO:0004797	AT5G23070.1		Thymidine kinase	NA
Sapur.005G179700.1	98.999987	-0.465783236	0.040620027	-11.4668	1.94E-30	7.35E-30	cyan	-0.690128593	1.56E-23		AT3G23280.2	XBAT35	XB3 ortholog 5 in Arabidopsis thaliana	NA
Sapur.001G037300.1	96.03381024	-0.771372466	0.067290027	-11.4634	2.01E-30	7.64E-30	cyan	-0.689293882	1.86E-23		AT4G31880.1			NA
Sapur.005G096000.2	23.71253643	1.026276964	0.089549517	11.46044	2.08E-30	7.90E-30	cyan	0.640024007	1.81E-19	GO:0006468,GO:0005524,GO:0004672	AT2G18170.1	ATMPK7,MPK7	MAP kinase 7	MAP kinase
Sapur.001G001100.1	21.77582417	0.902750173	0.078772136	11.46027	2.09E-30	7.92E-30	cyan	0.626116355	1.81E-18	GO:0008270,GO:0005515	AT5G56340.1	ATCRT1	RING/U-box superfamily protein	zinc finger protein
Sapur.010G068500.1	45.29874694	-0.513813688	0.044847807	-11.4568	2.17E-30	8.24E-30	cyan	-0.679540621	1.32E-22	GO:0003676,GO:0017069,GO:0000398	AT2G30260.1	U2B\'\'	U2 small nuclear ribonucleoprotein B	NA
Sapur.003G145800.1	91.07139581	-0.547152004	0.047761669	-11.4559	2.20E-30	8.33E-30	cyan	-0.684476603	4.94E-23	GO:0006355,GO:0005739,GO:0003690	AT5G07900.1		Mitochondrial transcription termination factor family protein	mTERF protein
Sapur.016G034300.1	595.2334447	-0.463039474	0.040425664	-11.4541	2.24E-30	8.50E-30	cyan	-0.692775793	9.05E-24	GO:0030170	AT3G57050.1	CBL	cystathionine beta-lyase	cystathionine beta-lyase
Sapur.007G039800.1	318.5991216	-0.768896884	0.067156929	-11.4493	2.37E-30	8.98E-30	cyan	-0.673433063	4.34E-22		AT5G66800.1			hypothetical protein
Sapur.15ZG052200.1	7.715677731	-1.940712861	0.169533953	-11.4473	2.42E-30	9.18E-30	cyan	-0.604756742	4.97E-17		AT1G10940.2	ASK1.SNRK2-4.SNRK2.4.SRK	Protein kinase superfamily protein	NA
Sapur.004G153500.1	20.76655167	2.50109043	0.218565083	11.44323	2.54E-30	9.63E-30	cyan	0.520741799	2.73E-12	GO:0009910,GO:0003712	AT2G27550.1	ATC	centroradialis	terminal flower 1
Sapur.003G073800.1	17.92033555	1.509252615	0.131898886	11.4425	2.56E-30	9.71E-30	cyan	0.580127607	1.69E-15	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G08850.1		Leucine-rich repeat receptor-like protein kinase family protein	receptor-like kinase
Sapur.019G009000.1	23.33460326	-0.982381121	0.085855405	-11.4423	2.57E-30	9.73E-30	cyan	-0.613084769	1.41E-17	GO:0006783,GO:0004325	AT2G30390.1	ATFC-II,FC-II,FC2	ferrochelatase 2	ferrochelatase
Sapur.016G076200.1	2120.063925	0.442488538	0.038676267	11.44083	2.61E-30	9.89E-30	cyan	0.646728284	5.73E-20	GO:0019236,GO:0007186,GO:0016021	AT5G18520.1		Lung seven transmembrane receptor family protein	lung seven transmembrane receptor, putative

Sapur.01G027700.1	4.76543999	3.93502837	0.169154086	-11.4384	2.66E-30	1.01E-29	cpm	-0.617708891	6.79E-18						NA
Sapur.0006183000.1	3591.633066	-0.699360984	0.061191743	-11.429	3.00E-30	1.13E-29	cpm	-0.715159622	6.91E-26	G0.0003723	ATSG15530.1		Ribosomal protein S3 family protein		40S ribosomal protein S3
Sapur.0002604200.1	106.8533809	0.775342403	0.067602746	-11.4373	3.06E-30	1.15E-29	cpm	-0.67607771	8.23E-22	G0.0008270;G0.0005515	ATSG28623.1		RING/U-box superfamily protein		RING-H2 zinc finger protein
Sapur.0006091800.1	566.5440441	-0.711992812	0.062306965	-11.4372	3.06E-30	1.16E-29	cpm	-0.714986994	7.08E-26		ATMG01790.1				hypothetical protein
Sapur.0006330700.1	145.0841934	-0.459855562	0.040150676	-11.4231	3.32E-30	1.21E-29	cpm	-0.703682315	8.91E-25	G0.0002047;G0.0006468;G0.0004672	ATSG28383.1		Protein kinase superfamily protein		receptor-like kinase, putative
Sapur.0003123500.1	232.4062503	0.542093552	0.047658944	11.42237	3.23E-30	1.22E-29	cpm	-0.710202971	2.12E-25		ATG23349.1		hydroxyproline-rich glycoprotein family protein		hydroxyproline-rich glycoprotein family protein, putative
Sapur.0096275300.1	186.6618143	0.466396703	0.040856617	11.42035	3.31E-30	1.25E-29	cpm	-0.668184168	5.20E-21	G0.0008270;G0.0005515	ATSG48852.1		RING/U-box superfamily protein		RING-H2 zinc finger protein, putative
Sapur.0010201100.1	24.14844552	1.277379621	0.111862298	11.41921	3.35E-30	1.27E-29	cpm	-0.637577701	2.74E-19	G0.0016791;G0.0008152	ATG17720.1		Pyridoxal phosphate-phosphatase-related protein		inorganic diphosphatase
Sapur.0115113500.1	776.6546525	-0.432114243	0.037860907	-11.4132	3.59E-30	1.35E-29	cpm	-0.698870285	2.51E-24		ATG16500.1				hypothetical protein
Sapur.7000500.1	2398.719653	0.573183997	0.10253318	11.41086	3.68E-30	1.38E-29	cpm	-0.63630329	1.38E-21	ATMYB21;ATMYB3;MYB21	ATG27819.1		myb domain protein 21		MYB transcription factor
Sapur.0021860000.2	25.29095919	-0.184481867	0.08892722	-11.408	3.81E-30	1.44E-29	cpm	-0.67892979	1.49E-22		ATG07030.1		Alba DNA/RNA-binding protein		Rpp20 subunit of nuclear RNase MRP and P protein
Sapur.0010541700.2	67.55677739	1.670129504	0.092428845	11.40624	3.86E-30	1.47E-29	cpm	-0.644575953	4.32E-20		ATG27580.1		Pathogenesis-related thaumatin-superfamily protein		thaumatin and allergen;brittle;agel;thaumatin-like; plant-like protein
Sapur.0031422300.1	1.361239393	-2.123619584	0.282645825	-11.4052	3.94E-30	1.49E-29	cpm	-0.623637909	2.69E-18		ATG02890.2	2PR2	protein binding		hypothetical protein
Sapur.0175168800.2	53.33633366	-0.888778826	0.077670729	-11.4035	3.95E-30	1.49E-29	cpm	-0.642182616	4.88E-22	G0.0003677;G0.0006334;G0.0005634;G0.0000786	AHMGA		high mobility group A		high mobility group family protein
Sapur.0011461400.1	153.8441107	-0.377378651	0.033111917	-11.4031	4.03E-30	1.52E-29	cpm	-0.67977226	1.26E-22		ATG21295.1		Tudor/PWWP/MBT superfamily protein		NA
Sapur.0042859000.1	16.78829476	-0.363640881	0.163625749	-11.3984	4.12E-30	1.56E-29	cpm	-0.572344221	1.56E-19						NA
Sapur.0102509000.1	670.8894859	0.635511827	0.05578079	11.39374	4.49E-30	1.69E-29	cpm	0.6373079	2.86E-19		ATG26230.1				hypothetical protein
Sapur.0106216300.1	1046.002875	0.674815868	0.059234947	11.39219	4.57E-30	1.72E-29	cpm	0.634999561	4.21E-19	G0.0006468;G0.0004672	ATG54380.1	THI1	protein kinase family protein		receptor-like kinase, putative
Sapur.0105194500.1	51.22376616	-0.455275597	0.06319413	-11.3888	4.75E-30	1.79E-29	cpm	-0.664664597	2.28E-21		ATG19180.1		Peptidase family M48 family protein (ZUF677)		transmembrane protein, putative
Sapur.0031410400.1	142.1340027	0.518842139	0.045313713	11.38727	4.84E-30	1.82E-29	cpm	0.672404742	5.66E-22		ATG38970.1		Zinc finger (C3HC4-type RING finger) family protein		Von willebrand factor type A domain protein
Sapur.0113025700.1	161.4497665	0.501017504	0.05038884	11.38189	5.11E-30	1.91E-29	cpm	0.671883181	6.05E-21		ATG02610.1		ELMO/CED-12 family protein		ELMO/CED-12 family protein
Sapur.0061362500.1	112.1497606	-0.8572832	0.075312513	-11.3772	5.43E-30	2.04E-29	cpm	-0.645179787	7.52E-20		ATG15800.1	RALR13	raf-like 13		rapid alkalinization factor
Sapur.0006330900.1	26.2558612	0.683362026	0.148040699	-11.3736	5.68E-30	2.12E-29	cpm	-0.618232119	3.40E-19	G0.0016020;G0.0006897	ATG28602.1		Adaptin ear-binding coat-associated protein 1 NECAP-1		NA
Sapur.0106207000.1	201.3250626	-0.696583076	0.061255278	-11.3718	5.78E-30	2.17E-29	cpm	-0.688771406	2.07E-23	G0.0043531	ATG45520.1		Leucine-rich repeat (LRR) family protein		disease resistance RPP13-like protein, putative
Sapur.0106522600.1	5.228746579	-2.244776619	-0.197414259	-11.3709	5.84E-30	2.19E-29	cpm	-0.624665969	3.80E-18	G0.0005114;G0.0020037;G0.0006879;G0.0004601	ATG52630.1	ATPA2;PA2	peptidase T		peptidase
Sapur.0020309000.3	8.968888884	1.700122999	0.149663364	11.3598	6.63E-30	2.46E-29	cpm	-0.602880955	7.39E-17		ATG22930.1		T-complex protein 11		T-complex protein
Sapur.0070267500.1	957.2162602	0.558054454	0.049153736	11.35325	7.15E-30	2.68E-29	cpm	-0.658848707	6.64E-21	G0.0004554;G0.0005681;G0.0000398	ATG08290.1	YLS8	mRNA splicing factor, thioredoxin-like US snRNP		thioredoxin-like protein 4A
Sapur.0105293800.1	100.1018826	-0.351208168	0.110038878	-11.3493	7.48E-30	2.80E-29	cpm	-0.731882004	1.02E-27		ATG44570.1	ATKCR2;KCR2	beta-ketoacyl reductase 2		NA
Sapur.0030041000.1	811.988261	0.501431211	0.044184044	11.34831	7.56E-30	2.83E-29	cpm	0.675308329	3.02E-22		ATG49960.1				ion channel pollux protein, putative
Sapur.0010699100.1	190.6593732	0.5128129	0.102048577	11.34748	7.63E-30	2.86E-29	cpm	0.632993707	5.87E-19						NA
Sapur.7027900.1	8.835123844	1.602997032	0.141280407	11.34621	7.74E-30	2.90E-29	cpm	0.663977207	3.75E-21						NA
Sapur.0051310800.1	127.8800774	0.868255141	0.076436147	11.34268	8.11E-30	3.04E-29	cpm	0.671883181	7.38E-19		ATAG36710.1		GRAS family transcription factor		GRAS family transcription factor
Sapur.0030640600.1	1819.722474	0.40495413	0.035703771	11.34205	8.12E-30	3.04E-29	cpm	-0.663779913	3.36E-23	G0.0006351;G0.0005634;G0.0003677	ATSG12130.1	ATIWS1;IWS1	Transcription elongation factor (TFIIS) family protein		transcription elongation factor (TFIIS) family protein
Sapur.0010201300.1	60.38867507	-0.383882326	0.122050628	-11.3385	8.46E-30	3.17E-29	cpm	-0.6524158	2.11E-20		ATG11810.1	SIS1	sigma factor binding protein 1		VQ motif protein
Sapur.0120203800.1	898.1034937	-0.627734201	0.055382708	-11.3345	8.86E-30	3.31E-29	cpm	-0.700001737	1.07E-24		ATG53460.2		Tetratricopeptide repeat (TPR)-like superfamily protein		thylakoid lumenal 17.4 kDa protein
Sapur.0062871000.1	152.3017448	0.132864408	0.100016148	11.3335	8.96E-30	3.35E-29	cpm	-0.623279902	2.64E-18						transmembrane protein, putative
Sapur.0106049600.1	11.3654718	1.132317331	0.099911787	11.33317	8.99E-30	3.36E-29	cpm	0.65401509	1.59E-20		ATG03100.1	CRM18;XPO18	exportin 18		NA
Sapur.0130224200.1	1095.593529	0.389838901	0.034398181	11.33312	8.99E-30	3.36E-29	cpm	0.665323503	5.08E-21	G0.0005634;G0.0008296;G0.0005737;G0.0004496	ATG27492.2	MK;MVK	mevalonate kinase		mevalonate kinase
Sapur.0194502200.1	303.2824674	0.586067298	0.169476565	11.33258	9.05E-30	3.38E-29	cpm	0.47837	2.86E-10	G0.0016157;G0.0005988	ATG73370.1	ATSUC5;SUC5	sucrose synthase 5		NA
Sapur.0061679000.1	1107.788054	-0.460691173	0.038872396	-11.3317	9.14E-30	3.42E-29	cpm	-0.698731607	2.59E-24	G0.0005114;G0.0051928;G0.0016491	ATSG06290.1	2-Cys Prx B;2CPB	2-cysteine peroxiredoxin B		2-cys peroxiredoxin
Sapur.0070067300.1	2008.707597	-0.472202293	0.033296878	-11.3312	9.20E-30	3.44E-29	cpm	-0.674828232	1.58E-23	G0.0003054;G0.0004418	ATG38290.1	HEMC	hydroxymethylbilane synthase		porphobilinogen deaminase
Sapur.0180263000.1	357.1514788	1.188457455	0.104900367	11.32939	9.39E-30	3.51E-29	cpm	0.602137603	7.31E-17	G0.0005114;G0.0051287;G0.0004471	ATG79750.1	ATNADP-ME4;NADP-ME4	NADP-malic enzyme 4		NADP-dependent malic enzyme
Sapur.0113050500.1	1.483926202	2.307549145	0.276708319	11.31615	9.72E-30	3.63E-29	cpm	0.597973146	2.16E-16	G0.0016021;G0.0008410;G0.0005137	ATG52120.1	ATEMT1;EMT1;FUR1	Phosphoribosyltransferase family protein		equilibrative nucleoside transporter
Sapur.0103045500.1	151.0723174	0.757155769	0.068376692	11.325	9.87E-30	3.69E-29	cpm	0.629347256	1.86E-18	G0.0006468;G0.0004672	ATG08720.1	ATEDR1;EDR1	Protein kinase superfamily protein		enhanced disease resistance protein
Sapur.0102250600.1	13.87619268	1.614363633	0.14238184	11.3249	9.92E-30	3.71E-29	cpm	0.620014561	7.86E-18	G0.0008270;G0.0005632	ATG27310.1		B box type zinc finger protein		B box zinc finger protein
Sapur.0161922300.1	11.55491043	1.173891563	0.121392045	11.31813	1.07E-29	3.99E-29	cpm	0.655064632	2.89E-20		ATG13600.1		Carbohydrate-binding X8 domain superfamily protein		carbohydrate-binding module family protein
Sapur.0175101300.1	2066.958641	0.439565588	0.03807165	11.31747	1.08E-29	4.02E-29	cpm	0.657456859	8.51E-21	G0.0005515;G0.0006413	ATG77840.1		Translation initiation factor IF2/IF5		eukaryotic translation initiation factor 5
Sapur.0090647700.1	160.9667131	-0.438159582	0.036368803	-11.3139	1.12E-29	4.18E-29	cpm	-0.678538041	2.22E-22		ATG52105.1				hypothetical protein
Sapur.0061991000.1	16.79835055	-1.669504044	0.103368898	-11.3138	1.12E-29	4.19E-29	cpm	-0.559124474	2.02E-16		ATG25770.3		alpha/beta-Hydrolases superfamily protein		acetyl xylan esterase
Sapur.0170204500.1	4.331639393	1.158006129	0.179025078	-11.3132	1.13E-29	4.21E-29	cpm	-0.629877058	1.23E-18	G0.0006468;G0.0005134;G0.0004672	ATG82861.1	PRSK	PRS-like receptor kinase		NA
Sapur.0082699800.1	539.1943	-0.683311458	0.060407404	-11.3084	1.19E-29	4.45E-29	cpm	-0.731641513	2.87E-32		ATG68233.1		Protein of unknown function (DUF1218)		fiber protein Fb34
Sapur.0100271700.1	11.90021004	1.528345149	0.135193669	-11.3049	1.24E-29	4.61E-29	cpm	-0.656317561	1.05E-20	G0.0008897;G0.0000287	ATG11470.1		A*-phosphotransferase family protein		NA
Sapur.0135291500.1	47.28647001	-1.539242598	0.136164512	-11.3041	1.25E-29	4.67E-29	cpm	-0.649719334	3.40E-20		ATG14920.1		Gibberellin-regulated family protein		NA
Sapur.0051311600.1	600.8593627	-0.325649181	0.034802777	-11.3033	1.26E-29	4.71E-29	cpm	-0.689601887	7.22E-22		ATG19320.1		Tetratricopeptide repeat (TPR)-like superfamily protein		PPR containing plant protein
Sapur.0080693500.1	109.5597512	0.094846569	0.362408378	11.30094	1.30E-29	4.84E-29	cpm	0.594869892	2.59E-16		ATG39770.2	CYT1;EMB101;GMP1;SD21	Glucose-1-phosphate adenylyltransferase family protein		NA
Sapur.0130280400.1	8.830139348	1.311318488	0.115987583	-11.2955	1.38E-29	5.15E-29	cpm	-0.680973813	9.94E-23		ATG41865.1				hypothetical protein
Sapur.0112095600.1	31.54188252	1.392926579	0.12333752	11.29362	1.41E-29	5.26E-29	cpm	0.619890032	4.87E-18	G0.0048544;G0.0006468;G0.0004672	ATG27290.1		S-locus lectin protein kinase family protein		NA
Sapur.0102612700.2	2.163212764	2.878091229	0.254956433	11.28857	1.49E-29	5.57E-29	cpm	0.672302164	6.58E-22		ATG23102.1		Pre-rRNA-processing protein TSR2, conserved region		Pre-rRNA-processing protein TSR2
Sapur.0030262300.1	21.81783604	0.808979309	0.070268119	11.28818	1.50E-29	5.59E-29	cpm	0.666349663	4.42E-24	G0.0003676	ATG17720.1		RNA-binding (RRM/RNP motifs) family protein		RNA recognition motif (RRM) containing protein
Sapur.0041319500.1	174.0714668	-1.362524764	0.102988129	-11.2878	1.51E-29	5.61E-29	cpm	-0.674358781	3.84E-22		ATG58150.1	ATOXS1;OXS3	oxidative stress 3		hypothetical protein
Sapur.0175101400.1	4.107521357	1.192164111	0.178724994	11.2864	1.53E-29	5.68E-29	cpm	0.587206991	2.27E-16	G0.0008270	ATG23175.2		RING/FYVE/PHD zinc finger superfamily protein		zinc finger protein
Sapur.0092049800.1	325.8448298	-0.492027481	0.03463736	-11.2789	1.67E-29	6.21E-29	cpm	-0.658160005	8.51E-21	G0.0005515;G0.0006413	ATG26880.2	AGL26	AGAMOUS-like 26		tRNA (cytidine(34)-2'-O-methyl)transferase, putative
Sapur.0061891000.1	7.69942025	-0.641182317	0.142876144	-11.2785	1.68E-29	6.24E-29	cpm	-0.658075285	7.64E-21						hypothetical protein
Sapur.7184200.1	3.825585876	-2.970162086	0.265582813	11.26842	1.88E-29	6.99E-29	cpm	-0.581627536	1.37E-15						NA
Sapur.0170204300.1	66.80845082	-0.587980291	0.087164446	-11.2682	1.88E-29	7.01E-29	cpm	-0.647836836	4.75E-20		ATG27930.3		DNA glycosylase superfamily protein		NA
Sapur.0020884600.1	15.2144617	-1.538493006	0.136605162	-11.2623	2.01E-29	7.49E-29	cpm	-0.609807853	2.28E-17						hypothetical protein
Sapur.0036460500.1	208.0161241	-0.614187384	0.054716149	-11.2606	2.03E-29	7.58E-29	cpm	-0.681651343	4.69E-23		ATG16695.1				transmembrane protein, putative
Sapur.0042589000.1	2164.993038	0.634176665	0.056332792	11.25968	2.08E-29	7.71E-29	cpm	0.619690085	5.02E-18		ATG03820.1		nonsense-mediated mRNA decay NMD3 family protein		60S ribosomal export protein NMD3
Sapur.0042814000.3	20.26254001	-0.748033477	0.066498425	-11.2513	2.28E-29	8.48E-29	cpm	-0.674116665	8.80E-22		ATG38600.1		Proline-rich spliceosome-associated protein (CWC15/CWC22) / zinc knuckle (CCHC-type) family protein		nucleic acid-binding protein, putative
Sapur.0105201600.1	174.1317234	-0.598097879	0.093135618	-11.2508	2.30E-29	8.53E-29	cpm	-0.637432867	2.75E-19	G0.0005114;G0.0020037;G0.0016705;G0.0005506	ATG63526.1	CYP718;36	cytochrome P450, family 71, subfamily A, polypeptide 36		NA
Sapur.0062049900.1	411.6648877	0.437120075	0.038557044	11.24944	2.33E-29	8.65E-29	cpm	0.672288079	5.41E-22		ATG29170.1		Eukaryotic protein of unknown function (DUF872)		transmembrane protein, putative
Sapur.0186200500.1	176.1003314	-0.373802022	0.033218473	-11.2485	2.35E-29	8.74E-29	cpm	-0.676612952	2.46E-22	G0.0015267;G0.0031011;G0.0006255;G0.0006338;G0.0006281	ATG35120.1	ABINA;ATABP6;ESD1;SUF3	actin-related protein 6		actin-like protein arp6
Sapur.0161657500.1	185.3040943	0.751284073	0.067153029	-11.2472	2.39E-29	8.87E-29	cpm	-0.702103125	1.28E-24		ATG01620.1	MED17	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein		import inner membrane translocase subunit TIM22
Sapur.0042155100.1	168.9094053	0.972072282	0.086764096	11.24168	2.42E-29	9.00E-29	cpm	0.678815065	1.94E-22		ATG27255.1	PHT3;3	phosphate translocator 3		phosphate carrier protein
Sapur.0061327200.1	5.913318872	-1.341785539	0.119356638	-11.2418	2.54E-29	9.43E-29	cpm	-0.724994621	6.07E-27		ATG32450.1		Pentatricopeptide repeat (PPR) superfamily protein		NA
Sapur.0161279700.2	10.80161758	0.518608150	0.097046158	11.24066	2.57E-29	9.55E-29	cpm	0.648822541	1.34E-20						NA
Sapur.0041658000.1	37.32618233	-2.426499417	0.216050233	-11.2312	2.87E-29	1.06E-28	cpm	-0.647383222	5.11E-20		ATG07150.2		Protein of unknown function (DUF567)		NA
Sapur.0020602000.2	7.998924241	-1.200201934	0.108378859	-11.2283	2.98E-29	1.10E-28	cpm	-0.673995527	1.89E-22	G0.0006662;G0.0003824	ATG33630.1		NAD(P)-binding Rossmann-fold superfamily protein		3-beta-hydroxy-delta5-steroid dehydrogenase
Sapur.0030681000.1	2.833058849	-2.292021991	0.201831168	-11.214	3.48E-29	1.29E-28	cpm	-0.657408208	6.06E-22		ATG49310.1		Protein of unknown function, DUF617		DUF617/28 domain protein
Sapur.0030247000.1	539.5719016	0.740659961	0.066002343	11.21152	3.58E-29	1.32E-28	cpm	0.629001163	1.10E-18	G0.0005515	ATG15760.1		Sterile alpha motif (SAM) domain-containing protein		SAM domain (sterile alpha motif) protein
Sapur.0192672500.1	589.1267679	0.440591495	0.039322292	11.20345	3.92E-29	1.45E-28	cpm	0.66092296	9.90E-22		ATG03140.1		Tudor/PWWP/MBT superfamily protein		PWWP domain protein
Sapur.0092581000.1	136.9638077	1.191852258	0.106418622	11.19969	4.09E-29	1.51E-28	cpm	0.665379079	1.99E-21	G0.0005515;G0.0051087	ATG17580.1	ATBAG4;BAG4	BCL-2-associated athanogene 4		BCL-2 binding anthanogene-1 protein, putative
Sapur.0161118300.1	101.9258664	-0.764828746	0.068219978	-11.1974	4.20E-29	1.55E-28	cpm	-0.664421539	2.52E-21	G0.0016887;G0.0005534;G0.0005885;G0.0004262;G0.0016021;G0.0006830	ATG82670.1	ATATM3;ATM3;ST1A1	ABC transporter family of the family protein		ABC transporter family of the family protein
Sapur.0010941000.1	247.674484	0.714707271	0.063811443	-11.1935	4.39E-29	1.62E-28	cpm	-0.627543837	1.51E-18		ATG25130.1		Uncharacterized conserved protein (UCP012943)		hypothetical protein
Sapur.0174444077	1.736144477	-1.183287924	0.173664113	-11.1924	4.41E-29	1.62E-28	cpm	-0.572345455	1.30E-12	G0.0007165;G0.0005515;G0.0043531	ATG38930.2		Disease resistance protein (TIR-NBS-LRR class) family		NA
Sapur.0061832000.1	1073.021987	-0.741717358	0.066279245	-11.1916	4.48E-29	1.66E-28	cpm	-0.689823437	1.67E-23	G0.0016020;G0.0015979;G0.0006253	ATG06520.1	PSBX	photosystem II subunit X		NA
Sapur.0161281600.1	170.8838805	-0.816138169	0.059168768	-11.1825	4.97E-29	1.83E-28	cpm	-0.662265067	5.21E-21		ATG20340.1				NA
Sapur.0131267000.2	25.88016066	-1.362175759	0.121818797	-11.182	5.00E-29	1.84E-28	cpm	-0.643186786	1.06E-19	G0.0016491;G0.0008152	ATG54190.1	PORA	protochlorophyllide oxidoreductase A		NADPH;protochlorophyllide oxidoreductase
Sapur.0020680700.3	7.079042313	-1.292293	0.115612527	-11.1778	5.24E-29	1.93E-28	cpm	-0.645513944	1.67E-19	G0.0004;G0.0005;G0.0003700;G0.0003677	ATG46060.1	ATHB-16;ATHB16;HB16	homeobox protein 16		homeobox leucine zipper protein
Sapur.0080807800.1	8.985808766	-1.003764015	0.106788725	-11.1774	5.26E-29	1.94E-28	cpm	-0.623616198	4.08E-19		ATG39100.1		Protein of unknown function, DUF437		DUF4228 domain protein
Sapur.0192017100.1	5.193683922	-2.783609667	0.15690276	-11.1753	5.34E-29	1.96E-28	cpm	-0.685408428	4.26E-22	G0.0007165;G0.0005515;G0.0043531	ATG36930.2		Disease resistance protein (TIR-NBS-LRR class) family		NA
Sapur.0060520500.1	4.93072906	-1.730571266	0.159524568	-11.1715	5.42E-29	2.07E-28	cpm	-0.727535438	3.28E-27	G0.0005114;G0.0051928;G0.0005680	ATG70050.1		Glucose-methanol-choline (GMC) oxidoreductase family protein		NA
Sapur.0020249600.1	1.557585544	3.401352988	0.304693029	11.17052	5.68E-29	2.09E-28	cpm	-0.544931671	1.60E-13	G0.0004668;G0.0004672	ATG45160.2				Serine/Threonine kinase domain protein
Sapur.0062685000.1	140.4473232	-0.68371444	0.065118876	-11.1682	5.77E-29	2.12E-28	cpm	-0.660051045	1.56E-22		ATG71777.1	BNS	Protein of unknown function (DUF1012)		hypothetical protein
Sapur.0061720000.2	21.38603444	0.951857792	0.085197056	11.16336	6.16E-29	2.27E-28	cpm	-0.78045508	1.88E-32	ATPK19;ATPK2;ATSER2;SER2	ATG08730.2	ATPK19	serine/threonine protein kinase 2		ribosomal protein S6 kinase, putative
Sapur.0012028700.1	304.3604733	1.306191212	0.117038292	11.16037	6.37E-29	2.34E-28	cpm	-0.575602021	1.12E-15		ATG06060.1	HMGB1;NFD03;NFD3	high mobility group B1		NA
Sapur.0162061400.2	2.907556738	2.460309689	0.220482762	11.15874	6.46E-29	2.38E-28	cpm	-0.545876654	1.45E-13	G0.0003077;G0.0005986	ATG35840.3		Succinate-CoA ligase(ADP-forming) beta-subunit family protein		succinate phosphate phosphatase
Sapur.0062032300.1	132.8737334	-0.556087243	0.049828333	-11.1579	6.91E-29	2.41E-28	cpm	-0.668284184	1.05E-22		ATG18380.1		Pentatricopeptide repeat (PPR) superfamily protein		PPR containing plant protein
Sapur.0120050600.1	1001.447256	-0.253886484	0.022755302	-11.1573	6.60E-29	2.43E-28	cpm	-0.668839564	4.62E-21	G0.0004668;G0.0005534;G0.0004672	ATG64720.1	CPK21	calcium-dependent protein kinase 21		calcium-dependent kinase
Sapur.0080136700.1	273.2149679	-0.541423948	0.048535765	-11.1553	6.74E-29	2.48E-28	cpm	-0.68310575	6.50E-23		ATG42310.1		CCP1-interacting protein-related		NA
Sapur.0042686600.1	175.2426494	-0.765645591	0.070787072	-11.154	6.85E-29	2.52E-28	cpm	-0.643853691	1.07E-19		ATG60645.1				hypothetical protein
Sapur.0086111200.1	122.1931795	-0.364464178	0.032680693	-11.1523	6.98E-29	2.57E-28	cpm	-0.678902797	1.23E-22	G0.0043565;G0.0006355;G0.0005634;G0.0003700	AT-HSFAB;HSFA8	heat shock transcription factor A8			heat shock transcription factor
Sapur.0102647100.1	64.83564684	-0.582583839	0.097875548	-11.1476	7.35E-29	2.70E-28	cpm	-0.679945568	6.93E-22	G0.0005515	ATG10580.1		Transducin/WD40 repeat-like superfamily protein		NA
Sapur.7004200.1	3021.025337	0.620639151	0.055679727	11.14659	7.44E-29	2.73E-28	cpm	0.629112149	1.11E-18	G0.0008810;G0.0006629;G0.0008889	ATG26660.1	GPDL2;MIH5;SHV3	PLC-like phosphodiesterase family protein		glycerophosphoryl diester phosphodiesterase family protein
Sapur.0051390000.1	101.4575274	0.379039415	0.053885116	11.14518	7.54E-29	2.77E-28	cpm	0.667618668	2.21E-22	G0.0006884;G0.0005855;G0.0005622	ATG88500.1		SNARE-like superfamily protein		NA
Sapur.0070207000.2	5.968763624	-0.401029881	0.125761812	-11.1403	7.98E-29	2.93E-28	cpm	-0.669134182	8.55E-22	G0.0005515;G0.0006468;G0.0004672	ATG65700.1	BAM1	Leucine-rich receptor-like protein kinase family protein		LRR receptor-like kinase
Sapur.7078500.1	6.017818174	-1.424908353	0.126263345	-11.1373	8.04E-29	2.95E-28	cpm	-0.654184965	5.06E-20		ATG66160.1	ATO	splicing factor ATO		NA
Sapur.0051189100.1	5.180519793	-1.935865571	0.173838055	-11.1366	8.32E-29	3.05E-28	cpm	-0.655214886	3.11E-20	G0016767	ATG67152.1		HXXXD-type acyl-transferase family protein		anthranilate N-hydroxycinnamoyl/benzoyltransferase, putative
Sapur.0180641000.1	229.0694579	-0.932261697	0.083706649	-11.1347	8.58E-29	3.12E-28	cpm	-0.705269086	6.30E-25		ATG44260.1		Plant protein of unknown function (DUF946)		vacuolar protein sorting-associated protein, putative
Sapur.0130272400.1	344.7740256	-0.100365151	0.088696477	-11.1339	8.58E-29	3.12E-28	cpm	-0.637619612	2.72E-19	G0.0055085;G0.0016020;G0.0015297;G0.0015238;G0.0008855	ATG68260.1		MATE efflux family protein		NA
Sapur.0051057500.1	65.79945665	1.367767431	0.118840651	11.13387	8.58E-29	3.15E-28	cpm	0.620497621	6.42E-18	G0.0005515	ATG19080.1		SWIB complex BAF60b domain-containing protein		upstream activation factor subunit spp27, putative
Sapur.0161884800.1	3448.108569	0.573183997	0.05518814	11.1329	8.79E-29	3.20E-28	cpm	0.617188207	8.77E-19	G0.0016020;G0.0006253	ATG17840.1	ABCG11;ATWBC11;COF1;O6	white-brown complex ABC transporter family protein		white-brown complex ABC transporter family protein
Sapur.0130132300.1	3.631941767	2.085661743	0.187312121	11.31516	8.81E-29	3.23E-28	cpm	-0.519189789	9.21E-18						hypothetical protein
Sapur.0161881000.1	8.406611348	2.220207193	0.200346652	11.1307	8.86E-29	3.25E-28	cpm	0.619966386	1.68E-17	G0.0016020;G0.0005515;G0.0016639;G0.0015927	ATG45190.1	ALDH7B4	aldehyde dehydrogenase family 7 protein		aldehyde dehydrogenase family 7 protein
Sapur.7108900.1	796.5404667	0.765857582	0.069163731	-11.1309	8.87E-29	3.25E-28	cpm	-0.679298826	2.49E-22		ATG52530.1		DNA-binding storekeeper protein-related transcriptional regulator		transcription regulator, putative
Sapur.0145126000.1	839.1611548	-0.457205224	0.06761903	-11.1218	9.83E-29	3.60E-28	cpm	-0.682060299	7.38E-23	G0.0016021;G0.0006468;G0.0005783	ATG42570.1		E-cell receptor-associated-like protein		E-cell receptor-associated-like protein
Sapur.0081551600.1	21.19135372	-0.019199536	0.091640122	-11.1218	9.83E-29	3.60E-28	cpm	-0.649737078	5.05E-20	G0.0006468;G0.0004672	ATG70520.1	CRK2	cysteine-rich RLK (RECEPTOR-like protein kinase) 2		cysteine-rich RLK (RECEPTOR-like protein kinase) 2
Sapur.0161247000.1	394.3409872	-0.466231532	0.042185193	-11.1216	9.85E-29	3.61E-28	cpm	-0.680970038	1.02E-23	G0.0008168;G0.0008152	ATG35660.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein		methyltransferase, putative
Sapur.0161010000.1	1903.887962	0.422188847	0.037966491	11.1203	9.99E-29	3.66E-28	cpm	0.645268964	7.41E-20		ATG51460.1		LMBR1-like membrane protein		LMBR1 family protein OsSlg0128200
Sapur.0106157200.1	5.630

Sapur.018G204300.1	9.62368287	3.91882831	0.178018456	10.77862	4.34E-27	1.54E-26	opsin	0.56349678	1.58E-14	GO:0046884;GO:0003677	ATSCG5520.1	ATCCD1ATNCED1.CCD1.NC	carotenoid cleavage dioxygenase 1	retinal pigment epithelial membrane protein
Sapur.016G204100.1	6.27584205	1.50965059	0.140112562	10.77669	4.44E-27	1.57E-26	opsin	0.62880551	1.16E-18	GO:0046884;GO:0003677	ATSCG5680.1		MADS-box transcription factor family protein	SRF-type transcription factor (DNA-binding and dimerization domain) protein
Sapur.016G241200.1	403.8842134	87.4068715138	0.140875116	10.77436	4.51E-27	1.61E-26	opsin	0.63193335	4.96E-23	GO:0055114;GO:0016491	ATSRG1;SRG1	senescence-related gene 1	flavonol synthase/flavanone 3-hydroxylase, putative	flavonol synthase/flavanone 3-hydroxylase, putative
Sapur.006G160800.1	46.8418254	6.60946157	0.05657006	-10.7736	4.59E-27	1.62E-26	opsin	-0.67611046	1.44E-22	GO:0005515	ATSDG6320.1	ATXR5;SDG18	SET domain protein 18	NA
Sapur.005G340800.1	4.72066263	1.02822087	0.140026771	-10.7732	4.61E-27	1.63E-26	opsin	-0.63060873	8.95E-19	GO:0009229;GO:0004417	ATSDH2B3.1		hydroxyethylthiazole kinase family protein	NA
Sapur.012G022300.1	987.758412	1.27584665	0.11839718	10.77302	4.62E-27	1.63E-26	opsin	0.65674532	9.72E-21		ATSGB23J2.2		Calcium-binding EF-hand family protein	calcium-binding protein CML27, putative
Sapur.017G204400.1	6.95349086	1.35408277	0.12397911	-10.7712	4.71E-27	1.66E-26	opsin	-0.64705857	5.41E-20	GO:0005515;GO:0042531	ATSGA3730.1		Disease resistance protein (CC-NBS-LRR class) family	NA
Sapur.018G224400.1	686.9475192	6.42220026	0.09205835	10.76881	4.81E-27	1.71E-26	opsin	0.65489611	1.48E-20		ATSC56010.1	AKT1;ATAKT1;KT1	K+ transporter 1	AKT1-like potassium channel protein
Sapur.003G062400.1	10.48349855	-1.36005388	0.126397481	-10.7671	4.92E-27	1.74E-26	opsin	-0.65616603	1.08E-20		ATSG31600.2	PTAC6	plastid transcriptionally active 6	hypothetical protein
Sapur.012G088300.1	224.6603692	42.5006192	0.095117742	10.7661	4.98E-27	1.76E-26	opsin	0.67970741	1.51E-22		ATSGP4740.1		Uncharacterized conserved protein yrf60	TIC protein 20-V, putative
Sapur.016G044500.4	6.88138554	1.19945671	0.11147720	10.7569	5.34E-27	1.88E-26	opsin	0.64962838	3.45E-20		ATSG12150.1			transmembrane protein, putative
Sapur.018G204500.4	4.97606027	1.26804184	0.1499129	10.7543	5.35E-27	1.88E-26	opsin	0.60234262	7.06E-17		ATSG12462.1		Transmembrane amino acid transporter family protein	NA
Sapur.006G092800.2	9.20612801	-1.38712842	0.138935899	-10.7582	5.42E-27	1.91E-26	opsin	-0.58796836	5.68E-16	GO:0006412;GO:0005840;GO:0005622;GO:0003735	ATSG54230.1		Ribosomal protein L17 family protein	SDS-ribosomal protein L17
Sapur.010G225400.1	537.8394658	81.8118209	0.15396117	10.7329	5.51E-27	1.98E-26	opsin	0.65604115	1.10E-20		ATSG7535.1		anthocyanin 5-aromatic acyltransferase, putative	NA
Sapur.005G045400.2	14.60670666	-0.99882129	0.092975382	-10.7543	5.68E-27	1.99E-26	opsin	-0.64818272	4.45E-20	GO:0009378;GO:0006310;GO:0006281	ATSG64580.1		AAA-type ATPase family protein	AAA-type ATPase family protein
Sapur.005G285800.1	301.4413604	38.2206436	0.092885449	10.7527	5.75E-27	2.01E-26	opsin	-0.61835016	6.68E-19		ATSG8140.1			integrin-membrane protein
Sapur.004G000100.1	193.3614552	-6.44877727	0.041751443	-10.7488	6.03E-27	2.12E-26	opsin	-0.68155295	8.86E-23		ATSG60870.1		Regulator of chromosome condensation (RCC1) family protein	regulator of chromosome condensation repeat protein
Sapur.013G100800.3	2.76192487	-2.06280261	0.19192035	-10.7483	6.03E-27	2.12E-26	opsin	-0.62887867	3.03E-18		ATSGD9910.1			hypothetical protein
Sapur.018G224900.1	29.24007593	7.05121705	0.107397834	-10.7467	6.09E-27	2.17E-26	opsin	-0.66977632	2.18E-17	GO:0006355;GO:0003700	ATERF_1;ERF-1	ATERF_1;ERF-1	ethylene responsive element binding factor 1	ethylene-responsive transcription factor 2
Sapur.010G086300.5	49.07518656	-0.68570981	0.062841732	-10.7407	6.55E-27	2.31E-26	opsin	-0.66319148	2.99E-21	GO:0016567;GO:0006402;GO:0005515	ATSG30030.1		ARM repeat superfamily protein	E3 ubiquitin ligase PUB14, putative
Sapur.003G041200.1	93.46378947	-2.00015365	0.075968812	-10.7384	6.68E-27	2.36E-26	opsin	-0.67997265	2.22E-22		ATSG31885.1		Protein of unknown function (DUF581)	DUF581 family protein
Sapur.001G059100.1	29.06266539	-0.93162942	0.086904985	-10.7383	6.73E-27	2.37E-26	opsin	-0.62731965	1.88E-18		ATSG20190.1			hypothetical protein
Sapur.013G200100.1	191.728057	-5.76587574	0.079413459	-10.7361	6.89E-27	2.42E-26	opsin	-0.67881005	1.50E-22	GO:0008950	ATSG21520.1		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress A-like protein
Sapur.013G106500.1	979.765688	6.46250456	0.041233833	10.73419	7.03E-27	2.47E-26	opsin	0.66728623	1.40E-21		ATSG34350.1			Lon protease-like protein, putative
Sapur.006G056000.1	49.46211583	6.81188209	0.075628241	10.7329	7.12E-27	2.51E-26	opsin	0.64050669	2.79E-19	GO:0005515	ATSNP03;NPR3	ATNPR3;NPR3	NPR1-like protein 3	NPR1/NIM1-like regulatory protein, putative
Sapur.004G240600.1	36.71534143	-0.90243671	0.094089933	-10.7318	7.32E-27	2.54E-26	opsin	-0.68054975	1.08E-22	GO:0005515;GO:0006468;GO:0004672	ATSG45800.1	MEE62	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.003G019200.1	37.19049415	-0.69621979	0.064882304	-10.7305	7.32E-27	2.57E-26	opsin	-0.67483068	3.31E-22	GO:0006412;GO:0005840;GO:0005622;GO:0003735	ATSG19730.1		Ribosomal L28e protein family protein	60S ribosomal protein L28
Sapur.013G125200.1	18.25626937	-0.56386689	0.422283547	-10.7292	7.41E-27	2.60E-26	opsin	-0.52624203	1.46E-12		ATSG63670.1		ankyrin repeat family protein	NA
Sapur.006G005000.1	46.4978257	-0.54522724	0.060145561	-10.7275	7.58E-27	2.66E-26	opsin	-0.65072245	2.95E-20		ATSG57062.1			transmembrane protein, putative
Sapur.017G041200.1	2.80126086	2.40522444	0.22621615	-10.7268	7.62E-27	2.68E-26	opsin	-0.61521873	1.01E-17	GO:0006355	ATSG3120.2	SNL1	SIN3-like 1	paired amphipathic helix Sin3-like protein, putative
Sapur.005G201400.1	63.22404881	1.58204171	0.148199991	-10.7236	7.89E-27	2.77E-26	opsin	-0.59370293	2.51E-16	GO:0005085;GO:0016021	ATSG47330.2		Major facilitator superfamily protein	sugar porter (SP) family MFS transporter
Sapur.012G100300.1	1.95166307	1.81899937	0.169698305	-10.7215	8.04E-27	2.82E-26	opsin	-0.58127947	1.46E-15		ATSG25040.1		UV-C-induced protein (UVR9407)	UV-C-like protein POPTR0047-823420 protein
Sapur.010G043300.1	57.18379948	-0.92316282	0.086046729	-10.7188	8.31E-27	2.92E-26	opsin	-0.62693976	4.13E-18	GO:0006355;GO:0005739;GO:0003690	ATSG08830.1		Mitochondrial transcription termination factor family protein	NA
Sapur.012G200100.1	86.05606937	-1.14710302	0.10702588	-10.7184	8.34E-27	2.93E-26	opsin	-0.68137001	9.38E-23		ATSG62915.1			NA
Sapur.011G007000.1	3.78089333	-1.90780373	0.178014218	-10.7172	8.46E-27	2.97E-26	opsin	-0.62672916	1.64E-18		ATSG19315.1			transmembrane protein, putative
Sapur.013G133200.1	15.28812895	-0.85492265	0.054122977	-10.7155	8.61E-27	3.02E-26	opsin	-0.68624586	2.28E-23	GO:0006468;GO:0004672	ATSG60460.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.017G075200.1	31.86885844	-0.77261459	0.071831044	-10.7138	8.76E-27	3.07E-26	opsin	-0.68798763	2.43E-23		ATSG73170.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.003G039900.1	836.2574657	6.34370586	0.022748231	10.71381	8.77E-27	3.07E-26	opsin	0.67849963	1.62E-22	GO:0006468;GO:0005524;GO:0004672	ATSG60940.1	SNRK2-10;SNRK2-10;SRK2B	SNF1-related protein kinase 2.10	Serine/Threonine kinase domain protein
Sapur.007G122900.1	11.35722989	-1.15161468	0.107588972	-10.7012	1.08E-26	3.52E-26	opsin	-0.63009741	9.56E-19					NA
Sapur.004G063900.1	25.8178948	-1.15767385	0.108171129	-10.6998	1.02E-26	3.57E-26	opsin	-0.64790722	4.67E-20					hypothetical protein
Sapur.003G009900.2	15.46280519	-1.34913274	0.126105191	-10.6986	1.03E-26	3.62E-26	opsin	-0.64399052	5.10E-20		ATSG22930.1		T-complex protein 11	T-complex protein
Sapur.010G184900.1	213.2248915	0.35816725	0.03347553	10.6975	1.05E-26	3.66E-26	opsin	-0.66635296	1.08E-21		ATSG04440.1		Protein of unknown function (DUF2997)	RAP annotation release 2, galactose-binding-like domain protein
Sapur.006G066000.1	126.8224904	5.70067294	0.074056149	10.6949	1.06E-26	3.70E-26	opsin	0.61155677	1.83E-17		ATSG18661.1			NA
Sapur.004G171200.1	93.8950014	6.39158849	0.068092212	10.69641	1.08E-26	3.70E-26	opsin	0.63179071	2.59E-19		ATSG63570.1		Lung seven transmembrane receptor family protein	lung seven transmembrane receptor family protein
Sapur.003G038800.1	565.9648889	6.44438486	0.041445103	10.69624	1.09E-26	3.70E-26	opsin	0.62022546	4.62E-18	GO:0046983	ATSG44432.2	bHLH104	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	helix loop helix DNA-binding domain protein, putative
Sapur.006G230400.1	203.8262223	-0.43253459	0.04046192	-10.6899	1.13E-26	3.87E-26	opsin	-0.67760664	1.28E-21		ATSG60560.1		SWIM zinc finger family protein	plant/FRAG-10 protein, putative
Sapur.016G184600.1	179.1498087	6.05972281	0.061719943	-10.689	1.13E-26	4.01E-26	opsin	-0.66473216	2.94E-21	GO:0008168	ATSG26180.2		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NDL1/NOP2/sun family protein
Sapur.016G027300.1	47.26126251	5.98418125	0.08828195	-10.6878	1.17E-26	4.08E-26	opsin	-0.62605455	1.18E-18	GO:0000266	ATSG70590.1	BIG/FH;FIS1A	Transmembrane protein	Transmembrane protein
Sapur.014G058000.1	5.96347769	-1.58719969	0.148539756	-10.6849	1.20E-26	4.19E-26	opsin	-0.64982408	3.24E-20		ATSG01860.1	PFC1	Ribosomal RNA adenine dimethylase family protein	ribosomal RNA small subunit methyltransferase A
Sapur.005G134300.1	42.69820605	-1.15151448	0.109068931	-10.6801	1.26E-26	4.41E-26	opsin	-0.64676165	3.43E-20		ATSG61630.1	ATSIP17;ATEXPA17;ATHDA9	expansin A17	alpha-expansin
Sapur.006G177500.1	390.618804	0.32664551	0.030575496	10.67669	1.31E-26	4.57E-26	opsin	0.64053848	1.66E-19	GO:0005524	ATSG17530.1	RPT1A	regulatory particle triple-A 1A	26S proteasome regulatory subunit
Sapur.019G051100.1	92.2318314	0.32164224	0.03016809	10.6734	1.36E-26	4.75E-26	opsin	-0.64492182	4.36E-20		ATSG65120.1		Protein of unknown function (DUF 3339)	transmembrane protein, putative
Sapur.016G043600.1	205.9469551	-0.41341846	0.038733856	-10.6733	1.36E-26	4.75E-26	opsin	-0.64658124	5.88E-20	GO:0003674	ATSG57910.1		D111/G-patch domain-containing protein	DEAH box splicing factor-binding site protein
Sapur.013G135200.1	159.9833122	-0.42388729	0.038183379	-10.6319	2.11E-26	7.35E-26	opsin	-0.61811656	5.46E-18	GO:0008168;GO:0008152	ATSG16030.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase
Sapur.008G093000.2	14.60925012	0.83885278	0.076836269	-10.668	1.44E-26	5.01E-26	opsin	-0.65219029	2.07E-20		ATSG16860.1		Ubiquitin-specific protease family C19-related protein	transmembrane protein, putative
Sapur.003G038800.1	406.2625208	0.39238969	0.027539492	10.6659	1.47E-26	5.12E-26	opsin	0.64338404	2.86E-21	GO:0008138;GO:0006470	ATSG40550.1	DSPTP1E;IBR5	Jnoble-2-butanol and protein tyrosine phosphatase, putative	dual specificity protein phosphatase, putative
Sapur.15WG146200.1	5364.454879	0.52761875	0.049483332	10.66256	1.52E-26	5.31E-26	opsin	0.61292597	1.44E-17		ATSG48890.1	ATMAPR2;ATMPR2;NAPR3;N	membrane-associated progesterone binding protein 3	membrane steroid-binding protein
Sapur.018G204800.2	7.83977816	-1.34507047	0.11885404	-10.6589	1.58E-26	5.52E-26	opsin	-0.65427216	1.53E-20	GO:0003676	ATSG36160.1		Alba DNA/RNA-binding protein	nucleic acid-binding protein
Sapur.006G186700.2	3.45255756	-0.65175052	0.181618313	-10.6575	1.61E-26	5.60E-26	opsin	-0.67020812	8.04E-22		ATSG36465.1			hypothetical protein
Sapur.004G022900.1	9.40264212	1.20339665	0.206763274	10.65619	1.63E-26	5.68E-26	opsin	0.52953006	9.99E-13		ATSG61260.1		Protein of unknown function (DUF761)	NA
Sapur.005G138800.1	2132.528731	0.43492265	0.034932465	10.64963	1.75E-26	6.09E-26	opsin	0.65405641	5.44E-20	GO:0005515	ATSG9150.1	ATSIUR9I6	non-ATP hydrolase subunit 9	26S proteasome non-ATPase regulatory subunit 11
Sapur.009G075500.1	117.6761547	0.49928745	0.046887313	-10.6487	1.77E-26	6.15E-26	opsin	-0.64158788	6.62E-20		ATSG15260.1	ATTIC2;CLA5;PCL1;TIC21	translocon at inner membrane of chloroplasts 21	TIC21
Sapur.016G027300.1	68.16179629	5.01356057	0.066861913	10.64815	1.78E-26	6.18E-26	opsin	-0.53840078	1.07E-15		ATSG58090.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.003G075300.1	31.26270215	1.25188574	0.11418587	10.64794	1.78E-26	6.20E-26	opsin	0.62818195	1.26E-18					hypothetical protein
Sapur.006G034700.1	7.80688018	1.68124222	0.156826273	10.6369	1.87E-26	6.51E-26	opsin	0.64376476	3.91E-19		ATSG19820.1	emb2234	ARM repeat superfamily protein	NA
Sapur.002G056500.3	17.88196239	-0.67439571	0.1009518	-10.6412	1.92E-26	6.66E-26	opsin	-0.67589904	5.22E-22		ATSG48880.1	TBL7	TRICHOME BIREFRINGENCE-LIKE 7	Pm5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.004G064500.2	2.08491541	-2.33526207	0.21947156	-10.6403	1.93E-26	6.72E-26	opsin	-0.87349214	1.51E-49	GO:0004648;GO:0003677;GO:0005515	ATSG37060.1		Leucine-rich repeat protein kinase family protein	receptor kinase, putative
Sapur.002G076300.1	55.84515671	1.49346079	0.140367679	10.63989	1.94E-26	6.75E-26	opsin	0.59158271	3.40E-16	GO:0045454;GO:0005515	ATSG51681.1		tetratricopeptide repeat (TPR)-containing protein	heat shock protein binding protein, putative
Sapur.016G154100.1	17.74046618	-0.05046447	0.078570475	-10.6366	2.01E-26	7.00E-26	opsin	-0.62802548	1.16E-18		ATSG2110.2			CCP-like protein, putative
Sapur.019G022700.1	13.44910054	-0.03387761	0.07355577	-10.6352	2.04E-26	7.08E-26	opsin	-0.63893401	2.17E-19	GO:0016787	ATSG47282.1		Calcineurin-like metallo-phosphoesterase superfamily protein	manganese-dependent ADP-ribose/CDP-alcohol diphosphatase
Sapur.004G058100.1	18.96556473	1.06100143	0.099776301	10.63464	2.06E-26	7.14E-26	opsin	0.6110921	1.91E-17					NA
Sapur.018G011500.1	14.15016417	-2.21387279	0.208183379	-10.6319	2.12E-26	7.35E-26	opsin	-0.57885537	2.66E-15	GO:0055114;GO:0020037;GO:0006979;GO:0004601	ATSG31760.1		Peroxidase superfamily protein	peroxidase
Sapur.011G127300.1	48.51271997	-0.89245756	0.083945587	-10.631	2.14E-26	7.42E-26	opsin	-0.63817658	2.46E-19		ATSG00220.1	AAP2	amino acid permease 2	NA
Sapur.004G000400.1	57.83229966	-2.01607164	0.206822114	-10.6288	2.16E-26	7.50E-26	opsin	-0.66855463	1.04E-21		ATSG01450.1		Pathogen-responsive alpha-thaumatin superfamily protein	thaumatin-like protein
Sapur.002G012300.1	2.86035527	-2.30179348	0.216620608	-10.6258	2.26E-26	7.84E-26	opsin	-0.62492778	2.19E-18	GO:0042578;GO:0030134;GO:0005622;GO:0005515	ATSG02030.1	EMB2739;HAP15	PAM domain (PCI/PINT associated module) protein	phosphoenolpyruvate carboxylase
Sapur.006G180800.1	436.1057579	0.66384842	0.09997525	-10.622	2.35E-26	8.16E-26	opsin	-0.68088382	2.61E-23	GO:0015377;GO:0008904;GO:0008969	ATSG08750.1	ATPPCK;PPC4	phosphoenolpyruvate carboxylase kinase 4	kelch repeat F-box protein
Sapur.002G032200.1	202.8263499	0.77365343	0.068492331	10.61966	2.41E-26	8.37E-26	opsin	0.65960306	6.11E-15	GO:0005515	ATSG03030.1		Galactose oxidase/kelch repeat superfamily protein	kelch repeat F-box protein
Sapur.006G149800.1	1346.330837	-0.35200741	0.03348855	-10.6192	2.43E-26	8.41E-26	opsin	-0.65472722	1.39E-20		ATSG07020.1		proline-rich family protein	hypothetical protein
Sapur.013G067800.1	35.0669166	-0.55372455	0.052439324	-10.6181	2.46E-26	8.46E-26	opsin	-0.66042108	4.98E-21	GO:0005515	ATSG07610.1		F-box family protein	F-box protein interaction domain protein
Sapur.016G179600.1	5.65305515	-2.42708275	0.228588134	-10.6165	2.47E-26	8.54E-26	opsin	-0.55397671	4.07E-14		ATSG48800.1			NA
Sapur.002G048300.1	59.1418813	-0.41407151	0.132968748	-10.6173	2.48E-26	8.57E-26	opsin	-0.62688060	1.97E-18		ATSG02462.1	FLI	Protein kinase family protein with ARM repeat domain	NA
Sapur.018G081300.1	781.5156881	0.50139369	0.047241652	10.61338	2.58E-26	8.94E-26	opsin	0.65266412	2.02E-20	GO:0007165	ATSG3960.1	ATCP9KLCP9LG;SIP3;SNRK3.	SOI2-interacting protein 3	CBL-interacting Serine/Threonine-kinase
Sapur.019G085800.1	760.9804694	6.76680556	0.072263164	10.6118	2.63E-26	9.11E-26	opsin	0.62266062	3.96E-18		ATSG45570.1	TBL39	TRICHOME BIREFRINGENCE-LIKE 39	Pm5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.004G008700.2	5.67925862	-2.29893158	0.12245517	-10.6071	2.74E-26	9.56E-26	opsin	-0.64843143	2.20E-21	GO:0008168	ATSG06370.1		Met-10+ like family protein / kelch repeat-containing protein	tRNA wybutosine-synthesizing protein 2/2/4
Sapur.003G073200.1	23.20079422	-1.01378519	0.09015688	-10.605	2.83E-26	9.78E-26	opsin	-0.63193551	5.68E-19	GO:0008233;GO:0006508;GO:0004190	ATSG03220.1		Eukaryotic aspartyl protease family protein	aylglucosamine-specific endoglucanase inhibitor protein, putative
Sapur.007G130800.1	176.406021	-0.76782485	0.07240778	-10.6042	2.85E-26	9.86E-26	opsin	-0.63094205	9.46E-19	GO:0005515	ATSG59940.1		Galactose oxidase/kelch repeat superfamily protein	kelch repeat F-box protein
Sapur.013G085300.1	1.85715764	-3.76322308	0.354065123	10.60367	2.87E-26	9.91E-26	opsin	-0.54860018	2.01E-13	GO:0007165;GO:0005515	ATSG16690.2	RLM3	disease resistance protein (TIR-NBS class), putative	NA
Sapur.011G178000.1	26.07518813	-0.92765143	0.087509769	-10.6028	2.89E-26	9.99E-26	opsin	-0.63502957	4.19E-19		ATSG65290.1		ubiquitin family protein	ubiquitin family protein
Sapur.003G264600.1	527.7448822	-0.57588374	0.054326224	-10.6008	2.95E-26	1.02E-25	opsin	-0.6333473	5.55E-19	GO:0006355;GO:0003677	ATSG7320.1	ANAC002;ATAF1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC transcription factor, putative
Sapur.004G000500.1	682.1416418	-0.26896564	0.019675738	-10.5987	2.96E-26	1.02E-25	opsin	-0.64727292	1.36E-20	GO:0005515	ATSGC2F14.C2F8C3.MK.E9	Proteasome component (PC) domain protein	proteasome component (PC) domain protein	COP9 signalosome complex subunit 4
Sapur.016G210000.6	18.39538556	-1.37322073	0.104693837	-10.5952	3.14E-26	1.08E-25	opsin	-0.65161847	1.73E-20		ATSG7260.1		ARM repeat superfamily protein	armadillo repeat protein, putative
Sapur.013G080800.1	54.56412186	-0.7917594	0.08526045	-10.5892	3.18E-26	1.17E-25	opsin	-0.64815101	4.47E-20	GO:0005885;GO:0016021	ATSG18000.1		Major facilitator superfamily protein	UNC93b-like protein TLC1.D1c
Sapur.003G076500.1	3.07634796	2.23703133	0.211387773	10.58781	3.39E-26	1.17E-25	opsin	0.57530323	2.25E-15	GO:0055114;GO:0016616;GO:0016491;GO:0019752	ATSG17260.1		Lactate/malate dehydrogenase family protein	L-lactate dehydrogenase
Sapur.015G072400.1	24.78889974	0.96210888	0.093743338	10.5869	3.52E-26	1.22E-25	opsin	0.61464261	1.42E-20					hypothetical protein
Sapur.008G149800.4	5.85024886	5.59656383	0.15091905	-10.5796	3.70E-26	1.28E-25	opsin	-0.67616507	2.36E-22		ATSG7600.2		Phototropic-responsive NPH3 family protein	BTB/POZ domain protein
Sapur.018G181000.5	14.94871626	-1.31062934	0.12389046	-10.579	3.73E-26	1.29E-25	opsin	-0.62604816	4.66E-18	GO:0045454;GO:0015035;GO:0006662	ATSG07700.1		Thioredoxin superfamily protein	thioredoxin-like protein
Sapur.018G029700.1	51.69661019	-1.05405855	0.1049919	-10.5789	3.73E-26	1.29E-25	opsin	-0.63595761	5.01E-19	GO:0005634	ATSG61470.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	NA
Sapur.003G058800.1	73.32036445	-1.06806549	0.108471117	-10.5784	3.81E-26	1.32E-25	opsin	-0.63183857	4.54E-19		ATSG35570.1		Galactosyltransferase family protein	dolichol-phosphate mannosyltransferase, putative
Sapur.004G164800.1	592.1450621	0.33615382	0.0317941	10.57635	3.84E-26	1.32E-25	opsin	0.66913035	8.95E-22	GO:0016192;GO:0006886	ATSG8190.1	ATVAM2;ATVPS41;VAM2.VP	vacuolar protein sorting 41	vacuolar protein sorting-associated-like protein
Sapur.012G090100.1	170.9899972	1.95998545	0.18534869	10.57472	3.90E-26	1.35E-25	opsin	0.53215256	7.36E-13	GO:0043531	ATSG14470.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.016G080800.1	9.39641163	-1.01520088	0.096061155	-10.5716	4.04E-26	1.39E-25	opsin	-0.66225572	3.57E-21		ATSG65481.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.011G168300.3	5.21243879	-1.71299582	0.162031295	-10.5708	4.07E-26	1.40E-25	opsin	-0.6578821	7.91E-21	PRI	ATSG15840.3	PRI	post-illumination chlorophyll fluorescence increase, putative	post-illumination chlorophyll fluorescence increase, putative
Sapur.003G190000.8	-7.66724285	-1.21231786	0.114703145	-10.5682	4.14E-26	1.42E-25	opsin	-0.66087138	1.62E-17	GO:0003677	ATSG18820.1			endonuclease, putative
Sapur.005G196900.1	505.6904918	0.87408429	0.082701823	10.56911	4.14E-26	1.43E-25	opsin	0.73965713	1.91E-28		ATSG8420.1		DC1 domain-containing protein	nucleotrodan, putative
Sapur.005G208300.1	111.7618954	0.49822961	0.056002863	-10.5689	4.15E-26	1.43E-25	opsin	-0.64320208	1.52E-19		ATSG8700.1			transmembrane protein, putative
Sapur.018G039900.1	4.47827049	2.67137876	0.34700545	10.56763	4.20E-26	1.45E-25	opsin	0.68021092	2.00E-10	GO:0005515	ATSG15270.1		Plant regulator RWP-RK family protein	transcription factor, putative
Sapur.003G070500.1	1660.076063	0.54327371	0.051984784	10.56687	4.23E-26	1.46E-25	opsin	0.61358273	1.12E-17	GO:0006355;GO:0004252	ATSG14562.1		Subtilisin family protein	subtilisin-like protease
Sapur.016G242400.1	21.3007115	1.02976602	0.09746787	10.56502	4.33E-26	1.49E-25	opsin	0.61336958	1.40E-17	GO:0005524;GO:0005515	ATSG10780.1		LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.011G194000.1	20.44795521	-0.89769168	0.08501507	-10.5621	4.46E-26	1.54E-25	opsin	-0.64201116	1.16E-19					hypothetical protein
Sapur.003G075200.1	12.68160972	-1.31318216	0.12607782	10.5587	4.63E-26	1.59E-25	opsin	0.59197405	3.35E-16					NA
Sapur.017G127700.1	17.00243965	-0.06188858	0.100908251	-10.5581	4.66E-26	1.60E-25	opsin	-0.66175479	2.90E-21		ATSG14330.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.013G201200.1	604.2496426	0.52197109	0.024097578	-10.5564	4.75E-26	1.63E-25	opsin	-0.61252248	2.58E-20		ATSG46060.1		PRP38 family protein	PRP38 family protein
Sapur.007G049100.1	343.4139161	0.57069701	0.054007064	10.549	5.13E-26	1.77E-25	opsin	0.63880091	1.86E-19	GO:0016567;GO:0006402;GO:0005515	ATSG23140.2		RING/U-box superfamily protein with ARM repeat domain	U-box protein
Sapur.015G240400.1	15.53024814	0.79751794	0.108062356	-10.5487	5.15E-26	1.77E-25	opsin	-0.67728378	7.25E-22		ATSG60670.1		PLATZ transcription factor family protein	zinc ion-binding protein, putative
Sapur.015G201900.1	31.99463883	0.76688409	0.072654531	-10.5484	5.17E-26	1.78E-25	opsin	-0.63417195	4.86E-19		ATSG49830.1	EXO84B	exocyst complex component 84B	exocyst complex component 84B
Sapur.004G000600.1	1.09847476	1.00000000	0.138119664	10.54197	5.19E-26	1.79E-25	opsin	0.61319664	2.01E-17		ATSG45181.1		ARM repeat superfamily protein	NA
Sapur.018G058800.1	116.8010427	0.08132785	0.102637773	10.53434	6.00E-26	2.06E-25	opsin	0.60200763	7.47E-17		ATSG61640.1	AGP20;ARAGP20	arabinogalactan protein 20	transmembrane protein, putative
Sapur.006G143800.1	188.1556647	0.53237457	0.05368715	10.5384	6.06E-26	2.08E-25	opsin	-0.64750916	4.61E-20	GO:0008612	ATSG65030.1	DHS;ZGA2	deoxyhypusine synthase	deoxyhypusine synthase
Sapur.013G072800.1	1144.911662	0.38375959	0.036443361	-10.5308	6.23E-26	2.14E-25	opsin	-0.68420281	5.22E-23	GO:0016021;GO:0006952	ATMLO1;MLO1	Seven transmembrane MLO family protein	Seven transmembrane MLO family protein	MLO-like protein
Sapur.003G152400.1	4821.446542	1.80706527	0.095602248	10.52701	6.49E-26	2.23E-25	opsin	0.63168492	2.79E-19	GO:0055114;GO:0050661;GO:0050660;GO:0004499	ATSBP93J1	YLC10	Flav

Sapur.01G2239100.1	451.8745885	-0.27016737	0.036470636	-10.2055	1.87E-24	6.21E-24	cpen	-0.625514566	1.99E-18	ATSG50640.1	hypothetical protein
Sapur.007G011300.1	49.49145804	0.516879215	0.050671763	-10.2005	1.97E-24	6.54E-24	cpen	-0.673043853	6.85E-22	ATSG36430.1	Plant protein of unknown function (DUF247)
Sapur.006G145400.1	22.27616327	0.214080659	0.021000659	-10.1943	2.10E-24	6.97E-24	cpen	0.602032088	7.10E-17	GO:0005085,GO:0016020,GO:0051297,GO:0051338,GO:0006855	MATE efflux family protein
Sapur.008G096300.1	894.8828514	0.566256161	0.05555519	10.19328	2.12E-24	7.04E-24	cpen	0.591531749	3.42E-16		
Sapur.010G169800.1	562.3130837	0.380107079	0.037296878	10.1927	2.14E-24	7.08E-24	cpen	-0.63523011	4.05E-19	GO:0006796,GO:0005737,GO:0044237,GO:0000287	pyrophosphatase 6
Sapur.006G107400.1	103.7074025	-0.595537801	0.058468006	-10.1857	2.30E-24	7.60E-24	cpen	-0.652791058	1.97E-20		prolamine P1 family protein
Sapur.002G029400.1	110.074759	1.2962021	0.127267651	10.18485	2.32E-24	7.67E-24	cpen	0.573936341	4.14E-13	GO:0005114,GO:0020037,GO:0016705,GO:0005506	cytochrome P450, family 83, subfamily B, polypeptide 1
Sapur.003G007300.1	15.15145037	0.946131885	0.092959131	-10.178	2.49E-24	8.22E-24	cpen	-0.62291009	1.86E-08		ubiquitin-like domain CTD phosphatase, putative
Sapur.003G021900.2	6.817682383	-1.262521585	0.124097874	-10.1736	2.60E-24	8.60E-24	cpen	-0.634596481	4.51E-19	GO:0016787	purple acid phosphatase 12
Sapur.7G018800.1	32.64180937	0.587662602	0.057846222	10.17009	2.76E-24	9.11E-24	cpen	0.602021288	9.70E-17	ATCBM1,ATKP01,HIT2,KPO	exportin 1A
Sapur.005G153500.1	124.1034432	-0.44802622	0.044071737	-10.1646	2.85E-24	9.42E-24	cpen	-0.642461227	2.11E-19	GO0080270	DHHC-type zinc finger family protein
Sapur.009G151700.2	11.45078542	0.917382211	0.090207163	10.1584	3.01E-24	9.93E-24	cpen	-0.622302311	1.47E-18		E1 ubiquitin-protein ligase, putative
Sapur.003G141200.1	4.164410011	-1.714839992	0.168862092	10.15521	3.14E-24	1.04E-23	cpen	0.60051273	9.31E-17	GO0005509,GO:0016021,GO:0004674,GO:0003047,GO:0004468,GO:0004672	wall-associated receptor kinase-like protein, putative
Sapur.006G205000.2	19.23129271	-0.588230822	0.058000127	-10.1529	3.28E-24	1.08E-23	cpen	-0.619150149	5.16E-18		uridylyltransferase
Sapur.009G038500.1	262.4695402	0.874287571	0.086164421	10.14663	3.43E-24	1.13E-23	cpen	0.59853892	1.22E-16		hypothetical protein
Sapur.003G045700.1	2193.153087	-0.95015853	0.094488347	-10.1476	3.61E-24	1.19E-23	cpen	0.62032963	2.32E-19	GO0005515,GO:0006468,GO:0004672	LRR receptor-like kinase
Sapur.006G237800.1	57.8026794	0.50601018	0.058256627	10.13756	3.78E-24	1.24E-23	cpen	0.608128688	2.99E-17		WRKY family transcription factor
Sapur.010G243600.2	5.844489139	-1.454878899	0.145468384	-10.1338	3.91E-24	1.29E-23	cpen	-0.617581515	7.08E-19		plastid developmental protein DAG, putative
Sapur.005G051100.1	436.8662741	0.591691692	0.058050655	10.11083	4.31E-24	1.42E-23	cpen	-0.645027618	1.90E-20	GO0005515	RNA polymerase II carboxy-terminal domain phosphatase-like protein, putative
Sapur.018G101100.1	589.191999	0.315168727	0.030942943	10.13377	3.91E-24	1.29E-23	cpen	0.62805396	1.32E-18	GO0016887,GO:0005524	phosphate ABC transporter ATP-binding protein
Sapur.7G046100.1	1.137962883	2.425425204	0.239006879	10.1045	4.09E-24	1.32E-23	cpen	0.569838923	5.21E-14		NA
Sapur.017G079500.1	15.69655608	2.247217772	0.221820276	10.13103	4.02E-24	1.32E-23	cpen	0.58434258	7.13E-16		Malectin/receptor-like protein kinase family protein
Sapur.006G176400.1	71.56832052	0.671531607	0.066462149	10.1027	4.14E-24	1.37E-23	cpen	-0.676478916	2.40E-22		zinc or iron-chelating domain protein, putative
Sapur.003G145300.1	178.3044647	0.489398883	0.048313621	-10.1355	4.26E-24	1.40E-23	cpen	-0.643991751	9.20E-20		NA
Sapur.003G007700.1	2.804667212	-2.362605819	0.231418575	-10.1222	4.40E-24	1.45E-23	cpen	-0.748362421	1.30E-17		Arabidopsis protein of unknown function (DUF241)
Sapur.010G142600.1	179.5114622	-1.259189877	0.124664437	-10.1183	4.58E-24	1.51E-23	cpen	-0.612236432	5.60E-17		early responsive to dehydration protein, putative
Sapur.016G088900.1	8.820831882	1.485961236	0.146889459	10.11604	4.68E-24	1.54E-23	cpen	0.598322209	1.28E-16	GO0009931,GO:0007165,GO:0006159	serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' protein
Sapur.012G160500.1	82.76161607	-0.645234101	0.057338873	-10.1159	4.79E-24	1.58E-23	cpen	-0.677297245	5.91E-22	GO0046564,GO:0006468,GO:0005524,GO:0004672	lectin protein kinase family protein
Sapur.010G009200.1	249.1374226	0.361613341	0.035795461	10.11386	4.81E-24	1.58E-23	cpen	0.638538936	2.33E-19	GO0055114,GO:0016491,GO0016787	Gro/S-like zinc-binding alcohol dehydrogenase family protein
Sapur.007G123200.1	22.70776373	-0.902224	0.08925585	-10.1124	4.87E-24	1.60E-23	cpen	-0.61518812	1.01E-17	GO0003700,GO0009058	Tyrosine transaminase family protein
Sapur.003G167700.1	279.1950107	1.503258897	0.148720425	-10.1079	5.10E-24	1.67E-23	cpen	-0.553672222	5.61E-14	GO0046564,GO:0006468,GO:0005524,GO:0004672	receptor-like protein kinase 1
Sapur.005G206500.1	119.5450449	-0.365261428	0.036006879	-10.1045	5.24E-24	1.73E-23	cpen	-0.614164238	1.19E-17	GO0003700,GO0006355	FAR1-related sequence protein
Sapur.017G112100.1	26.53972869	1.918661584	0.189692455	10.10343	5.33E-24	1.75E-23	cpen	0.52147667	2.51E-12	GO0005114,GO0016491	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.008G028300.1	215.591876	0.417162261	0.041292266	-10.1027	5.37E-24	1.76E-23	cpen	-0.622328607	6.66E-19		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.003G069100.1	391.6947712	0.504363727	0.049931128	-10.1008	5.48E-24	1.80E-23	cpen	-0.605291825	4.58E-17		Ankyrin repeat family protein
Sapur.005G201500.1	11.79134243	0.968000192	0.097000966	10.1026	5.51E-24	1.81E-23	cpen	0.613204657	4.97E-17	GO0006355,GO:0003677	NAC domain containing protein 90
Sapur.15WG121300.2	10.98808429	-0.191871143	0.019197091	-10.1076	5.57E-24	1.83E-23	cpen	-0.629307184	1.88E-17		signal recognition particle-related / SRP-related
Sapur.019G087400.1	107.0674227	-0.644621134	0.063984111	-10.0974	5.67E-24	1.86E-23	cpen	-0.628805123	1.57E-18		ARM repeat superfamily protein
Sapur.016G280500.3	12.19969958	-0.853910246	0.092231036	-10.0955	5.78E-24	1.89E-23	cpen	-0.580091995	1.70E-15		NA
Sapur.005G207300.1	4.480013635	2.855937869	0.28324497	10.09493	5.82E-24	1.90E-23	cpen	0.547863119	1.12E-11		Mitochondrial ribosomal protein L27
Sapur.009G151200.1	193.1483251	-0.940301182	0.079636747	-10.0934	5.91E-24	1.94E-23	cpen	-0.642629298	1.34E-20	GO0008408,GO:0006139,GO:0003676,GO:0006260,GO:0003887,GO:0003677	DNA polymerase I
Sapur.016G201700.1	114.4651504	0.595824868	0.059057528	-10.0923	5.97E-24	1.96E-23	cpen	-0.626550862	1.68E-18		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.006G146400.1	8770.844884	-0.577291259	0.057234759	-10.0921	5.98E-24	1.96E-23	cpen	-0.622326008	2.12E-18	GO0016020,GO:0009765	light harvesting complex of photosystem II 5
Sapur.010G030600.1	115.3372448	0.464733949	0.046046699	10.09201	5.98E-24	1.96E-23	cpen	0.52147667	6.51E-16		Domain of unknown function (DUF23)
Sapur.003G083900.1	23.54019015	-0.752806379	0.0726275	-10.0907	6.07E-24	1.99E-23	cpen	-0.633930601	6.80E-19	GO0070617,GO:0005875	Dynein light chain type 1 family protein
Sapur.008G103200.1	9.26075833	1.704869946	0.168988132	10.08898	6.18E-24	2.02E-23	cpen	0.506060142	1.29E-11		fasciclin-like arabinogalactan protein, putative
Sapur.7G57900.1	19.99204943	0.856879071	0.085118887	10.08738	6.28E-24	2.05E-23	cpen	0.668792294	1.05E-21		exportin 1A
Sapur.005G038700.1	24.06514578	0.775243486	0.076844122	-10.0871	6.30E-24	2.06E-23	cpen	-0.605631153	4.36E-17		ATP binding;nucleic acid binding;helicases
Sapur.001G135900.9	25.35710413	-0.691549884	0.068600045	-10.0808	6.72E-24	2.19E-23	cpen	-0.636691244	3.18E-19		endonuclease, putative
Sapur.016G125000.1	123.5450810	-0.252588472	0.025067197	-10.0798	6.80E-24	2.22E-23	cpen	-0.72668875	4.74E-27	GO0008168	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.7G06800.1	41.57228905	-0.465515651	0.046192443	-10.0777	6.93E-24	2.26E-23	cpen	-0.627786837	1.38E-18		Mitochondrial ribosomal protein L27
Sapur.004G154600.1	29.00048855	-0.625000192	0.058650105	-10.0759	7.06E-24	2.31E-23	cpen	-0.648218566	4.42E-20		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.003G136300.2	9.729442622	-0.082419549	0.107446379	-10.0738	7.22E-24	2.36E-23	cpen	-0.617501501	7.54E-18		Ribosomal RNA processing Brix domain protein
Sapur.5G018800.1	87.53157642	-0.329192202	0.04064801	-10.0717	7.50E-24	2.45E-23	cpen	-0.643410107	1.05E-19	GO0008270	DHHC-type zinc finger family protein
Sapur.15WG011800.1	795.9979098	-0.499126059	0.049565801	-10.0699	7.51E-24	2.45E-23	cpen	-0.642343013	6.24E-20		HSP20-like chaperones superfamily protein
Sapur.015G031500.1	35.75533897	0.612241429	0.061885345	10.0678	7.63E-24	2.50E-23	cpen	-0.656304879	9.36E-21		Pentatricopeptide repeat (PPR)-like superfamily protein
Sapur.018G091300.1	17.85094656	-0.95901729	0.095261508	-10.0672	7.71E-24	2.52E-23	cpen	-0.635460456	3.90E-19	GO0003151,GO:0030488,GO:0016429	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.001G150400.1	89.13403963	-0.352131412	0.034981378	-10.0663	7.79E-24	2.54E-23	cpen	-0.630918808	9.47E-19		Plant ubiquitin regulatory and proteasome activator family protein
Sapur.004G269400.1	2.918439912	-0.803680695	0.23495862	-10.066	7.81E-24	2.55E-23	cpen	-0.716073226	6.26E-22	LSH10	Protein of unknown function (DUF640)
Sapur.002G061100.1	520.8545842	0.452477045	0.044594072	10.06532	7.86E-24	2.56E-23	cpen	0.57681024	2.65E-15	GO0005515	BTB/POZ domain-containing protein
Sapur.019G026600.1	8066.054572	0.7189964	0.071394	10.0688	8.00E-24	2.61E-23	cpen	0.615305568	9.90E-18	ACT7	actin 7
Sapur.004G161300.1	76.60803949	-0.52339029	0.052014491	-10.0624	8.10E-24	2.64E-23	cpen	-0.615390003	1.20E-17	GO0046872	Leucine-rich repeat protein kinase family protein
Sapur.005G038700.1	48.2608843	1.224285152	0.121675433	10.06119	8.14E-24	2.65E-23	cpen	-0.585898136	1.14E-15	BLT	brassinosteroid-regulated protein BRI1-5
Sapur.002G012300.1	7.732461178	1.777751445	0.17068859	10.0601	8.17E-24	2.66E-23	cpen	-0.534802247	5.40E-13	GO0016788	GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.15WG114200.1	65.75432205	0.587128009	0.057396	10.0588	8.30E-24	2.70E-23	cpen	-0.544673652	1.06E-13	GO0005886,GO:0006886,GO:0006605	secE/sec61-gamma family protein
Sapur.016G043000.1	178.5402906	-0.611432343	-0.05976	8.51E-24	2.77E-23	cpen	-0.608614406	2.76E-17	GO0003676	RNA-binding (RNA)(RBD/RNP motifs) family protein
Sapur.003G075500.1	5179.588852	0.97103281	0.095668517	10.05618	8.62E-24	2.81E-23	cpen	-0.644997818	2.39E-20	GO0016491,GO:0005975,GO:0004553	glycosyl hydrolase family 10 protein
Sapur.016G062300.1	176.57356	-0.658220117	0.065461331	-10.0551	8.72E-24	2.84E-23	cpen	-0.667626193	2.28E-17	GO0046411,GO:0005840,GO0003735,GO:0015934	Ribosomal protein L22p/L17e family protein
Sapur.013G115100.1	1.220037043	3.031613024	0.297448831	10.05393	8.83E-24	2.87E-23	cpen	0.538295529	3.57E-13	GO0080270	RING/FYVE/PHD zinc finger superfamily protein
Sapur.003G038300.1	106.8409009	-0.583881654	0.059393791	-10.0482	9.35E-24	3.04E-23	cpen	-0.64679129	4.57E-20		hypothetical protein
Sapur.005G053300.1	3.827694601	-1.703404518	0.169547905	-10.0456	9.61E-24	3.13E-23	cpen	-0.61493131	1.06E-17		NA
Sapur.003G204100.1	136.3173026	0.729028815	0.075757321	10.04555	9.64E-24	3.13E-23	cpen	0.624731883	2.51E-18	GO0020146,GO:0005975,GO:0004553	beta galactosidase 1
Sapur.017G029900.1	20.23146283	-1.10838434	0.110337329	-10.0454	9.62E-24	3.13E-23	cpen	-0.578397201	2.14E-15	GO0020147,GO:0006468,GO:0005524,GO:0004672	receptor serine/threonine kinase, putative
Sapur.003G011500.1	143.6274799	0.175277152	0.018121917	10.0422	9.94E-24	3.23E-23	cpen	-0.502232741	2.38E-11		ankyrin repeat family protein
Sapur.003G081400.1	156.5447752	-0.511947344	0.051080529	-10.0365	1.05E-23	3.42E-23	cpen	-0.659052646	2.73E-20	GO0016597,GO:0008152	ACT domain repeat 8
Sapur.003G059400.1	2249.270027	-0.464181751	0.046276532	-10.0318	1.12E-23	3.65E-23	cpen	-0.601874429	2.26E-17	GO0003729,GO0006508,GO:0008843,GO:0006520	Tetratricopeptide (TPR)-like superfamily protein
Sapur.004G165200.1	125.1.35436	-0.465570879	0.046535298	-10.0047	1.45E-23	4.71E-23	cpen	-0.652305395	2.27E-20	GO0055114,GO:0020037,GO:0016705,GO:0005506	aspartate aminotransferase, putative
Sapur.005G049900.1	165.4727576	0.361559388	0.036148836	10.00251	1.49E-23	4.81E-23	cpen	-0.638438856	2.37E-19	GO0005515	cytochrome P450 family protein
Sapur.019G007800.1	20.84691021	-0.597838223	0.059908286	-9.99913	1.54E-23	4.88E-23	cpen	-0.607063615	2.24E-17	GO0046872	Cytochrome P450, family 83, subfamily B, polypeptide 1
Sapur.7G08000.1	107.1830187	-0.46958076	0.046966105	-9.99829	1.55E-23	5.02E-23	cpen	-0.6181793	6.37E-18		synthase
Sapur.010G126000.1	1000.25484	0.514868202	0.051531619	9.996544	1.58E-23	5.11E-23	cpen	0.600610265	3.77E-17	GO0016020,GO0006886	double-stranded RNA-binding protein 4
Sapur.009G072200.1	679.8615101	0.401825682	0.040212971	9.99244	1.64E-23	5.32E-23	cpen	0.655169397	3.15E-20	GO0005515	Vesicle transport protein SFT2 / WD-40 repeat family protein
Sapur.016G093000.1	13.8278232	1.223418319	0.122457604	9.988317	1.71E-23	5.54E-23	cpen	0.559918896	1.86E-16		transducin family protein / WD-40 repeat family protein
Sapur.005G050500.1	14.43861696	-0.352618847	0.035439585	-9.98694	1.74E-23	5.62E-23	cpen	-0.60667654	3.72E-17	GO0043531	Putative lysine decarboxylase family protein
Sapur.003G000300.1	9.141687968	-1.211791061	0.121377218	-9.98368	1.80E-23	5.80E-23	cpen	-0.583984576	4.68E-16		NB-ARC domain-containing disease resistance protein
Sapur.013G030600.1	487.7868205	-0.823481495	0.082490454	-9.98251	1.82E-23	5.87E-23	cpen	-0.629510556	1.04E-18		NA
Sapur.009G040400.1	492.0206635	-0.352478515	0.035278515	-9.98229	1.82E-23	5.88E-23	cpen	-0.613280195	5.97E-17	GO0046872	methionine sulfoxide reductase B 2
Sapur.005G171300.1	2.890663395	2.009243809	0.201292058	9.981734	1.83E-23	5.92E-23	cpen	0.574036683	1.82E-15		
Sapur.014G001700.1	612.2905881	-0.098858862	0.010079916	-9.9808	1.85E-23	5.97E-23	cpen	-0.581951649	1.31E-15	GO0043531	NB-ARC domain-containing disease resistance protein
Sapur.013G131700.1	247.2951888	-0.660651344	0.067056575	-9.97682	1.93E-23	6.21E-23	cpen	-0.600218962	9.78E-17		Jiburoid-responsive family protein
Sapur.004G123700.1	44.88238371	-0.275354744	0.127843861	-9.97588	1.94E-23	6.27E-23	cpen	-0.626637371	1.01E-18	GO0009733	SAUR-like auxin-responsive protein family
Sapur.015G110100.1	363.5157571	-0.103624889	0.010414571	-9.97456	1.97E-23	6.37E-23	cpen	0.61870604	1.41E-17	GO0008289	lipid-binding serum glycoprotein family protein
Sapur.15WG077800.1	74.12612099	-0.628505108	0.063028181	-9.97181	2.03E-23	6.53E-23	cpen	-0.629632318	1.07E-18		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.003G008300.1	4.620559207	1.223418319	0.161170484	9.968317	2.05E-23	6.61E-23	cpen	-0.729126455	1.61E-25		Putative lysine decarboxylase family protein
Sapur.005G017400.2	12.3716108	-0.864326461	0.086675539	-9.97023	2.06E-23	6.64E-23	cpen	-0.609488881	2.43E-17	GO0046355	FAR1-related sequence 7
Sapur.013G040000.1	15.63864224	-0.807184152	0.08909786	-9.96887	2.08E-23	6.72E-23	cpen	-0.61693773	1.58E-17		ATP binding;nucleic acid binding;helicases
Sapur.002G060000.1	10.18166695	-1.070276688	0.107374025	-9.96774	2.11E-23	6.80E-23	cpen	-0.583146471	1.12E-15		UDP-Glycosyltransferase superfamily protein
Sapur.002G089500.1	5.965193886	-2.366223617	0.237685126	-9.96678	2.13E-23	6.87E-23	cpen	-0.602505983	4.12E-17	GO0046385	phosphatidylinositol monophosphate 5 kinase
Sapur.003G093800.1	574.3060278	-0.267575793	0.026207949	-9.96601	2.15E-23	6.93E-23	cpen	-0.629690365	2.01E-18	GO0005515,GO:0016021,GO:0051979,GO:0009523	photosystem II core complex proteins psb31
Sapur.011G085800.1	4.379797228	1.298323364	0.130392142	9.958601	2.31E-23	7.45E-23	cpen	0.641812017	1.34E-19	GO0005515	F-box/RNI-like/FBD-like domains-containing protein
Sapur.005G119300.1	87.48607713	-0.622142294	0.062502188	-9.95783	2.33E-23	7.51E-23	cpen	-0.629834593	8.97E-19		m-nonadecane family protein
Sapur.016G217500.1	1128.705887	0.529932341	0.053235524	9.956357	2.37E-23	7.62E-23	cpen	0.614939953	1.16E-17	GO0005515,GO:0005886,GO:0005783	protein pump interactor 1
Sapur.015G015900.1	66.78085138	-0.323535057	0.032775938	-9.95617	2.37E-23	7.62E-23	cpen	-0.592138467	5.14E-16	GO0016021,GO0004190	SIGNAL PEPTIDE PEPTIDASE-LIKE 1
Sapur.003G138500.1	7.430424277	-2.010615304	0.216461398	-9.94745	2.59E-23	8.33E-23	cpen	-0.635937244	3.60E-19		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.004G088800.1	201.7153846	-0.564228882	0.056819	-9.9443	2.67E-23	8.58E-23	cpen	-0.657608112	1.38E-21		alpha/beta-hydrolases superfamily protein
Sapur.014G122200.1	202.7655583	0.579086487	0.058265205	-9.93884	2.82E-23	9.07E-23	cpen	-0.659181163	6.25E-21		U3 containing 90S pre-ribosomal complex subunit
Sapur.005G038800.1	14.16617863	-0.152884388	0.015996427	-9.93885	2.82E-23	9.07E-23	cpen	-0.629846908	5.41E-18	GO0006468,GO0005524,GO0004672	N/MA-related serine/threonine kinase 1
Sapur.010G133400.1	1.595603025	3.803210099	0.382791762	9.935454	2.92E-23	9.38E-23	cpen	0.515383295	7.57E-12		NA
Sapur.006G073400.1	14.02668737	2.210531117	0.221890427	-9.93131	3.04E-23	9.78E-23	cpen	-0.579413053	1.86E-15		NADP/5-binding Rossmann-fold superfamily protein
Sapur.015G145300.1	175.1458336	0.614826667	0.062115884	9.930522	3.07E-23	9.85E-23	cpen	0.560723558	3.84E-16		GO0047838.1
Sapur.018G103000.1	351.863251	0.284927682	0.028698884	9.92818	3.14E-23	1.01E-22	cpen	0.636201815	3.45E-19	GO0008270	zinc finger (ubiquitin-hydrolase) domain-containing protein
Sapur.014G077200.1	23.01888859	-0.452207321	0.045611763	-9.92613	3.21E-23	1.05E-22	cpen	-0.58470271	8.97E-16		NA
Sapur.007G096400.1	29.82074866	-0.981206688	0.098870857	-9.92412	3.27E-23	1.05E-22	cpen	-0.595118841	2.05E-16		Chaperone DnaJ-domain superfamily protein
Sapur.002G081100.1	12.7911888	1.328950686	0.133661388	9.920464	3.28E-23	1.06E-22	cpen	0.609164258	1.47E-17	GO0005515	prenylcysteine methyltransferase leftwardly expressed protein 1
Sapur.007G018900.1	645.4294642	1.325451357	0.133605194	9.920388	3.28E-23	1.06E-22	cpen	-0.578498547	2.11E-15	GO0008168	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.008G138300.1	93.11270659	-0.512218432	0.051661	-9.91845	3.40E-23	1.11E-22	cpen	-0.676378114	6.68E-22		hypothetical protein
Sapur.019G083000.1	720.477422	-0.258504046	0.026065516	-9.91696	3.51E-23	1.13E-22	cpen	-0.631916576	7.02E-19		Protein of unknown function (DUF668)
Sapur.016G184500.2	26.94502761	1.024269725	0.103307366	9.914779	3.53E-23	1.15E-22	cpen	-0.498079681	3.19E-11	GO0055114,GO:0016491,GO0080270	cinnamyl alcohol dehydrogenase 9
Sapur.018G054000.1	3.818664574	-0.874561665	0.271609002	-9.9142	3.64E-23	1.17E-22	cpen	-0.677289866	2.61E-20	GO0005515,GO0006468,GO0005524,GO0004672	Leucine-rich repeat transmembrane protein kinase family protein
Sapur.003G091900.1	155.0420669	0.356444661	0.035967962	-9.91007	3.78E-23	1.21E-22	cpen	-0.630378689	9.05E-19		Mitochondrial substrate carrier family protein
Sapur.013G005500.1	101.3192503	0.280240441	0.028272208	-9.90806	3.84E-23	1.23E-22	cpen	-0.613102351	1.98E-17		NADP/5-binding Rossmann-fold superfamily protein
Sapur.014G066600.1	207.567485	0.537488843	0.054275197	9.903025	4.04E-23	1.29E-22	cpen	0.618791889	5.79E-18		LDL receptor wingless signaling/trafficking chaperone protein
Sapur.007G204000.1	28.74016858	-0.642422924	0.065265186	-9.9015	4.07E-23	1.31E-22	cpen	-0.593392679	2.42E-16		NA
Sapur.010G189800.1	4.930664498	1.756843279	0.177492288	9.900537	4.14E-23	1.33E-22	cpen	0.592363824	2.91E-16	GO0080270,GO0005515	RING-H2 zinc finger protein
Sapur.006G188800.1	22.27575224	0.743827565	0.075113785	9.89889	4.21E-23	1.35E-22	cpen	-0.64966837	4.02E-20		Pentatricopeptide repeat (PPR)-like superfamily protein
Sapur.010G097400.1	1233.828697	0.378695561	0.038304121	9.893702	4.43E-23	1.42E-22	cpen	0.684595042	4.82E-23	GO0046468,GO0006672	kinase domain protein
Sapur.003G075200.1	47.28313137	0.652017829	0.065925571	-9.89246	4.46E-23	1.44E-22	cpen	-0.624364567	3.14E-18		cell-like 11
Sapur.004G030400.1	0.829932132	2.139466029	0.217375446	9.891963	4.51E-23	1.46E-22	cpen	-0.583170328	1.77E-15		Late embryogenesis abundant protein (LEA) family protein
Sapur.017G135200.1	131.7001294	-0.450874291	0.04558425	-9.89101	4.55E-23	1.46E-22	cpen	-0.614395403	1.19E-17	GO0005515	ARM repeat superfamily protein
Sapur.003G170500.1	53.71998298	0.818292686	0.082745382	9.889732	4.61E-23	1.48E-22	cpen	-0.616980851	6.16E-15	GO0016758,GO0008152	UDP-glucose/thymidine 7 TBK 7
Sapur.013G027700.1	48.71821209	-0.884263739	0.08941377	-9.88957	4.62E-23	1.48E-22	cpen	-0.649975834	1.25E-20		Protein of unknown function, DUF584
Sapur.006G202000.1	10.94654649	0.379414496	0.09908324	-9.88476	4.85E-23	1.55E-22	cpen	-0.639307704	5.64E-19		FAD-dependent oxidoreductase, putative
Sapur.014G061600.1	2825.743945	0.267943872	0.027107827	9.884378	4.87E-23	1.56E-22	cpen	0.655819705	2.90E-20	GO0055114,GO0004471,GO:0051287	NAD-dependent malic enzyme 2
Sapur.013G086200.1	166.9644718	1.586727319	0.156237378	9.882452	4.94E-23	1.58E-22	cpen	0.554432247	4.94E-14	GO0016787	Calcineurin-like phosphoesterase superfamily protein
Sapur.016G278900.1	61.13400797	1.208575101	0.123386674	9.875055	5.34E-23	1.71E-22	cpen	-0.63363441	5.26E-19		NA
Sapur.003G150500.1	70.12883378	-0.612084788	0.06207769	-9.87445	5.38E-23	1.71E-22	cpen	-0.636209202	4.98E-19		AGCF3 interacting protein 1
Sapur.15WG074900.1	11.61431884	1.301912578	0.131847352	-9.87436	5.38E-23	1.72E-22	cpen	-0.585261015	4.55E-16		NA
Sapur.019G018800.1	1477.412351	0.562214449	0.057000249	9.872158	5.47E-23	1.75E-22	cpen	0.628540082	5.81E-19	GO0006783,GO0004325	ferrochelatase 1
Sapur.001G139900.1	46.31599679	0.730075884	0.07400947	9.86428	5.93E-23	1.89E-22	cpen	-0.588578942	5.21E-16		hypothetical protein
Sapur.002G293400.1	12.60494348	0.926870937	0.093965214	-9.86388	5.96E-23	1.90E-22	cpen	-0.64644514	6.02E-20		Erythronate-4-phosphate dehydrogenase family protein
Sapur.018G082400.1	209.4123997	0.637930155	0.064680947	-9.86281	6.04E-23	1.93E-22	cpen	-0.6176162	7.20E-18	GO0043531	Rib-ARC domain-containing disease resistance protein
Sapur.017G031300.1	26.39573655	-1.462622033	0.148370168	9.85797	6.33E-23	2.02E-22	cpen	-0.567240606	9.52E-15		uncoupling protein 5
Sapur.015G181300.1	62.33632224	-0.882421199	0.093918487	-9.85627	6.36E-23	2.04E-22	cpen	-0.61583707	9.50E-18	GO0080270,GO0003676	DEAD-box protein abstract, putative
Sapur.15WG084600.1	63.78075545	-0.845276809	0.085853371	-9.85133	6.76E-23	2.16E-22	cpen	-0.61147661	1.80E-17	GO0016851,GO0005975	DNA-damage-repair/toleration protein (DRT102)
Sapur.005G096400.1	319.1542517	-0.622037209	0.054317417	-9.84418	7.28E-23	2.31E-22	cpen	-0.623572509	1.98E-18	GO0005515	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.003G140000.3	15.70496325	-0.032064683	0.104873179	-9.84099	7.50E-23

Sapur.002G169500.1	321.8268867	0.31386476	0.032514591	-9.65221	4.83E-22	1.50E-21	ppm	-0.62091586	4.22E-18	ATSG43090.1	Ubiquitin carboxyl-terminal hydrolase family protein	plant organelle RNA recognition domain protein
Sapur.001G029000.1	637.4335588	0.41312667	0.046694495	9.650487	4.89E-22	1.52E-21	ppm	-0.61640392	8.41E-18	ATSG54360.1	zinc ion binding	E3 ubiquitin-protein ligase CHFR protein
Sapur.001G026700.1	35.45021906	-0.88568399	0.091757623	-9.64573	5.12E-22	1.60E-21	ppm	-0.60504527	4.38E-17	GO:0005515;GO:0045531	LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.004G150100.1	577.7997718	0.31767776	0.032546894	-9.64048	5.39E-22	1.68E-21	ppm	-0.62702852	1.56E-18	GO:0016810;GO:0006807	nitrilase	nitrilase/nitrile hydratase N-ITA
Sapur.006G030600.1	23.52705314	0.78973767	0.081926396	9.639284	5.46E-22	1.70E-21	ppm	-0.58733225	6.22E-16		5-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosylmethionine-dependent methyltransferase domain protein
Sapur.008G051500.1	102.0139261	0.56182784	0.05830589	9.635703	5.65E-22	1.76E-21	ppm	-0.61509234	8.41E-17	GO:0005524;GO:0016226;GO:0005506	NFU domain protein 4	iron-sulfur cluster assembly protein NFU4
Sapur.010G144500.1	16.22575295	0.93480765	0.097003859	9.634131	5.74E-22	1.79E-21	ppm	-0.61473176	1.09E-17	GO:0003047	RNJRS domain-containing protein	RNJRS domain protein
Sapur.010G005100.1	150.6434936	0.82029459	0.085105059	-9.62541	6.25E-22	1.95E-21	ppm	-0.63458012	4.52E-19	GO:0043531	NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.008G014200.1	65.19436317	1.13326154	0.11772659	9.625066	6.27E-22	1.95E-21	ppm	-0.57637275	6.30E-15		RmlC-like cupins superfamily protein	oxalate oxidase
Sapur.006G015500.1	90.58883928	0.57182257	0.059429126	9.624326	6.31E-22	1.97E-21	ppm	-0.6273073	1.05E-20	tic20-IV	Translocon at the inner membrane of chloroplasts 20-IV	NA
Sapur.010G024000.1	1329.92957	0.63761958	0.066301083	9.616946	6.78E-22	2.11E-21	ppm	-0.59175834	3.32E-16			transmembrane protein, putative
Sapur.004G027500.1	2.33877762	0.92578238	0.09624804	9.614168	6.97E-22	2.17E-21	ppm	-0.61468131	5.19E-18		Uncharacterized protein family (UPF0467)	plant integral membrane protein
Sapur.013G141200.1	24.64826911	-0.87160259	0.090673776	-9.6135	7.01E-22	2.18E-21	ppm	-0.57796812	2.27E-15	ATSG43650.1	EMB2777	Sas10/U3 ribonucleoprotein (utp) family protein	NA
Sapur.003G000300.1	2614.834114	0.71309942	0.074178882	9.613353	7.04E-22	2.18E-21	ppm	-0.59081287	5.17E-16	ATSG49560.1	CKB1	casein kinase II beta subunit	casein kinase II beta subunit
Sapur.010G094500.2	2.52315651	-1.86575793	0.196311249	-9.6122	7.10E-22	2.21E-21	ppm	-0.60501928	4.78E-17	GO:0004412;GO:0005840;GO:0005622;GO:0003735;GO:0008097	ribosomal protein L5 B	60S ribosomal protein L5
Sapur.004G131700.1	4.66853331	-1.06125166	0.110432581	-9.61062	7.16E-22	2.26E-21	ppm	-0.62636718	1.26E-19	GO:0005524	TCP-1/cpn60 chaperonin family protein	RuBisCO large subunit-binding protein subunit alpha
Sapur.017G055500.1	16.4283364	-0.74577689	0.077671255	-9.60171	7.88E-22	2.46E-21	ppm	-0.57837896	2.14E-15		CCT domain	TCP transcription factor
Sapur.008G020400.1	26.18384029	0.75664256	0.078813388	9.600479	7.98E-22	2.47E-21	ppm	0.60284607	6.60E-17	GO:0008270	RING/FYVE/PHD zinc finger superfamily protein	NA
Sapur.007G039000.2	7.73377713	-0.97637884	0.101705112	-9.60033	7.97E-22	2.47E-21	ppm	-0.57948484	1.84E-15		Phosphatidic acid phosphatase family protein	phosphatidic acid phosphatase (PAP2) family protein
Sapur.018G049000.1	1542.460018	0.52475708	0.054638347	-9.59616	8.30E-22	2.58E-21	ppm	-0.62637845	1.75E-18	GO:0016020;GO:0015979;GO:0009523	photosystem II subunit X	ultraviolet-B-responsible protein
Sapur.013G117001.1	458.07005	0.41612204	0.043344879	-9.59565	8.33E-22	2.58E-21	ppm	-0.61467393	5.97E-17	GO:0005415;GO:0005741	eukaryotic translation initiation factor 2 beta subunit	eukaryotic translation initiation factor 2 beta subunit
Sapur.008G035400.3	3.47037825	-1.42728184	0.14885139	-9.58864	8.93E-22	2.77E-21	ppm	-0.6051755	4.66E-17	GO:0006468;GO:0006672	Protein kinase superfamily protein	receptor Serine/Threonine kinase, putative
Sapur.010G144800.1	68.18616377	0.89888163	0.087517325	9.58306	9.04E-22	2.82E-21	ppm	0.59616726	1.76E-16			NA
Sapur.001G088800.1	333.916425	-0.40017262	0.041786286	-9.57664	9.60E-22	3.11E-21	ppm	-0.62811187	1.31E-18	GO:0005515;GO:0006468;GO:0004672	Leucine-rich repeat protein kinase family protein	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.006G078300.5	27.84916515	0.71309942	0.074476882	9.574364	1.04E-21	3.38E-21	ppm	-0.59081287	5.17E-16		RING/U-box superfamily protein	RING/U-box protein
Sapur.001G095600.1	327.5161854	-0.84842205	0.088675707	-9.5679	1.08E-21	3.38E-21	ppm	-0.61026207	2.18E-17			hypothetical protein
Sapur.016G180000.1	5.05343149	1.72181344	0.179990135	9.565994	1.11E-21	3.46E-21	ppm	0.52238825	2.38E-12	GO:0005524;GO:0004386;GO:0006281;GO:0003678;GO:0000723	FIP1 helicase	NA
Sapur.007G021100.1	88.49504646	-0.61264182	0.064084683	-9.56487	1.13E-21	3.46E-21	ppm	-0.67750026	2.07E-22		Pectate methyltransferase family protein	methyltransferase, putative
Sapur.T178000.1	3.66763141	1.38058631	0.144357073	9.563889	1.14E-21	3.52E-21	ppm	0.67988319	3.30E-17		splicing factor-related	NA
Sapur.T145500.1	3.42189679	1.29750224	0.136154152	9.561938	1.16E-21	3.58E-21	ppm	0.66968553	3.76E-24		splicing factor-related	NA
Sapur.001G097900.1	6.62928851	-1.22488447	0.128150434	-9.55829	1.20E-21	3.71E-21	ppm	-0.58132874	8.22E-16			substition-like protease, putative
Sapur.013G113200.1	436.0060779	0.64838765	0.067836802	9.558165	1.20E-21	3.71E-21	ppm	0.60001734	1.46E-17	GO:0003700	TCP family transcription factor 4	transcription factor TCP4
Sapur.014G141200.1	109.8623023	-0.72769168	0.076149475	-9.5561	1.22E-21	3.78E-21	ppm	-0.60423816	5.37E-17			NA
Sapur.002G169300.1	90.3847791	0.92087664	0.052632121	9.553168	1.28E-21	3.95E-21	ppm	0.63370015	7.57E-18		NF-YB8	nuclear transcription Y subunit B
Sapur.001G059700.1	5.80407974	-1.15388599	0.120800149	-9.55138	1.28E-21	3.96E-21	ppm	-0.63670585	3.17E-19	GO:0006290	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing protein
Sapur.001G269100.1	17.20614982	-0.71928357	0.075352112	-9.54999	1.30E-21	4.01E-21	ppm	-0.61466088	8.6E-17	GO:0006290	Pentatricopeptide repeat (PPR-like) superfamily protein	PPR containing plant protein
Sapur.001G149300.1	102.5353212	0.70091877	0.073424448	9.546138	1.35E-21	4.16E-21	ppm	-0.57841508	2.13E-15		Excinuclease ABC, C subunit, N-terminal family protein	GIY-YIG catalytic domain protein
Sapur.016G267900.1	274.8642906	0.64136214	0.067181792	-9.54521	1.38E-21	4.30E-21	ppm	-0.63943074	2.00E-19	GO:0008270;GO:0005515	BRH1	zinc-RING finger protein
Sapur.018G054600.1	199.2062113	0.87281237	0.091458805	9.540058	1.40E-21	4.41E-21	ppm	0.60703324	3.55E-17		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	iron-heme dioxygenase in morphine synthesis amino-terminal protein
Sapur.016G088200.2	87.30595289	0.62576688	0.065588081	9.539151	1.44E-21	4.45E-21	ppm	-0.59943494	1.09E-16			hypothetical protein
Sapur.004G023200.1	74.93995249	0.92544786	0.096056297	9.53197	1.54E-21	4.76E-21	ppm	-0.62737405	5.68E-18			hypothetical protein
Sapur.T102300.1	0.75280994	2.80105052	0.293918079	9.531059	1.56E-21	4.80E-21	ppm	0.60948837	2.43E-17			NA
Sapur.008G179200.1	188.9070095	0.85027158	0.091812226	9.530076	1.56E-21	4.80E-21	ppm	0.60291223	5.64E-17	GO:0046983	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	bHLH transcription factor, putative
Sapur.003G037600.1	2350.776772	0.69682329	0.073119325	9.528289	1.60E-21	4.93E-21	ppm	0.62476331	1.63E-18	GO:0005515;GO:0055114;GO:0046872;GO:0016702	LOX3	lipoxygenase 3
Sapur.003G166000.1	15.79867862	-0.96530009	0.104512388	-9.52259	1.68E-21	5.20E-21	ppm	-0.58231768	1.10E-15	ATGA2OXA;ATGA2OXG;ATGA	gibberellin 2-oxidase 6	gibberellin 2-oxidase
Sapur.009G079500.1	171.2173463	0.53022069	0.055685276	-9.52174	1.70E-21	5.25E-21	ppm	-0.6223751	7.08E-17	GO:0016567;GO:0006842	PUB26	plant U-box 26
Sapur.009G084100.1	24.3890213	-0.65865002	0.069379304	-9.51969	1.73E-21	5.35E-21	ppm	-0.60257619	6.87E-17			NA
Sapur.013G029300.1	699.2967994	0.66083368	0.069404591	9.521619	1.73E-21	5.25E-21	ppm	0.62936576	4.52E-18	GO:0005515	Calcium-dependent phospholipid-binding Copine family protein	copine protein, putative
Sapur.011G069600.1	578.2519097	0.81705589	0.085839556	9.520626	1.73E-21	5.30E-21	ppm	0.59201269	3.20E-16	GO:0550085;GO:0016021	4-Oxo;AHOCT4	organic cation/carnitine transporter4
Sapur.013G071200.1	43.03510593	1.14258879	0.120029155	9.519324	1.74E-21	5.32E-21	ppm	0.58837368	5.36E-16		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	Transducin/WD40 repeat-like superfamily protein
Sapur.016G308000.1	11.15929057	-1.54345305	0.162115278	-9.51837	1.76E-21	5.42E-21	ppm	-0.60026913	9.67E-17	GO:0016787;GO:0008152	alpha/beta-Hydrolases superfamily protein	alpha/beta-hydrolases superfamily protein
Sapur.004G022300.1	846.8285016	0.59132748	0.07767263	9.51207	1.87E-21	5.75E-21	ppm	-0.63729765	1.26E-17		Galactose oxidase/kelch repeat superfamily protein	kelch motif protein
Sapur.001G182300.1	36.96463399	0.75168809	0.394439709	9.510159	1.90E-21	5.85E-21	ppm	0.57627431	2.69E-15	GO:0055114;GO:0020037;GO:0016705;GO:0005506	cytochrome P450, family 81, subfamily D, polypeptide 8	NA
Sapur.003G001700.1	1.09984852	2.07109192	0.637138437	9.505883	1.93E-21	5.90E-21	ppm	0.56642764	8.66E-14	GO:0016787	NB-ARC domain-containing protein	CC-NBS-LRR resistance protein
Sapur.017G035500.1	485.9176049	-0.65452079	0.068832157	-9.50504	2.08E-21	6.15E-21	ppm	-0.59651034	1.67E-16	GO:0043531	LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.003G155500.1	31.27898886	0.68451134	0.07255137	9.50355	2.10E-21	6.24E-21	ppm	-0.59556804	1.36E-16		tobamovirus multiplication protein 3	tobamovirus multiplication-like protein
Sapur.012G058100.1	121.4065931	-0.51032536	0.05371564	-9.5005	2.08E-21	6.42E-21	ppm	-0.63481998	4.23E-19			transmembrane protein, putative
Sapur.004G098200.1	2.96835137	-1.9272302	0.202938252	-9.49663	2.17E-21	6.66E-21	ppm	-0.64172016	8.15E-19	GO:0046872	C2H2 and C2HC zinc fingers superfamily protein	zinc finger protein, putative
Sapur.008G116005.5	7.167794136	-0.88026025	0.325207542	-9.49662	2.17E-21	6.67E-21	ppm	-0.58201022	1.46E-16			zinc finger protein, putative
Sapur.017G060900.1	104.67514	0.352184	0.037103025	9.496355	2.17E-21	6.68E-21	ppm	0.59737332	1.52E-16	GO:0006532	CW14	Protein of unknown function (DUF1336)	plant/SYN623-31 protein, putative
Sapur.005G102300.1	13.83861355	-0.77162972	0.082611964	-9.4948	2.22E-21	6.82E-21	ppm	-0.61767241	4.46E-18			NA
Sapur.010G192300.1	18.67283467	-1.18161217	0.124657589	-9.49412	2.22E-21	6.82E-21	ppm	-0.56725501	1.16E-14			hypothetical protein
Sapur.003G000100.1	54731.11501	0.70268367	0.074881332	9.49409	2.22E-21	6.82E-21	ppm	-0.61852425	2.96E-20	ATGA2OXA;ATGA2OXC;ATGA		NA
Sapur.001G142500.1	2.21171548	1.18469348	0.230404164	9.482117	2.49E-21	7.65E-21	ppm	-0.53948406	3.09E-13	GO:0055114;GO:0016491	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.012G056000.3	16.57432244	0.87864	0.088678624	9.47884	2.57E-21	7.88E-21	ppm	-0.61878852	6.27E-18		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.016G111700.1	151.004499	0.54766297	0.05781892	9.477283	2.62E-21	8.01E-21	ppm	-0.56182938	1.98E-14			hypothetical protein
Sapur.003G093000.1	524.3516496	-0.65605188	0.07463	-9.46019836	2.68E-21	8.22E-21	ppm	-0.61782878	6.96E-18	GO:0007264;GO:0005525	ASAR1;ATSAR2;ATSAR3;AS	secretion-associated RAS super family 2	GTP-binding protein SAR1, putative
Sapur.012G130700.1	1165.989185	0.30571663	0.032272708	9.472915	2.72E-21	8.35E-21	ppm	-0.59505575	2.07E-16			hydroxyproline-rich glycoprotein family protein	hydroxyproline-rich glycoprotein family protein
Sapur.011G082300.1	11.67963638	1.06412165	0.112410358	9.466416	2.90E-21	8.88E-21	ppm	0.61118761	1.88E-17		Protein of unknown function (DUF642)	transmembrane protein, putative
Sapur.012G081000.1	15.58916981	1.34171248	0.142595297	9.463037	2.93E-21	8.97E-21	ppm	0.53587215	4.80E-13			transmembrane protein, putative
Sapur.012G068800.1	6.49035815	-0.92062816	0.108088855	-9.46519	2.93E-21	8.98E-21	ppm	-0.5175937	3.31E-14			oligopeptide transporter
Sapur.016G091100.1	770.0277	-0.38047626	0.040202715	-9.46038	2.97E-21	9.08E-21	ppm	-0.61835596	6.30E-18	GO:0003676	RING-type E3 ubiquitin transferase 1B	RING-recognition motif 2 in nucleolysin TIA-1 (p40-TIA-1)-like protein
Sapur.016G165500.1	66.92173529	-0.60127723	0.063153492	-9.46096	3.05E-21	9.34E-21	ppm	-0.59255308	2.98E-16	GO:0016758;GO:0008152		UDP-glycosyltransferase superfamily protein
Sapur.004G146200.1	788.0818102	0.40760163	0.043020581	-9.45689	3.11E-21	9.52E-21	ppm	-0.64452795	5.96E-20	GO:0005525		GTP binding
Sapur.004G169500.1	345.8619527	-0.61755566	0.065296879	-9.45794	3.14E-21	9.67E-21	ppm	-0.60164506	8.47E-17			lipid transfer protein 5
Sapur.005G042800.1	399.5197568	0.56580072	0.059922916	9.45155	3.21E-21	9.88E-21	ppm	0.58596223	7.52E-16		TBL31	PMR5/CaCa2p GDSL/SGNH-like acyl-esterase family protein	
Sapur.004G008800.1	16254.37638	-0.8603221	0.091009674	-9.45308	3.29E-21	1.01E-20	ppm	-0.69823224	2.98E-17	GO:0055114;GO:0020037;GO:0008979;GO:0004601	PRXR1	Peroxidase superfamily protein	cationic peroxidase
Sapur.010G042000.1	788.8797148	0.74375274	0.078697267	9.451084	3.35E-21	1.03E-20	ppm	-0.60620651	4.08E-17			Nucleotide-diphosphe-sugar transferases superfamily protein	hypothetical protein
Sapur.017G071700.1	81.61010663	-2.85601199	0.302313945	-9.447931	3.46E-21	1.06E-20	ppm	-0.52268229	7.72E-13	GO:0016021;GO:0006810	emp24/gp25L/p24 family/GOLD family protein	NA
Sapur.008G109200.1	66.87586672	0.54601487	0.05768851	9.463877	3.59E-21	1.10E-20	ppm	0.54324885	1.35E-13	GO:0005515	Rubisco methyltransferase family protein	SET domain protein
Sapur.005G017600.1	4.56683604	-0.49088163	0.05790525	-9.45946	3.75E-21	1.15E-20	ppm	-0.54400023	9.86E-16		Dna/HisMD cytosine-rich domain superfamily protein	protein disulfide-isomerase U2T1, putative
Sapur.006G180000.1	41.61692334	-0.54651419	0.057700276	-9.43688	3.84E-21	1.17E-20	ppm	-0.62276672	1.09E-18	GO:0006355;GO:0005739;GO:0003690	Mitochondrial transcription termination factor family protein	mTERF protein
Sapur.001G064100.1	9.97329252	-1.36992249	0.148319707	-9.43645	3.86E-21	1.18E-20	ppm	-0.57681617	2.64E-15	GO:0006355;GO:0005700	Integrase-type DNA-binding superfamily protein	AP2/EREBP domain transcription factor
Sapur.003G016600.1	127.3195008	-0.57801179	0.061294888	-9.43151	4.04E-21	1.23E-20	ppm	-0.62493979	2.96E-18			transmembrane protein, putative
Sapur.004G000600.1	2507.618694	0.52540026	0.056054482	9.428402	4.09E-21	1.25E-20	ppm	0.59223232	2.00E-16	AE3;IN1;EIN3	Ethylene insensitive 3 family protein	ethylene insensitive 3 class transcription factor
Sapur.018G058800.2	9.55722619	-0.97280653	0.103197011	-9.42647	4.24E-21	1.29E-20	ppm	-0.60596235	4.14E-17	GO:0016020;GO:0008236;GO:0006508	PLSP1	plastidic type I signal peptidase 1	signal peptidase I
Sapur.013G037000.1	19.91974321	1.54837247	0.164247664	-9.42586	4.27E-21	1.30E-20	ppm	-0.60209284	2.7E-17			NA	NA
Sapur.009G008000.8	3.80984076	-1.49006861	0.15817125	-9.4206	4.48E-21	1.37E-20	ppm	-0.58523042	7.67E-16	GO:0007275	Plant-specific transcription factor YABBY family protein	YABBY2-like transcription factor YAB2
Sapur.002G015500.1	2039.734309	-0.56890469	0.060409532	-9.41872	4.57E-21	1.39E-20	ppm	-0.60486554	4.89E-17		CP12-3	CP12 domain-containing protein 3	CP12 domain protein
Sapur.006G086000.1	5.77001468	-0.42008798	0.051934854	-9.41843	4.58E-21	1.40E-20	ppm	-0.62201111	4.40E-18	GO:0005515	UBQ10	polyubiquitin 10	NA
Sapur.T022800.1	1.96174136	-2.01039632	0.213457524	9.417543	4.62E-21	1.41E-20	ppm	0.62811886	3.06E-18	GO:0005681;GO:0003198;GO:0003887	ARM repeat superfamily protein	RNA polymerase sigma subunit SIGA
Sapur.010G151200.1	7.02272656	-1.49478938	0.15874697	-9.41561	4.78E-21	1.46E-20	ppm	-0.56437819	1.01E-14		Dna/HisMD cytosine-rich domain superfamily protein	DUF177 domain protein
Sapur.013G138600.1	71.71584292	-0.62167327	0.066026759	-9.41546	4.79E-21	1.46E-20	ppm	-0.59778626	1.39E-16		myb-like HTH transcriptional regulator family protein	telomeric repeat-binding factor, putative
Sapur.005G066500.1	2.49036777	-1.46040026	0.154582629	9.397555	5.47E-21	1.66E-20	ppm	-0.42860214	1.11E-08	GO:0016787	ATNUDT11;ATNUDX13;NUE	nudix hydrolase 11	nudix hydrolase
Sapur.010G028200.1	99.3096829	-0.42568426	0.045288157	-9.39954	5.48E-21	1.67E-20	ppm	-0.64357987	9.87E-20	GO:0006355;GO:0005739;GO:0003690	Mitochondrial transcription termination factor family protein	mTERF protein
Sapur.003G174300.1	53.32741439	0.81376029	0.08872249	9.39718	5.60E-21	1.71E-20	ppm	-0.61267606	1.50E-17	GO:0009733	SAUR-like auxin-responsive protein family	SAUR-like auxin-responsive protein
Sapur.001G088400.1	22.51706658	1.51388644	0.161090598	9.396493	5.64E-21	1.72E-20	ppm	-0.51282801	6.58E-12	GO:0016021;GO:0016020;GO:0022857	nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4
Sapur.013G084000.1	0.80576266	1.03537584	0.110627364	9.335202	5.70E-21	1.74E-20	ppm	-0.55357452	5.24E-14	GO:0005515	F-box/RNI-like superfamily protein	NA
Sapur.007G074100.1	687.5469713	0.33834211	0.036020089	9.393125	5.82E-21	1.77E-20	ppm	-0.59421026	2.16E-16	GO:0015536;GO:0003824;GO:0015539;GO:0016892;GO:0009107	lipoic acid synthase 1	LIP1	lipoyl synthase
Sapur.016G249100.1	8390.678224	-0.77650946	0.08273851	-9.39222	5.87E-21	1.79E-20	ppm	-0.62377278	3.61E-18	GO:0055114;GO:0006097;GO:0016491;GO:0008152			polyphenol oxidase
Sapur.005G127600.1	4.26052731	-1.26232429	0.134988738	-9.38924	6.22E-21	1.89E-20	ppm	-0.56286907	1.80E-14			CARA	carbamoyl phosphate synthetase A
Sapur.007G134000.1	8.25022188	1.64225157	0.175058183	9.381175	6.52E-21	1.98E-20	ppm	0.57680893	2.96E-15	GO:0005507;GO:0004144	D-aspartate/serine (WSD1-like) family protein	CARA	D-aspartate/serine (WSD1-like) family protein
Sapur.016G087500.1	2521.818854	0.58016129	0.061844932	9.380932	6.54E-21	1.99E-20	ppm	0.58314495	1.95E-16	GO:0046872;GO:0030001	Heavy metal transport/detoxification superfamily protein	NA
Sapur.T134300.1	1.20200178	2.8727255	0.306725689	9.380549	6.56E-21	1.99E-20	ppm	0.54501729	2.86E-13			NA
Sapur.006G208000.1	5.30679682	-1.20268357	0.128214803	-9.3801	6.59E-21	2.00E-20	ppm	-0.57226437	4.91E-15		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.010G013100.1	153.9614926	-0.54097523	0.05784613	-9.37817	6.71E-21	2.04E-20	ppm	-0.61047758	2.00E-17	GO:0016758;GO:0008152	UDP-glycosyl transferase 73B1	UGT73B1	UDP-glucose flavonoid 3-O-glucosyltransferase
Sapur.013G026700.1	51.53809475	0.65380107	0.062446349	9.375729	6.87E-21	2.08E-20	ppm	-0.60378742	3.50E-17		UDP-Glycosyltransferase superfamily protein	UGT	UDP-glucuronosyltransferase/glycosyltransferase beta-N-acetylglucosaminyltransferase
Sapur.021G016800.1	8.19074583	-1.16145293	0.129909997	-9.37336	7.03E-21	2.13E-20	ppm	-0.58284103	1.20E-15	GO:0005515;GO:0003824	AMP-dependent synthetase and ligase family protein	CER8;LACS1	long-chain-fatty-acid-CoA ligase
Sapur.002G196200.1	128.0105523	1.32075989	0.149319378	9.372975	7.05E-21	2.14E-20	ppm	-0.51262718	8.17E-12	GO:0055114;GO:0020037;GO:0016705;GO:0005506	cytochrome P450 family protein	CYP76G1	cytochrome P450 family protein
Sapur.007G027000.1	195.9857951	-0.11342255	0.011889172	-9.37083	7.20E-21	2.18E-20	ppm	-0.54266779	2.01E-13	GO:0008270;GO:0005622;GO:0005515	6-box type zinc finger protein with CCT domain		constans-like zinc finger protein
Sapur.016G166600.1	216.9735894	0.31375937	0.034353504	9.367507	7.43E-21	2.25E-20	ppm	-0.59119093	2.73E-16		Mitochondrial substrate carrier family protein	GTOT10.1	substrate carrier family protein
Sapur.005G048200.1	263.2569998	0.87325969	0.09574667	9.356828	7.51E-21	2.27E-20	ppm	-0.64753988	4.98E-20				TPR protein
Sapur.003G141200.1	42.20406131	0.70609457	0.076605467	9.362624	7.38E-21	2.36E-20	ppm	0.58154724	1.26E-15		Hydroxyl dehalogenase-like hydrolase family protein	NAD(P) binding Rossmann-fold superfamily protein	haloacid dehalogenase-like hydrolase domain protein
Sapur.010G139500.1	178.8170279	0.61767617	0.065905881	-9.36197	7.82E-21	2.37E-20	ppm	-0.59926347	1.14E-16				NAD(P)H-binding family protein
Sapur.006G078400.1	5.47887115	1.58237372	0.169654003	9.361838	7.84E-21	2.37E-20	ppm	0.51642916	4.42E-12	GO:0046983	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	RGE1;ZOU	basic helix-loop-helix (bHLH) DNA-binding family protein
Sapur.010G033700.1	155.4292931	-0.74205209	0.079329153	-9.36069	7.87E-21	2.41E-20	ppm	-0.57777148	2.38E-15		Low PSII Accumulation 1 protein	LPA1	Low PSII Accumulation, DUF647
Sapur.003G106300.1	309.8769189	0.38224449	0.040875327	9.351471	8.64E-21	2.62E-20	ppm	0.57777148	2.38E-15				hypothetical protein
Sapur.001G330000.1	8.21141794	0.81879652	0.09	9.346387	8.92E-21	2.85E-20	ppm	-0.56249428	2.67E-14	GO:0055114;GO:0016630	glycerolehyde 3-phosphate dehydrogenase A subunit 2	GAPA-2	glyceraldehyde 3-phosphate dehydrogenase A subunit 2
Sapur.002G146300.1	35.56314842	1.03971264	0.111290981	9.34229	9.43E-21	2.85E-20	ppm	-0.56320287	1.61E-14			TBL25	PmS/CaCa2p GDSL/SGNH-like acyl-esterase family protein
Sapur.008G141900.1	33.43274831	1.95965203	0.208302244	9.338864	9.74E-21	2.96E-20	ppm	0.60493839	4.82E-17			BLI;KD51	BLISTER
Sapur.009G073800.2	2.04667312	2.02295385	0.216581019	9.33866	9.76E-21	2.96E-20	ppm	-0.61291042	1.46E-17	GO:0005515			SWIB/MDM2 domain protein
Sapur.004G030900.1	48.33028861	0.92688945	0.099303294	-9.33372	1.02E-20	3.09E-20	ppm	-0.57349831	5.42E-15	GO:0005634;GO:0003677	squamosa promoter-binding protein-like 12	SPL12	squamosa promoter-binding-like protein
Sapur.008G144500.1	87.93328067	0.61185	0.066	9.33	1.03E-20	3.13E-20	ppm	-0.56231884	1.85E-14	GO:0005515	ARABIDOPSIS TOXICOSIS RESPONSIVE PROTEIN 5	ATWRC;SG155	histone-lysine N-methyltransferase ATWRC, putative
Sapur.006G130400.1	450.8696237	-0.96362478	0.102737399	-9.33081	1.05E-20	3.17E-20	ppm	-0.58182134	1.31E-15	GO:0055114;GO:0020037;GO:0008979;GO:0004601	Peroxidase superfamily protein		NA
Sapur.004G000400.1	154.7576324	0.54880824	0.11212706	9.32193	1.10E-20	3.32E-20	ppm	-0.54882821	1.02E-13	GO:0003723	Ribosomal protein S5 family protein		40S ribosomal protein S3
Sapur.T035200.1	13.07619324	0.94235551	0.101091294	9.323608	1.12E-20	3.39E-20	ppm	-0.5716629	2.53E-15				NA
Sapur.010G000300.1	93.46710074	-0.94361728	0.101017	-9.32327	1.13E-20	3.40E-20	ppm	-0.61308237	2.18E-17	GO:0016020;GO:0006810;GO:0005215	agent domain-containing protein	GAMMA-TIP;GAMMA-TIP1	aquaporin, MIP Family/AJC TIP subfamily protein
Sapur.010G065500.1	8.10515859	-2.56262543	0.135507126	-9.32248	1.14E-20	3.43E-20	ppm	-0.59813036	1.20E-16		gamma tonoplast intrinsic protein		NA
Sapur.007G023800.1	7343.74231	0.88889451	0.092456621	9.318608	1.18E-20	3.56E-20	ppm	0.58936317	1.28E-16	GO:0055114;GO:0016491	succinate dehydrogenase 1-4	SDH1-1	succinate dehydrogenase [ubiquinone] flavoprotein subunit
Sapur.001G075300.1	844.3518826	0.36297881	0.038182129	9.317251	1.19E-20	3.60E-20	ppm	0.60467656	5.07E-17	GO:0016161;GO:0000272	beta-amylase 1	BAM1;BMY7;TB-BAMY

Sapur.013G139400.1	24.7709422	-0.81540188	0.090091637	-9.05081	1.42E-19	4.16E-19	ppm	-0.625014954	2.16E-18	ATOP17,OPF17	ovate family protein 17	NA
Sapur.002G113400.1	595.3733189	0.46478894	0.051354201	9.050535	1.42E-19	4.17E-19	ppm	0.594087646	2.37E-16	GO:0016757	glycosyltransferase 12	NA
Sapur.004G087500.1	224.6090209	0.10286461	0.036518879	2.816022	1.43E-19	4.18E-19	ppm	0.593672187	2.52E-16	GO:0070671,GO:0005875	Dynein light chain type 1 family protein	dynein light chain type 1 protein
Sapur.001G012100.1	618.6340901	1.27620552	0.14102218	9.046644	1.43E-19	4.20E-19	ppm	0.553339793	8.24E-14	GO:0005515,GO:0055114,GO:0044872,GO:0016702	Lipoxygenase 2	lipoxygenase
Sapur.006G158800.1	231.9513073	-0.36365284	0.04012167	-9.04877	1.43E-19	4.20E-19	ppm	-0.58203054	1.30E-15	GO:0009003	DNAse I-like superfamily protein	endonuclease/exonuclease/phosphatase domain protein
Sapur.006G159100.1	497.2792386	0.24117163	0.026858478	9.046714	1.47E-19	4.31E-19	ppm	0.601553418	7.99E-17			colon cancer-associated protein Mic1-like containing protein
Sapur.018G254100.1	9.52297879	-0.90827825	0.100476211	-9.03974	1.57E-19	4.59E-19	ppm	-0.587511252	6.02E-10	GO:0004365,GO:0006355,GO:0003700	WRKY transcription factor	WRKY transcription factor
Sapur.015G025100.1	2.56047131	1.90358723	0.210265815	9.037887	1.68E-19	4.67E-19	ppm	0.569709334	6.88E-15			Myb/SANT-like DNA-binding domain protein
Sapur.159G123500.1	6.27212863	-1.46752405	0.160182614	-9.03671	1.61E-19	4.72E-19	ppm	-0.559996405	2.46E-14		Protein of unknown function (DUF594)	NA
Sapur.005G197600.1	3.48664561	-1.12663151	0.125413729	-8.98609	2.04E-19	5.66E-19	ppm	-0.606508884	5.61E-16	GO:0003677	HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain	high mobility group protein
Sapur.T175500.1	1.62062093	2.50186763	0.277108479	9.028413	1.74E-19	5.09E-19	ppm	0.55319181	5.77E-14			NA
Sapur.I161G100.1	188.8219031	1.12537079	0.124695029	9.024197	1.81E-19	5.29E-19	ppm	0.572841195	1.04E-15		ROTUNDIFOLIA like 5	DVL13
Sapur.T184300.1	1.07407828	2.36507481	0.261852766	9.023028	1.83E-19	5.34E-19	ppm	0.48899745	8.14E-11			NA
Sapur.003G089900.1	2.28042605	2.72607488	0.302104873	9.022547	1.84E-19	5.37E-19	ppm	0.491264056	6.6E-11		Protein of unknown function (DUF567)	NA
Sapur.007G130700.1	15.62630391	1.72112795	0.190134799	9.006913	2.12E-19	6.18E-19	ppm	0.56895518	9.89E-15	GO:0016021,GO:0006952	Seven transmembrane MLO family protein	ATMLO,MLO1
Sapur.010G082300.1	466.3523843	0.28385187	0.031508974	9.006163	2.12E-19	6.18E-19	ppm	0.568585827	8.66E-15	GO:0016491,GO:0016646	2-oxoglutarate(2OG) and Fe(II)-dependent oxygenase superfamily protein	2OG-Fe(II) oxygenase family oxidoreductase
Sapur.004G099800.1	103.1390857	-0.76984738	0.085554258	-8.99855	2.29E-19	6.68E-19	ppm	-0.593719586	2.92E-16	GO:0055114,GO:0020037,GO:0006979,GO:0004601	Peroxidase superfamily protein	peroxidase
Sapur.010G098200.1	673.4570841	-0.70128920	0.078020708	-8.9885	2.51E-19	7.30E-19	ppm	-0.644413484	8.53E-20	GO:0055114,GO:0016616,GO:0009055,GO:0003854	NADP(H)-dependent Rossmann-fold superfamily protein	dihydrofolinoyl-6-reductase, putative
Sapur.003G047105.1	9.01888999	-1.26187989	0.140798891	-8.98723	2.54E-19	7.39E-19	ppm	0.702121027	1.25E-24		Exostosin family protein	exostosin family protein
Sapur.002G141400.1	346.2218644	0.66443908	0.075953816	8.884417	2.60E-19	7.57E-19	ppm	0.567979968	8.64E-15	GO:0005524	P-loop containing nucleoside triphosphate hydrolases superfamily protein	AAA family ATPase
Sapur.006G211000.1	31.39465518	-0.97128209	0.110455179	-8.84969	2.68E-19	7.81E-19	ppm	-0.595054154	5.46E-16	GO:0055114,GO:0050661,GO:0050660,GO:0004499	Flavin-binding monooxygenase family protein	flavin-containing monooxygenase YUCCA6
Sapur.003G121200.1	241.8057067	-0.35762116	0.039879715	-8.97604	2.81E-19	8.16E-19	ppm	-0.593807043	4.97E-16			DUF1499 family protein
Sapur.003G121800.1	9.98070212	1.12473246	0.117926849	8.975603	2.82E-19	8.19E-19	ppm	0.56612605	1.05E-14	GO:0006355,GO:0003677	NAC transcription factor	NAC transcription factor
Sapur.005G141000.1	178.0226395	-0.39479847	0.043990704	-8.97451	2.85E-19	8.27E-19	ppm	-0.578846913	2.01E-15	GO:0008168	mcrA methyltransferase family protein	16S rRNA (cytosine(1402)-N(4))-methyltransferase
Sapur.T196G111300.1	2.50807778	0.58480207	0.065188681	8.9369	2.86E-19	8.32E-19	ppm	0.527872034	9.93E-13	GO:0005509	calmodulin like 38	polycitrin (un protein 5), putative
Sapur.T19900.1	0.84717574	-2.48548723	0.277025305	8.972072	2.91E-19	8.46E-19	ppm	0.608093915	3.01E-17			NA
Sapur.T186400.1	40.39145933	0.996317517	0.11106236	8.972044	2.91E-19	8.46E-19	ppm	0.466495827	7.37E-10	GO:0005524	chromatin remodeling 42	NA
Sapur.007G201100.1	102.9159227	1.04568107	0.116614571	8.97038	2.95E-19	8.59E-19	ppm	-0.529582891	9.93E-13		AAD-like 6	MYB transcription factor
Sapur.010G095000.1	740.7595643	-0.47281896	0.052687514	-8.97019	2.96E-19	8.60E-19	ppm	-0.590963526	2.71E-16		Protein kinase superfamily protein	stress responsive alpha-beta barrel domain protein
Sapur.002G000300.1	655.6805777	-0.46135197	0.05145811	-8.96896	2.98E-19	8.66E-19	ppm	-0.578628298	2.10E-15	GO:0005515,GO:0016567,GO:0004842	plant U-box 17	Arm/UCH-9 rapidly elicited protein
Sapur.004G049500.1	163.9328237	-0.99127526	0.110540607	-8.96752	3.03E-19	8.81E-19	ppm	-0.608040206	3.03E-17			transmembrane protein, putative
Sapur.T024900.1	5.56132622	1.38302969	0.15077419	8.967346	3.04E-19	8.83E-19	ppm	0.51077657	1.48E-16		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.006G095500.1	8.12423043	-1.12601428	0.125603736	-8.96482	3.11E-19	9.02E-19	ppm	-0.553025801	5.90E-14			DUF1159 family protein
Sapur.T000400.1	280.6898868	0.367182284	0.040962863	8.962443	3.15E-19	9.13E-19	ppm	0.586413484	7.06E-16	GO:0005385,GO:0046873,GO:0030001,GO:0016020	ZIP metal ion transporter family	ZIP family transporter
Sapur.T035400.1	13.94192888	0.87356769	0.097047025	8.953349	3.39E-19	9.82E-19	ppm	0.561788606	1.94E-14		against domain-containing protein	NA
Sapur.004G032000.1	76.3072744	0.85144158	0.095000172	8.95347	3.51E-19	1.02E-18	ppm	-0.578667725	2.32E-15			hypothetical protein
Sapur.003G040700.4	7.42629339	1.14371804	0.127808085	8.946221	3.58E-19	1.04E-18	ppm	0.491677847	6.19E-11	GO:0042578	Phosphoinositide phosphatase family protein	phosphoinositide phosphatase
Sapur.002G012200.1	280.6845054	0.537597912	0.060104528	-8.94408	3.74E-19	1.08E-18	ppm	-0.60292261	6.52E-17		SRS4 related sequence 5	short intermediate-related sequence protein, putative
Sapur.007G047700.1	160.2721898	0.54897793	0.059836064	-8.94058	3.87E-19	1.12E-18	ppm	-0.623332207	9.93E-18	GO:0006355,GO:0003700	DNA8 and EAR motif containing protein 3	AP2/EREBP domain transcription factor
Sapur.008G016100.1	75.3905885	0.81395789	0.091068223	8.939992	3.89E-19	1.13E-18	ppm	0.543429151	1.57E-14	GO:0004648,GO:0004672,GO:0005524	Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.T015500.1	11.38589325	1.12473246	0.127601814	8.91404	4.13E-19	1.19E-18	ppm	0.562312671	1.85E-14		against domain-containing protein	NA
Sapur.018G010000.1	7.11627973	1.13952487	0.127553458	8.933764	4.12E-19	1.19E-18	ppm	0.576302224	2.84E-15		Protein kinase superfamily protein	AarP domain kinase, putative
Sapur.010G005800.1	410.9721126	0.54486004	0.077022596	8.925166	4.45E-19	1.29E-18	ppm	0.5406161	2.70E-13		Protein kinase superfamily protein	apoptotic hydrolase
Sapur.008G069400.1	60.26101574	-0.60758397	0.18021188	-9.02027	4.65E-19	1.34E-18	ppm	-0.722403006	1.26E-22	ATMYB10SLOP2,MYB10S	myb domain protein 105	Myb transcription factor
Sapur.016G080100.1	331.3877949	0.272308486	0.041745505	6.519896	4.75E-19	1.36E-18	ppm	0.60451272	3.74E-16			plastid transcriptionally active protein
Sapur.009G032500.1	354.7797109	-0.32183082	0.036088271	-8.91835	4.73E-19	1.37E-18	ppm	-0.564535229	1.36E-14	GO:0005885,GO:0016021	ANTR1,PHT4;1	phosphate transporter 4;1	sodium-dependent phosphate transporter
Sapur.010G027700.1	23.28814603	0.58747616	0.069406573	8.913748	4.93E-19	1.42E-18	ppm	0.548653911	9.70E-15			transmembrane protein, putative
Sapur.003G144900.1	375.0667959	-0.62735357	0.072236169	-8.91054	5.06E-19	1.46E-18	ppm	0.567506082	9.69E-15		zinc ion binding	E3 ubiquitin protein ligase CHFR protein
Sapur.007G107300.1	93.88763073	-0.52031175	0.058406413	-8.90847	5.17E-19	1.49E-18	ppm	-0.582241185	1.26E-15			NA
Sapur.006G012500.1	272.8211609	1.04568107	0.12014956	8.708009	5.19E-19	1.50E-18	ppm	-0.579209779	1.80E-15	GO:0008270		transcriptional adaptor ADA2
Sapur.007G120900.1	215.6025518	-0.55184475	0.061971223	-8.90647	5.27E-19	1.52E-18	ppm	-0.604919005	5.40E-17		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing protein
Sapur.016G237700.1	288.2752968	-0.61164205	0.070480251	-8.68562	5.31E-19	1.53E-18	ppm	-0.58125768	1.44E-15	GO:0003676	DUF1611/zf-ssr/ssr-containing protein	DNA-damage-repair/toleration protein DRT111
Sapur.006G189400.1	170.1410604	-0.81181958	0.091892257	-9.00293	5.44E-19	1.57E-18	ppm	-0.559431224	2.62E-14			NA
Sapur.007G001700.2	2.30705457	1.96568107	0.227221889	8.650267	5.54E-19	1.60E-18	ppm	-0.597912864	1.36E-16	GO:0003824	cyclocortexi synthase 1	cyclocortexi synthase
Sapur.010G138100.1	10.24801881	-0.96089529	0.107988356	-8.89799	5.68E-19	1.64E-18	ppm	-0.576178843	1.92E-15	GO:0008270,GO:0005515	RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.003G060600.1	15.45188867	-0.57436127	0.065186866	-8.89368	5.91E-19	1.70E-18	ppm	-0.553816842	1.27E-14			NA
Sapur.001G180200.1	278.5457922	-0.52920388	0.059507955	-8.89294	5.95E-19	1.71E-18	ppm	-0.563810964	1.49E-14	GO:0005737,GO:0003879,GO:0000287,GO:0000105		ATP phosphoribosyltransferase
Sapur.004G085500.1	244.9061243	0.57796288	0.06503195	8.888814	6.18E-19	1.78E-18	ppm	0.582934344	1.15E-15	GO:0016811,GO:0016021,GO:0006672	Alkaline phytoceramidase (aPHC)	alkaline ceramidase
Sapur.014G127900.1	2.24613788	-1.78618725	0.204153527	-8.88809	6.26E-19	1.80E-18	ppm	-0.552570998	6.24E-14		plastidal transcriptionally active protein 18	plastid transcriptionally active protein
Sapur.003G051100.1	4.30942255	-1.27753372	0.143768824	-8.88749	6.25E-19	1.80E-18	ppm	-0.609084774	2.59E-17			NA
Sapur.010G151500.1	118.0143131	0.85180167	0.09671649	8.807883	6.28E-19	1.81E-18	ppm	0.570224688	4.21E-15	GO:0003993	HAD superfamily, subfamily IIIB acid phosphatase	acid phosphatase, putative
Sapur.014G037000.1	986.7820024	0.549278692	0.061889491	-8.88307	6.50E-19	1.87E-18	ppm	-0.519270338	2.67E-16	GO:0006426,GO:0005737,GO:0005524,GO:0004820,GO:0000166	glycine-tRNA ligases	glycyl-tRNA synthetase
Sapur.008G000200.1	180.5843481	0.50180133	0.057225076	-8.8798	6.76E-19	1.94E-18	ppm	-0.575026761	3.36E-15	GO:0005634	PHT	FRAGILE HISTIDIN TRIAD
Sapur.013G091000.1	26.21624852	-0.67692465	0.076195032	-8.87266	7.14E-19	2.05E-18	ppm	-0.570055509	6.57E-15		PAP/OAS1 substrate-binding domain superfamily	NA
Sapur.004G021500.1	1278.132064	0.49114997	0.055386169	8.871758	7.20E-19	2.06E-18	ppm	-0.52-13.6409	1.25E-13	GO:0016491,GO:0016021	2-methylthiazolinate 1	NA
Sapur.017G042200.1	20.74413973	-0.75187511	0.084585821	-8.86895	7.38E-19	2.12E-18	ppm	-0.573731622	4.02E-15			plastid/T23J11-6 protein, putative
Sapur.005G137800.1	27.53182	2.00535122	0.228000316	8.868016	7.68E-19	2.20E-18	ppm	-0.568948968	5.01E-15	GO:0003723	APUM1,PUM1	pumilio protein, putative
Sapur.008G147200.1	2956.226908	-0.49428142	0.055765414	-8.86358	7.75E-19	2.22E-18	ppm	-0.657418813	9.05E-21	GO:0005515,GO:0016021,GO:0015979,GO:0009523	PSB7,YCF32	photosystem II 8Y	photosystem II core complex protein psbY
Sapur.016G139800.1	3900.0038	-0.56626955	0.063934846	-8.85653	8.25E-19	2.37E-18	ppm	-0.584862434	8.77E-16	GO:0016020,GO:0005765	LHCB2,LHCB2.1	photosystem II light harvesting complex gene 2.1	photosystem I light harvesting chlorophyll A/B-binding protein
Sapur.T031600.1	11.40382506	0.96148238	0.107446563	8.853377	8.34E-19	2.39E-18	ppm	0.559229174	2.68E-14		against domain-containing protein	NA
Sapur.015G099300.1	5062.745884	1.62246193	0.183253791	8.848696	8.85E-19	2.54E-18	ppm	0.582476687	6.74E-16		polyubiquitin 10	NA
Sapur.004G081600.1	44.45008814	0.62606948	0.070117558	8.84623	9.04E-19	2.59E-18	ppm	-0.579896547	2.36E-15		decapping 5	Sc35-like Sm domain protein
Sapur.012G089000.1	8.97147825	2.16206687	0.137579569	8.845218	9.13E-19	2.62E-18	ppm	0.579181776	1.87E-15			NA
Sapur.003G000600.1	10.11845434	0.91870383	0.103889954	8.84319	9.30E-19	2.67E-18	ppm	-0.588334763	1.57E-16			DUF1499 family protein
Sapur.016G088300.1	8.95065265	-0.97676504	0.110486604	-8.84057	9.52E-19	2.73E-18	ppm	-0.565848021	2.26E-14		myb domain protein 68	NA
Sapur.006G082600.1	4.81041369	0.92142667	0.104197873	8.838522	9.97E-19	2.85E-18	ppm	0.545213802	1.05E-13	GO:0004648,GO:0004672	Calcium-dependent protein kinase 1	calcium/calmodulin-dependent kinase
Sapur.001G030300.4	0.91838365	-2.40144564	0.271157571	-8.83311	1.02E-18	2.92E-18	ppm	0.697539284	3.33E-24		Pectin lyase-like superfamily protein	pectate lyase, putative
Sapur.001G097600.1	155.4827899	0.723806552	0.081963714	-8.83204	1.03E-18	2.94E-18	ppm	-0.623479182	3.23E-18		myb domain protein 42	Myb transcription factor
Sapur.003G042500.2	11.36201568	0.97280853	0.106149438	-8.82982	1.05E-18	3.00E-18	ppm	-0.603109136	4.20E-17	GO:0016818,GO:0008026,GO:0006139,GO:0005524,GO:0003676,GO:0005634,GO:0004400	RADA-like DNA/RNA helicase protein	DNA repair helicase (rad3)
Sapur.002G001000.7	1.52760947	-2.32396939	0.26245321	-8.82129	1.13E-18	3.24E-18	ppm	-0.751842988	7.76E-30		Protein of unknown function, DUF547	electron transporter, putative
Sapur.T016800.1	15.74678882	0.90535129	0.10264787	8.816981	1.14E-18	3.27E-18	ppm	0.5383095	5.9E-14			hypothetical protein
Sapur.013G105900.5	7.46325092	1.05119513	0.125232083	-8.8183	1.16E-18	3.32E-18	ppm	-0.569219407	7.34E-15	GO:0003676	arginine/serine-rich 45	RNA recognition motif, a.k.a. RRM/RNC RBD protein
Sapur.004G086100.1	4.73283016	1.76532285	0.20796391	8.81469	1.18E-18	3.42E-18	ppm	0.544218072	1.75E-13	GO:0005515,GO:0006396	Pentatricopeptide repeat-like 51	NA
Sapur.004G141900.1	888.1556239	-0.46326481	0.05320259	-8.81382	1.22E-18	3.49E-18	ppm	-0.618635734	5.93E-18	GO:0008283,GO:0008085,GO:0005576	PHYTOSULFOKINE 3 PRECURSOR	phytosulfokine precursor protein
Sapur.T000500.1	136.5047471	0.62257251	0.047984847	8.806514	1.29E-18	3.68E-18	ppm	-0.560908384	2.14E-14		myb domain protein 101	MYB transcription factor
Sapur.017G081000.1	19.49007042	1.93256258	0.219893327	8.805434	1.30E-18	3.72E-18	ppm	-0.440329883	7.98E-09		PLC-like phosphodiesterases superfamily protein	phosphoipase C, putative
Sapur.004G139800.1	18.28684674	0.56347239	0.064066633	-8.80543	1.36E-18	3.72E-18	ppm	-0.601779756	7.72E-17			NA
Sapur.003G077700.1	5.87004222	-2.21664546	0.1383349	-8.80138	1.35E-18	3.86E-18	ppm	-0.576691509	2.70E-15	GO:0016021,GO:0008233,GO:0006465,GO:0005787	peptidases	microsomal signal peptidase 12 kDa subunit
Sapur.002G061200.1	3.46068333	1.56062456	0.175058856	8.800703	1.36E-18	3.88E-18	ppm	0.55483653	4.75E-14	GO:0007568,GO:0008152	AtUSP,USP	UDP-sugar pyrophosphorylase
Sapur.019G085000.1	426.1823985	0.307468684	0.040632016	8.76832	1.38E-18	3.96E-18	ppm	0.528474744	1.01E-12		prenylated RAB acceptor 1.B4	PRA1 family protein
Sapur.003G149200.2	2.89189483	1.75246125	0.199247566	8.795296	1.43E-18	4.07E-18	ppm	0.46828212	1.51E-10		Protein kinase superfamily protein	choline/ethanolamine kinase
Sapur.005G153800.1	327.4889944	0.558056281	0.063454679	8.795151	1.44E-18	4.08E-18	ppm	0.58318938	1.64E-15	GO:0008299	geranylgeranyl pyrophosphate synthase	geranylgeranyl pyrophosphate synthase
Sapur.005G020800.1	139.2669551	0.50551173	0.057536171	8.787509	1.53E-18	4.36E-18	ppm	0.561992729	2.06E-14			homeodomain protein, putative
Sapur.016G151100.1	84.47179965	-1.56208729	0.178000772	-8.78628	1.54E-18	4.40E-18	ppm	-0.567292048	1.96E-15	GO:0016758,GO:0008152	UGT76E2	UT glucosyltransferase family protein
Sapur.001G179100.1	45.97005642	-2.31655688	0.263888037	-8.77822	1.66E-18	4.73E-18	ppm	-0.6091935	7.92E-17	GO:0003677	EDR4,RAV1	B3 DNA-binding domain protein
Sapur.004G045400.2	10.28803663	-0.69188737	0.08127611	-8.7755	1.76E-18	4.85E-18	ppm	-0.552774192	6.10E-14			adx/fdx reductase family oxidoreductase
Sapur.010G067200.1	1.48985261	2.69258763	0.306937461	8.773174	1.75E-18	4.96E-18	ppm	0.513325235	6.20E-12	GO:0016747,GO:0008610,GO:0016020,GO:0006633	KCS11	3-ketoacyl-CoA synthase 11
Sapur.013G139600.1	131.8134662	-0.06600529	0.119602678	-8.77087	1.77E-18	5.05E-18	ppm	-0.552310188	6.45E-14	GO:0042351	NB-ARC domain-containing disease resistance protein	NA
Sapur.010G049900.1	6.25302946	-1.14209105	0.130247882	-8.7686	1.81E-18	5.15E-18	ppm	-0.576638786	3.11E-15	GO:0016020	SPIN/Band 7/PHB domain-containing membrane-associated protein family	NA
Sapur.005G047800.1	13.14519464	-1.33269492	0.152030882	-8.76802	1.83E-18	5.17E-18	ppm	-0.574000052	1.79E-13		myb domain protein 69	R2R3-MYB transcription factor, putative
Sapur.019G085700.1	8.17649821	-0.97865579	0.111731552	-8.76794	1.83E-18	5.18E-18	ppm	-0.54591724	1.88E-13			NA
Sapur.008G044000.1	8093.989898	0.24755524	0.028240651	8.765928	1.85E-18	5.27E-18	ppm	0.555000455	4.92E-14	GO:0008152,GO:0004807	trioisophosphate isomerase	trioisophosphate isomerase
Sapur.010G019100.1	1024.680809	0.37887805	0.043238144	8.76281	1.90E-18	5.41E-18	ppm	-0.608032049	2.91E-17		beta-ketoacyl-CoA synthase	3-ketoacyl-CoA synthase
Sapur.006G178300.1	1440.18216	-0.28658288	0.032731722	-8.75811	1.99E-18	5.66E-18	ppm	-0.621715457	3.63E-18	GO:0016020	Transmembrane protein 14C	transmembrane protein 14C
Sapur.005G096600.1	742.8695278	-0.37037066	0.042338082	-8.75805	1.99E-18	5.66E-18	ppm	-0.55761414	5.1E-15			transmembrane protein, putative
Sapur.018G065000.1	43.50045588	-0.50982193	0.058232645	-8.75642	2.02E-18	5.75E-18	ppm	-0.603191361	6.27E-17		Nucleotide/sugar transporter family protein	NA
Sapur.016G080800.1	1.79017551	3.49341839	0.398933882	8.752229	2.06E-18	5.94E-18	ppm	0.463360658	2.58E-09	GO:0004674,GO:0048544,GO:0006468,GO:0004672	S-locus lectin protein kinase family protein	NA
Sapur.006G170100.1	21.10910514	-0.84850263	0.096972723	-8.75084	2.12E-18	6.01E-18	ppm	-0.552694616	6.14E-14			hypothetical protein
Sapur.018G070800.1	845.0597948	-0.45658236	0.05219318	-8.74674	2.20E-18	6.23E-18	ppm	-0.615887879	9.40E-18		Cellulose-synthase-like C5	cellulose synthase-like C1-1, glycosyltransferase family 2 protein
Sapur.015G075100.1	175.8391468	-0.26197107	0.144207171	-8.7433	2.28E-18	6.45E-18	ppm	-0.575570705	4.26E-15		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.017G021200.1	8.136238	-0.97150187	0.111135881	-8.74165	2.30E-18	6.52E-18	ppm	-0.56255226	1.75E-14	GO:0005515,GO:0043531	LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.001G034800.1	1.16973029	2.90364186	0.329486126	8.741431	2.30E-18	6.52E-18	ppm	0.529629737	9.88E-13		Protein kinase superfamily protein	NA
Sapur.019G071600.2	17.67046669	0.77571924	0.088819155	8.733611	2.47E-18	6.99E-18	ppm	0.578878134	2.14E-15		alpha/beta-Hydrolases superfamily protein	alpha/beta-hydrolase, putative
Sapur.008G007400.1	23.03192755	0.57546148	0.06601654	8.71528	2.52E-18	7.08E-18	ppm	-0.600917278	7.11E-17		Pentatricopeptide (PPR) superfamily protein	PPR containing plant protein
Sapur.007G141900.1	6.76277874	1.60418233	0.18370589	8.731991	2.52E-18	7.09E-18	ppm	-0.535249139	5.12E-13		ARM repeat superfamily protein	cyclin-like protein
Sapur.006G181500.2	19.24659444	0.75238227	0.086187	8.726969	2.61E-18	7.32E-18	ppm	-0.709708483	2.35E-25		Protein kinase family protein with ARM repeats/transporter family protein	protein transporter
Sapur.016G177900.1	3.48761456	-1.32649927	0.152010783	-8.72635	2.63E-18	7.45E-18	ppm	-0.569931011	6.68E-15		Protein of unknown function (DUF620)	lipase, putative
Sapur.010G080900.1	18.27853845	-0.64613104	0.07387165	-8.72458	2.67E-18	7.56E-18	ppm	-0.568681631	8.9E-15	GO:0007165,GO:0030155,GO:0000160	histidine kinase 5	histidine kinase cytokinin receptor
Sapur.007G109500.1	48.42460023	-0.78170764	0.089568322	-8.72374	2.69E-18	7.62E-18	ppm	-0.545017859	1.59E-13	GO:0006413,GO:0003743	Translation initiation factor SUI1 family protein	translation initiation factor SUI1, eukaryotic protein
Sapur.T060200.1	15.42642785	1.11785827	0.128164654	8.722046	2.73E-18	7.74E-18	ppm	0.53859743	3.44E-13		arm8274H	ARM repeat superfamily protein	NA
Sapur.017G052800.1	422.1479417	1.18185874	0.135585874	8.719343835	2.78E-18	7.86E-18	ppm	0.558793056	2.16E-14		RNA ligase/cyclic nucleotide phosphodiesterase family protein	cyclic phosphodiesterase
Sapur.015G019800.1	61.3299364	0.720342397	0.082618958	-8.71885	2.81E-18	7.96E-18	ppm	-0.61702866	7.66E-18		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.007G092200.1	1658.344327	0.37188102	0.04261611	8.715163	2.84E-18	8.21E-18	ppm	0.562469779	7.75E-14	GO:0006468,GO:0004672	Protein kinase superfamily protein	casein kinase II alpha subunit
Sapur.010G084500.1	0.76412651	2.67028689	0.307406562	8.714811	2.91E-18	8.25E-18	ppm	0.548269178	1.91E-13	GO:0006355,GO:0003677	NAC with transmembrane motif1	No apical meristem (NAM) protein
Sapur.003G176400.1	84.69770164	0.503866099	0.06162727	8.17144	2.94E-18	8.37E-18	ppm	-0.600917278	7.11E-17	GO:0016021	Aquaporin-like superfamily protein	aquaporin SIP1
Sapur.010G096600.1	380.1502526	-0.29535261	0.033904616	-8.7108	3.02E-18	8.54E-18	ppm	-0.563813536	1.49E-14	GO:0008168,GO:0008152	mRNA capping enzyme family protein	methyltransferase domain protein
Sapur.019G093000.1	2.50318536	-0.93187168	0.107018248	-8.70669	3.04E-18	8.61E-18	ppm	-0.567292048	1.96E-15		polygalacturonase-1 non-catalytic subunit beta	polygalacturonase-1 non-catalytic subunit beta
Sapur.001G113300.2	94.23682083	0.742868007	0.054621733	8.683002	3.85E-18	1.09E-17	ppm	0.58245067	1.30E-16	GO:0003950	WVE protein-interaction domain protein family	inactive poly [ADP-ribose] polymerase
Sapur.016G038800.2	7.09532977	1.44331577	0.166239302	-8.68296	3.86E-18	1.09E-17	ppm	-0.538505884	8.57E-13		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.016G018800.1	16.66714898	-0.64532185	0.074334908	-8.68245	3.87E-18	1.09E-17	ppm	-0.563396118	1.32E-15	GO:0005515	F-box family protein	F-box/LRR protein
Sapur.005G197000.1	686.4825701	0.49303353	0.056835327	8.676574	4.08E-18	1.15E-17	ppm	0.589466182	8.65E-16	GO:0008402,GO:0005515	ATPK2,TOD1,TA,PLDDELTA	phosphoipase D
Sapur.008G026000.1	3.38205243	1.70620441	0.196934608	8.670404	4.13E-18	1.16E-17	ppm	0.568719016	1.46E-15	GO:0006468,GO:0005524,GO:0004672	with no lysine (K) kinase 8	NA
Sapur.011G084700.1	0.70185674	2.60035585	0.2998319	8.672255	4.20E-18	1.18E-17	ppm	0.569414656	7.15E-15	GO:0006355,GO:0003677	NAC with transmembrane motif1	NAC transcription factor
Sapur.005G180300.1	112.1514463	0.56000224	0.064579477	8.67013	4.22E-18	1.22E-17	ppm	-0.578812343	1.94E-15	GO:0008193,GO:0006406,GO:0000287	tRNA(m1G37)methyltransferase family protein	tRNA(m1g37)methyltransferase
Sapur.007G084300.1	3080.84083	0.88965329	0.10267488	8.66627	4.45E-18	1.25E-17	ppm	-0.524298245	5.71E-13	GO:0005544,GO:0005509	ANNAT2	annexin 2	annexin
Sapur.008G000100.1	181.3162296	0.46785429	0.054056464	-8.66605	4.47E-18	1.26E-17	ppm	-0.584882667	2.14E-16			hypothet

Sapur.008G067400.1	721.4003053	0.387673641	0.046173129	8.396088	4.62E-17	1.26E-16	cpm	0.51135233	7.72E-12		BPS1	Protein of unknown function (DUF793)	DUF793 family protein
Sapur.15WG153400.1	8.4452111	1.198102428	0.142797685	-8.39021	4.85E-17	1.33E-16	cpm	-0.54228605	2.21E-13	GO:0010621,GO:0004190		SIGNAL PEPTIDE PEPTIDASE-LIKE 1	NA
Sapur.01G022200.1	273.0128648	0.98518994	0.11748286	8.385831	5.04E-17	1.38E-16	cpm	-0.63203176	2.46E-19	GO:0008008,GO:0006222		Zinc/in-like metalloproteases family protein	oligopeptidase A
Sapur.15WG146300.2	22.19433321	0.711305402	0.084863154	8.381793	5.23E-17	1.42E-16	cpm	0.56933828	2.33E-14	GO:0005515		RNI-like superfamily protein	F-box/LRR protein
Sapur.01G023200.1	62.38884633	0.823101168	0.08252181	8.37742	5.41E-17	1.48E-16	cpm	-0.57309379	5.79E-15			alpha/beta-Hydrolases superfamily protein	gibberellin receptor GID1, putative
Sapur.00G058600.1	118.7023134	-0.478895866	0.057175098	-8.37595	5.48E-17	1.49E-16	cpm	-0.59585781	1.81E-16			Oligosaccharyltransferase complex/magnesium transporter family protein	OST3/OST6 family protein
Sapur.15WG151200.1	368.3131597	-0.438985882	0.052410778	-8.37587	5.48E-17	1.50E-16	cpm	-0.57134769	5.56E-15	GO:0004674		Serine/threonine-protein kinase Rio1	Serine/Threonine-kinase RIO1
Sapur.05G068400.1	482.3187107	-0.515891229	0.062106361	-8.37128	5.78E-17	1.55E-16	cpm	-0.59413617	2.16E-16				NA
Sapur.007G022200.1	71.3664221	0.479855803	0.057322743	8.37111	5.71E-17	1.56E-16	cpm	0.53521884	5.08E-13	GO:0007264,GO:0005525		ADP-ribosylation factor family protein	ADP-ribosylation factor(Arf)/Arf-like (Art) small GTPase family protein
Sapur.01G056200.1	8.387832315	0.95128198	0.113847859	8.356109	5.76E-17	1.57E-16	cpm	-0.54345662	2.56E-15			HMG box (high mobility group) DNA-binding family protein	NA
Sapur.00G221600.1	5.841047403	1.225078427	0.146458157	8.364699	6.03E-17	1.64E-16	cpm	0.51861895	7.53E-13	GO:0007165,GO:0000155,GO:0000160		histidine kinase 5	histidine kinase cytokinin receptor
Sapur.01G029300.1	34.24606044	0.312461513	0.15691682	8.28376	6.07E-17	1.65E-16	cpm	0.38802923	1.50E-07				NA
Sapur.15WG029500.1	139.4803521	-0.468654461	0.056048845	-8.36154	6.19E-17	1.69E-16	cpm	-0.5450159	1.59E-13			Tetratricopeptide repeat (TPR)-like superfamily protein	fertility restorer, putative
Sapur.01T027500.1	20.71606666	0.252807148	0.030267148	8.352425	6.26E-17	1.70E-16	cpm	-0.4994373	2.75E-11	GO:0004648,GO:0004672		Protein kinase family protein	lysine kinase
Sapur.01G076200.1	133.5488716	-0.564155796	0.067510136	-8.35661	6.45E-17	1.76E-16	cpm	-0.53673927	4.30E-13				hypothetical protein
Sapur.00G413600.2	3.513969842	1.011631522	0.1213	8.3351247	6.51E-17	1.77E-16	cpm	-0.86827928	4.75E-09	GO:0055085,GO:0016020,GO:0006810,GO:0000215			nucleobase ascorbate transporter 12
Sapur.01G147300.2	41.79271343	-0.616686953	0.075823074	-8.35358	6.62E-17	1.80E-16	cpm	-0.45302055	2.43E-09	GO:0055114,GO:0016491	ATNAT12,NAT12	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	leucoanthocyanidin dioxygenase
Sapur.01G105600.1	3.050477668	-1.362169151	0.163141173	-8.34951	6.85E-17	1.86E-16	cpm	-0.55824255	6.50E-14	GO:0006950		Adenine nucleotide alpha hydrolases-like superfamily protein	adenine nucleotide alpha hydrolases-like superfamily protein
Sapur.00G026100.1	834.1128968	0.387576487	0.046396246	8.349133	6.88E-17	1.87E-16	cpm	-0.59329593	2.52E-14	GO:0016887,GO:0005524		P-loop containing nucleoside triphosphate hydrolases superfamily protein	anion-transporting ATPase
Sapur.004G143800.1	735.0164648	0.368201532	0.044083542	8.348275	6.93E-17	1.88E-16	cpm	-0.55419164	5.09E-14	GO:0005515		Tetratricopeptide repeat (TPR)-like superfamily protein	70 kDa peptidyl-prolyl isomerase, putative
Sapur.01G132700.2	57.46188228	-0.5	0.06931548	-8.34707	6.94E-17	1.89E-16	cpm	-0.56842598	2.36E-15				GPI-anchored protein, putative
Sapur.002G050900.3	99.22202382	-0.481127382	0.057634166	-8.34797	6.94E-17	1.89E-16	cpm	-0.57009621	6.61E-15		FB_GI	gigantea protein (GI)	gigantea protein, putative
Sapur.01G026700.1	151.3743429	-0.601281857	0.072443938	-8.34733	6.98E-17	1.90E-16	cpm	-0.55897462	2.78E-14				carbohydrate-binding module family 50 protein
Sapur.00G149900.1	44.8543042	0.923566955	0.110663354	8.345754	7.08E-17	1.92E-16	cpm	-0.55170873	6.95E-14				NA
Sapur.01G146100.1	4.582862723	-0.829867662	0.100192647	-8.34225	7.29E-17	1.98E-16	cpm	-0.53833242	3.42E-13				hypothetical protein
Sapur.04G118300.1	96.18735821	-0.686670263	0.08231506	-8.34198	7.31E-17	1.98E-16	cpm	-0.57349712	4.75E-15			Ribosomal protein S25 family protein	40S ribosomal protein S25, putative
Sapur.01B024900.1	1885.796697	0.305201488	0.031807882	8.331692	7.97E-17	2.16E-16	cpm	-0.54277519	2.08E-13	GO:0016787,GO:0005524,GO:0003677		eukaryotic translation initiation factor 4A1	eukaryotic initiation factor 4A
Sapur.00G196900.1	1307.778561	-0.263842426	0.031574229	-8.33188	7.99E-17	2.17E-16	cpm	-0.61884881	1.74E-17			Protein of unknown function (DUF810)	DUF810 family protein
Sapur.05G069500.1	0.751052111	2.546334065	0.306058131	8.319773	8.91E-17	2.39E-16	cpm	-0.49478016	4.02E-11			Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant hydroxyproline-rich glycoprotein, putative
Sapur.01T027200.1	1.097909577	1.308166324	0.157332136	8.31662	8.81E-17	2.39E-16	cpm	-0.59102286	3.95E-07			Protein of unknown function (DUF1336)	DUF1336 family protein
Sapur.001G142300.2	18.46794223	-0.788524382	0.094780158	-8.31943	8.84E-17	2.39E-16	cpm	-0.54897354	1.25E-13	GO:0004648,GO:0004672		protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	LysM type receptor kinase
Sapur.01G076200.1	792.3789628	-0.415580182	0.050017022	-8.31708	9.02E-17	2.44E-16	cpm	-0.58337464	2.46E-16			Leucine-rich repeat transmembrane protein kinase family protein	patellin protein
Sapur.01G021200.1	87.13224879	-0.917789910	0.110363179	-8.31589	9.10E-17	2.46E-16	cpm	-0.58907541	4.27E-16	GO:0005515		Tetratricopeptide repeat (TPR)-like superfamily protein	glutamine-5-transferase tau 7
Sapur.01G028300.1	84.66605546	-0.982116971	0.11832248	-8.29994	1.04E-16	2.82E-16	cpm	-0.55324887	4.40E-14			Chaperone DnaJ-domain superfamily protein	chaperone protein DnaJ
Sapur.002G049700.2	5.025177664	1.154577446	0.139241981	8.291877	1.11E-16	3.01E-16	cpm	-0.53475634	5.43E-13				transmembrane protein, putative
Sapur.004G174200.1	410.2916644	-0.433132564	0.05217502	-8.29165	1.12E-16	3.03E-16	cpm	-0.58742753	6.88E-16			Protein of unknown function (DUF341)	dehydrins core family protein, putative
Sapur.005G022300.1	149.5204321	-1.75601703	0.211922888	8.289005	1.14E-16	3.09E-16	cpm	-0.50493359	6.19E-11	GO:0007165:GO:0005515:GO:0043167:GO:0007018:GO:0005524:GO:003377		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.15WG006600.1	3838.810786	0.371466466	0.044834527	8.288528	1.15E-16	3.10E-16	cpm	-0.56789955	8.77E-15				NA
Sapur.005G080200.1	31.63840989	0.676062962	0.082002824	8.28817	1.16E-16	3.11E-16	cpm	-0.53833242	2.42E-13	GO:0055739,GO:0006139	ATCOX6B2,COX6B	cytochrome C oxidase 6B	cytochrome C oxidase subunit 6b
Sapur.01B021800.1	12.28641714	-1.307127528	0.157827145	-8.28202	1.21E-16	3.27E-16	cpm	-0.53458617	5.54E-13				transmembrane protein, putative
Sapur.005G012900.1	210.6024855	-0.767358584	0.0894222	-8.28145	1.22E-16	3.28E-16	cpm	-0.54953769	9.66E-14	GO:0016758,GO:0008152		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase family protein
Sapur.15WG015800.1	506.1978692	0.45019272	0.048453757	8.280002	1.23E-16	3.32E-16	cpm	-0.52861659	1.97E-12	GO:0055114,GO:0009916		alternative oxidase 1A	ubiquinol oxidase
Sapur.00G085600.1	68.02329263	-0.647896224	0.08	8.2799	1.26E-16	3.36E-16	cpm	-0.59742266	1.46E-16			Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	NA
Sapur.01G025500.1	17.15414664	-0.880913594	0.106438242	-8.27707	1.26E-16	3.41E-16	cpm	-0.58967773	6.96E-15		PHS1	poor homologous synapsis 1	synapsis 1-like protein, putative
Sapur.01B026600.1	186.8218667	-0.331616419	0.04023953	-8.25507	1.38E-16	3.45E-16	cpm	-0.54543075	1.51E-13			dolichyl-phosphate-mannose-protein mannosyltransferase-related	NA
Sapur.00B079100.1	6.853795531	1.18083302	0.142734594	8.272928	1.31E-16	3.52E-16	cpm	-0.55170868	6.95E-14		ECT7	evolutionarily conserved C-terminal region 7	YTH domain protein
Sapur.01G124700.1	5.450861683	1.175862604	0.142126265	8.266428	1.40E-16	3.76E-16	cpm	-0.47687628	7.72E-10			ankyrin repeat-containing protein	NA
Sapur.01G037500.1	228.6387734	-0.354686848	0.042886319	-8.26363	1.41E-16	3.81E-16	cpm	-0.55452778	8.88E-14			Telomerase activating protein Est1	Est1 DNA/RNA-binding domain protein
Sapur.002G130900.1	287.9143663	0.322008841	0.039105395	8.257965	1.48E-16	3.99E-16	cpm	-0.58265133	1.20E-15	GO:0005515		ARABIDILO-1	ubiquitin-protein ligase, putative
Sapur.008G112600.1	7051.708798	-0.476621622	0.057696154	-8.25669	1.51E-16	4.24E-16	cpm	-0.58065772	5.13E-15	GO:0015079,GO:0009538,GO:0009522	PSAD-1	photosystem I subunit D-1	photosystem I reaction center subunit II
Sapur.007G139800.1	11.71727904	-1.277585556	0.156790515	-8.24568	1.64E-16	4.42E-16	cpm	-0.55452736	8.89E-14				hypothetical protein
Sapur.006G012900.1	78.54092212	-0.524570195	0.063604413	-8.24531	1.66E-16	4.46E-16	cpm	-0.54497015	1.60E-13			Protein of unknown function (DUF567)	LURP-one-related protein
Sapur.01B026400.1	255.7076917	-0.299884566	0.036377841	-8.24361	1.67E-16	4.49E-16	cpm	-0.56354086	1.54E-14	GO:0051287		6-phosphogluconate dehydrogenase family protein	6-phosphogluconate dehydrogenase NAD-binding domain protein
Sapur.01G198200.1	80.02246211	-0.597498882	0.072439125	-8.24319	1.68E-16	4.51E-16	cpm	-0.50688045	1.34E-11	GO:0004648,GO:0004672		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.008G072000.1	122.4349697	-0.482852218	0.058578128	-8.24286	1.68E-16	4.52E-16	cpm	-0.75767927	2.67E-20		FLA17	Fasciclin-like arabinogalactan protein 17 precursor	fasciclin-like protein
Sapur.01G060500.1	148.3391524	-0.656077988	0.079545039	-8.24107	1.71E-16	4.59E-16	cpm	-0.57342033	2.46E-15	GO:0008017,GO:0007018,GO:0005524,GO:003777,GO:0005871		P-loop containing nucleoside triphosphate hydrolases superfamily protein	kinesin motor domain protein
Sapur.01G119700.1	60.2674071	0.979466038	0.118852945	8.240991	1.71E-16	4.59E-16	cpm	-0.49794187	1.34E-11	GO:0016887,GO:0005524,GO:0016020	ABCG37,ATPDRP8,PIS1	pleiotropic drug resistance 9	ABC transporter G family protein
Sapur.005G127500.1	22.26130949	0.597190179	0.072490875	-8.2378	1.75E-16	4.70E-16	cpm	-0.54817394	7.76E-13	GO:0006468,GO:0006672		Protein kinase superfamily protein	NA
Sapur.005G080800.1	51.97619356	-0.561661396	0.068013008	-8.2327	1.81E-16	4.86E-16	cpm	-0.53372819	6.12E-13	GO:0008270,GO:0005515		RING/U-box superfamily protein	RING-U-box superfamily protein
Sapur.006G041700.1	25.8654901	-0.769462999	0.092892273	-8.23264	1.83E-16	4.92E-16	cpm	-0.54722418	1.21E-13				hypothetical protein
Sapur.15WG014400.1	4.253018383	1.252014751	0.152	8.2604638	1.85E-16	4.98E-16	cpm	-0.51197025	7.26E-14			Plant protein of unknown function (DUF247)	DUF247 domain protein
Sapur.008G105100.1	329.3797964	-0.008416928	0.1235293	-8.22873	1.88E-16	5.08E-16	cpm	-0.5463271	2.88E-13	GO:0006468,GO:0005524,GO:0004672		MAP kinase 15	MAP kinase 15
Sapur.002G139600.2	12.84960171	-0.564483864	0.129486855	-8.22192	2.00E-16	5.37E-16	cpm	-0.52921425	1.52E-13	GO:0016491,PGLC,PGLCL		CBL-interacting protein kinase 9	CBL-interacting serine/Threonine-kinase
Sapur.15WG010000.1	19.42854272	-0.762015135	0.092732713	-8.21733	2.08E-16	5.58E-16	cpm	-0.56094653	2.41E-14	GO:0005885,GO:0016021	ATNRT2.5,NRT2.5	nitrate transporter2.5	high-affinity nitrate transporter
Sapur.01G220200.1	3.303889969	-1.450423129	0.1974383	-8.21493	2.12E-16	5.69E-16	cpm	-0.53952466	3.08E-13				transmembrane protein, putative
Sapur.001G125200.1	24.08447586	1.07621933	0.131016547	8.214277	2.13E-16	5.71E-16	cpm	-0.42824395	1.50E-08			Kinase interacting (KIP1-like) family protein	NA
Sapur.01G058500.1	161.9717501	-1.15261247	0.14014764	-8.2105	2.21E-16	5.92E-16	cpm	-0.55092664	1.84E-14	GO:0008019	FAR2,MS2	triplite acyl CoA reductase-related male sterility protein	fatty acyl-CoA reductase
Sapur.01G050100.1	5.867645589	1.253391171	0.152764718	8.204716	2.31E-16	6.19E-16	cpm	-0.52973735	9.76E-13	GO:0007010,GO:0003779	ATVIN2,VLN2	villin 2	villin-3 protein
Sapur.01B029700.1	210.1689512	-0.456469055	0.055603948	-8.20005	2.45E-16	6.43E-16	cpm	-0.55991017	2.46E-14			Protein of unknown function (DUF761)	transmembrane protein, putative
Sapur.01G285000.1	47.56894944	-0.597995519	0.072889919	-8.19171	2.58E-16	6.89E-16	cpm	-0.54601791	9.03E-14			Ubiquitin conjugating enzyme family protein	plant organelle RNA recognition domain protein
Sapur.003G090600.1	182.4868969	-0.470965768	0.057496662	-8.19041	2.60E-16	6.96E-16	cpm	-0.50633752	1.33E-11	GO:0006355,GO:0005634,GO:0016677,GO:0009725	ARF1	auxin response factor 1	auxin response factor 1
Sapur.01G027400.1	14.00413857	1.358456514	0.178007666	8.188009	2.66E-16	7.10E-16	cpm	-0.45060895	1.16E-09				transmembrane protein, putative
Sapur.01G016900.2	6.900676881	-1.012359206	0.123661237	-8.18788	2.66E-16	7.10E-16	cpm	-0.5159965	4.64E-12	GO:0019898,GO:0015979,GO:0009654,GO:0009523,GO:0005509	PPL1	PsbP-like protein 1	thylakoid lumenal 25.6 kDa protein, putative
Sapur.004G092200.1	181.1158369	0.413705656	0.050257561	8.187343	2.67E-16	7.14E-16	cpm	-0.47878819	2.26E-10	GO:0007165			NA
Sapur.003G062300.1	53.69022205	-0.648902865	0.079320295	-8.18104	2.83E-16	7.51E-16	cpm	-0.73180249	1.34E-27		SKL2	shikimate kinase like 2	shikimate kinase-like protein
Sapur.006G184200.1	9.016731351	0.227049988	0.031388844	-8.17341	3.05E-16	8.09E-16	cpm	-0.52416206	8.61E-12				NA
Sapur.15WG106800.1	525.6445713	1.259597542	0.154199101	8.16832	3.13E-16	8.34E-16	cpm	-0.46894904	7.07E-10			RPM1-interacting protein 4 (RIN4) family protein	RPM1-interacting protein
Sapur.15WG145400.1	110.5276907	-0.452842569	0.055426586	-8.16652	3.17E-16	8.47E-16	cpm	-0.54422081	1.75E-13		CC82,UCC82B	Protein of unknown function (DUF2930)	CC82, putative
Sapur.01G128800.1	373.8144876	-0.604939734	0.052286339	-8.16622	3.18E-16	8.49E-16	cpm	-0.53015174	3.94E-13	GO:0005975,GO:0004553	AtGH9B6,GH9B8	glycosyl hydrolase family 9 protein	glycosyl hydrolase family 9 protein
Sapur.003G074700.1	84.30931143	0.846069102	0.103609785	-8.16573	3.20E-16	8.52E-16	cpm	-0.55381287	5.34E-14			Protein of unknown function (DUF581)	DUF581 family protein
Sapur.003G011000.1	307.3283662	-0.307665182	0.037774419	-8.16524	3.22E-16	8.55E-16	cpm	-0.58441269	9.34E-16	GO:0016021		(2H)(5)(7)(8)-tetrahydrofolate synthase family	3-ketoacyl-CoA synthase
Sapur.001G185500.1	209.6189662	-0.263583806	0.03230802	-8.15846	3.39E-16	9.04E-16	cpm	-0.54276556	2.09E-13	GO:0009982,GO:0009451,GO:0003723,GO:0001522		Pseudouridine synthase family protein	RNA pseudouridine synthase
Sapur.01G065900.2	2.824868313	1.292406433	0.158402077	-8.1559	3.47E-16	9.22E-16	cpm	-0.55251042	4.31E-14	GO:0016787,GO:0005524,GO:0003677		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.15WG114800.1	151.8435377	-0.377267488	0.046264488	-8.15458	3.50E-16	9.31E-16	cpm	-0.58339289	1.98E-15	GO:0016788	NPC6	non-specific phosphodiester C6	phosphodiester C
Sapur.01G131600.1	1355.758711	-0.385884437	0.047122488	-8.15456	3.50E-16	9.31E-16	cpm	-0.58088853	5.56E-15	GO:0016192,GO:0006886		zinc ion binding	vacuolar sorting-associated-like protein
Sapur.01G022200.1	73.07664992	-0.424851862	0.052103327	-8.15401	3.52E-16	9.37E-16	cpm	-0.56939786	2.32E-14	GO:0016491,GO:0008152		short-chain dehydrogenase-reductase B	NA
Sapur.003G048800.1	271.9113257	0.367436302	0.045008725	8.153931	3.52E-16	9.38E-16	cpm	-0.52728588	1.28E-12				PAH-IV domain protein
Sapur.01G267800.1	238.9457258	0.515567741	0.062880478	8.151286	3.60E-16	9.58E-16	cpm	-0.52658209	1.40E-12	GO:0004674,GO:0048544,GO:0006468,GO:0004672		S-locus lectin protein kinase family protein	PPP06 protein phosphatase domain protein, putative
Sapur.003G048800.1	536.837823	0.236060464	0.028976047	8.146889	3.74E-16	9.93E-16	cpm	-0.54928644	1.40E-13			Transducin/WD40 repeat-like superfamily protein	flowering time control protein FY, putative
Sapur.001G022400.1	19.69849218	-0.750602842	0.09539087	-8.1445	3.81E-16	1.01E-15	cpm	-0.48240038	1.08E-10	GO:0005515	FY		hypothetical protein
Sapur.001G195000.1	326.9579821	-0.820595776	0.100815445	-8.13958	3.97E-16	1.05E-15	cpm	-0.54363504	1.88E-13				NA
Sapur.004G000300.1	1005.419664	0.268272271	0.032965429	8.131852	4.23E-16	1.12E-15	cpm	-0.52216258	1.56E-14		GDSL200	Protein kinase superfamily protein	ABC1 family kinase
Sapur.005G134100.1	0.91027943	1.2888775	0.406668852	8.129842	4.30E-16	1.14E-15	cpm	-0.43503374	1.20E-08	GO:0005975,GO:0004553		Glycosyl hydrolase superfamily protein	RNA pseudouridine synthase
Sapur.01G231300.1	58.16015833	-0.660202272	0.08181651	-8.11867	4.34E-16	1.15E-15	cpm	-0.55251042	4.31E-14	GO:0016787,GO:0005524,GO:0003677		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.01G304500.1	8523.104104	0.388019616	0.047742288	-8.11721	4.39E-16	1.17E-15	cpm	-0.57348704	5.51E-15	GO:0005180,GO:0006950,GO:0006457,GO:0005524	AtHsp90.4,Hsp90.4	non-specific phosphodiester C6	phosphodiester C
Sapur.01G000100.1	1.4124845	0.954881443	0.241060723	8.121567	4.46E-16	1.18E-15	cpm	-0.8141953	7.62E-19		ATRAF1,FIM1	Fimbrin 1	vacuolar sorting-associated-like protein
Sapur.01G024200.1	7.608443611	-0.952582385	0.117232839	-8.11556	4.45E-16	1.18E-15	cpm	-0.56245851	1.78E-14	GO:0055114,GO:0006788,GO:0004392	HO2	heme oxygenase 2	heme oxygenase
Sapur.01G136700.1	2.819457505	1.261458852	0.156951751	8.1409454	4.52E-16	1.19E-15	cpm	-0.60524949	1.38E-17				NA
Sapur.003G034000.1	800.0656876	0.363357606	0.044737342	8.123836	4.52E-16	1.20E-15	cpm	-0.51999259	7.20E-12	GO:0016788	NPC1	non-specific phosphodiester C1	acting on ester bonds hydrolase, putative
Sapur.003G067000.3	10.56389202	0.723689317	0.089116832	8.120454	4.64E-16	1.23E-15	cpm	-0.52493748	1.70E-12	GO:0008289	EDR2	ENHANCED DISEASE RESISTANCE 2	enhanced disease resistance 2 protein
Sapur.005G099400.1	491.5507914	-0.512507895	0.063095671	-8.11525	4.89E-16	1.29E-15	cpm	-0.55417456	5.04E-14	GO:0006631,GO:0016491,GO:0006098		6-phosphogluconate dehydrogenase family protein	decarboxylating 6-phosphogluconate dehydrogenase
Sapur.009G099500.1	99.92998883	0.490601797	0.05240171	8.109416	5.09E-16	1.35E-15	cpm	-0.53356592	2.51E-13	GO:0016627,GO:0016021,GO:0006629,GO:0005737		3-oxo-5-alpha-steroid 4-dehydrogenase family protein	3-oxo-5-alpha-steroid 4-dehydrogenase
Sapur.005G070200.1	205.3579944	-0.3767058	0.04647563	-8.10662	5.12E-16	1.36E-15	cpm	-0.52888525	1.98E-12	GO:0008152,GO:0008324	AAI1	acyl activating enzyme 1	NA
Sapur.01G161700.3	12.89122166	0.868384866	0.107122712	8.10611	5.23E-16	1.38E-15	cpm	-0.56306488	1.64E-14	GO:0003677		Homeodomain-like superfamily protein	homeobox leucine zipper protein, putative
Sapur.005G044000.1	174.4444667	-0.723383347	0.08926251	-8.10323	5.35E-16	1.42E-15	cpm	-0.51573825	4.78E-12	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	ATTT12,TT12	MATE efflux family protein	MATE transporter
Sapur.01G061400.1	4.731635534	1.407406041	0.173711197	8.102301	5.38E-16	1.43E-15	cpm	-0.65281934	1.97E-20	GO:0005307,GO:0005986		Sucrose-6F-phosphate phosphohydrolase family protein	sucrose phosphate phosphatase
Sapur.01G047300.1	481.1779642	-1.154684869	0.143523281	8.101323	5.44E-16	1.44E-15	cpm	-0.56788334	5.96E-15	GO:0005524		DNA2 domain-containine protein / helicase domain-containine protein / HINU endonuclease domain-containine an	NA
Sapur.01G248800.1	775.4521501	1.307060553	0.16139623	8.098334	5.57E-16	1.48E-15	cpm	-0.51318466	4.54E-12		ATEXPB2,ATHEXP BETA 1.4	expansin B2	expansin B
Sapur.005G093800.1	31.3454534	-0.81631861	0.100831157	-8.09569	5.68E-16	1.51E-15	cpm	-0.53898876	4.17E-13	GO:0007165:GO:0005515		Toll-interleukin-Resistance (TIR) domain family protein	NA
Sapur.004G154400.1	293.0105644	-0.47582762	0.058344411	8.09463	5.75E-16	1.53E-15	cpm	-0.52897409	1.34E-12	GO:0003677:GO:0006055		Cytochrome C1 family	cytochrome c1 heme protein
Sapur.005G108400.1	656.8107017	-0.217200304	0.026932205	-8.0922	5.86E-16	1.55E-15	cpm	-0.53814703	3.63E-13			Cysteine/heme bete-synthase (CBS) family protein	CBS domain protein
Sapur.T13870.1	22.91131131	0.833183665	0.103061671	8.081185	6.04E-16	1.60E-15	cpm	-0.64438805	5.77E-09			Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.01G073800.1	11.02000231	-0.835829859	0.103488652	-8.07666	6.66E-16	1.76E-15	cpm	-0.51464658	5.52E-12				hypothetical protein
Sapur.01G026100.1	41.39648889	1.737078223	0.215080444	8.075266	6.68E-16	1.77E-15	cpm	-0.51072842	4.28E-12		GIL1	Plant protein of unknown function (DUF641)	DUF641 family protein
Sapur.002G012500.1	5.289313344	1.059457946	0.131185127	8.066901	7.04E-16	1.86E-15	cpm	-0.53468781	5.47E-13				light-stress-responsive one-helix-like protein, putative
Sapur.15WG110000.1	115.3663151	-0.875174197	0.108539875	-8.06091	7.08E-16	1.87E-15	cpm	-0.66424171	3.86E-11	GO:0005525	ATRAB-F2A,ATRABSA,ATRAI	RAB homolog 1	Ras-related protein Rab1
Sapur.01G035600.1	126.6404716	-0.988471782	0.122664015	-8.05949	7.66E-16	2.02E-15	cpm	-0.54087528	2.56E-14	GO:0007264,GO:0005525	ARABH1a,RABH1a	RAB GTPase homolog H1E	NA
Sapur.01G034300.1	14.59115585	-0.668649449	0.088338377	8.1147	8.11E-16	2.14E-15	cpm	-0.53029804	1.31E-12			Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.01G054000.1	4.08614675	-1.126568289	0.139248807	-8.0511	8.21E-16	2.16E-15	cpm	-0.55452791	5.12E-14			S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	16S rRNA (guanine(527)-N(7))-methyltransferase
Sapur.009G091400.1	95.33946238	-0.72715677	0.090319357	-8.05095	8.22E-16	2.17E-15	cpm	-0.53824795	5.59E-13			Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.01B026200.1	88.47574627	-0.624822974	0.077634344	-8.04828	8.46E-16	2.22E-15	cpm	-0.56265602	1.80E-14				DUF688 family protein
Sapur.01G004700.1	19.70167319	-0.795259016	0.09882182	-8.0474	8.48E-16	2.23E-15	cpm	-0.53974582	5.21E-14	GO:0005515		Calcium-dependent lipid-binding (CaLB domain) family protein	Arf-GTPase activator, putative
Sapur.003G065200.1	6.765437314	-0.811229192	0.101061751	-8.04577	8.55E-16	2.25E-15	cpm	-0.55948531	2.58E-14	GO:0016491,GO:0008152	RPM1,RPS3	NB-ARC domain-containing disease resistance protein	NA
Sapur.01G076600.1	13.37782689	-1.093761768	0.135828519	-8.04657	8.51E-16	2.24E-15	cpm	-0.51892572	3.11E-12	GO:0055085,GO:0016021,GO:0016020,GO:0006810,GO:0005215		Major facilitator superfamily protein	NA
Sapur.01B005200.1	221.6895723	-0.847692169	0.105405152	-8.0425	8.86E-16	2.32E-15	cpm	-0.57664743	2.02E-15			Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/LTP family protein
Sapur.01G242800.1	83.21972368	-0.519566443	0.064607145	-8.04193	8.84E-16	2.33E-15	cpm	-0.56305444	1.64E-14				hypothetical protein
Sapur.01G088900.1	1341.661349	0.262808081	0.108649455	8.037699	9.15E-16	2.41E-15	cpm	-0.52472071	2.81E-12	GO:0055114,GO:0016491,GO:0005507	LAC14	laccase 14	laccase
Sapur.001G131700.3	3.515789809	-0.262808081	0.117494979	-8.0349	9.37E-16	2.46E-15	cpm	-0.53811291	8.61E-13	GO:0016020		Uncharacterized protein family (UPF0016)	transmembrane protein TPA81, putative
Sapur.01G

Sapur.005G105100.6	1.633876752	-1.652904262	2.013766027	-7.73231	1.06E-14	2.69E-14	cpen	-0.551670069	6.98E-14	GO:0043565,GO:0006355,GO:0003700	AT4G36730.1	GBF1	G-box binding factor 1	bZIP transcription factor
Sapur.017G121100.1	17.27194439	-0.805077267	0.106133706	-7.73119	1.07E-14	2.72E-14	cpen	-0.509017995	1.25E-11		AT5G11120.1			NA
Sapur.006G011300.4	4.576271941	1.068205308	0.138184024	-7.70287	1.07E-14	2.74E-14	cpen	-0.523287056	1.98E-12	GO:0003676	AT5G07910.1		RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein A1
Sapur.015G072200.1	510.9105545	-0.232478428	0.030087978	-7.72662	1.10E-14	2.82E-14	cpen	-0.549819065	1.56E-11	GO:0005789	AT4G21450.1		PapD-like superfamily protein	MSP (major sperm protein) domain protein
Sapur.005G269700.1	10.87583655	-0.757070404	0.098127952	-7.72431	1.12E-14	2.87E-14	cpen	-0.538656562	1.67E-12	GO:0016351,GO:0003677	AtNAC20/ LCU/CLA/CAC368	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC transcription factor 007	
Sapur.007G024300.1	2771.713991	-0.241200663	0.031238253	-7.72132	1.15E-14	2.93E-14	cpen	-0.522011617	2.36E-12	GO:0003676	AT5G50670.1	LS-70K/U1SNRNP	U1 small nuclear ribonucleoprotein-70K	U1 small nuclear ribonucleoprotein 70 kDa protein, putative
Sapur.002G046300.1	160.610842	-0.610302238	0.079107116	-7.71672	1.19E-14	3.04E-14	cpen	-0.488352538	1.84E-10					NA
Sapur.010G284400.1	51.05428814	-0.664758815	0.086158877	-7.71566	1.20E-14	3.07E-14	cpen	-0.1574385	4.78E-15	GO:0006457,GO:0003755,GO:0000413	AT5G56370.2	ROC2	rotamase cyclophilin 2	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.001G107300.1	78.41428881	-0.37338014	0.048609728	-7.70838	1.27E-14	3.24E-14	cpen	-0.558826984	2.83E-14		AT5G61360.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.002G069900.1	142.863984	-0.766026193	0.09941211	-7.70664	1.29E-14	3.30E-14	cpen	-0.544691171	1.75E-13		AT5G38131.1		O-fucosyltransferase family protein	GDP-fucose protein O-fucosyltransferase
Sapur.014G108300.1	12.25363347	1.174319367	0.152510202	7.688571	1.38E-14	3.50E-14	cpen	0.511856647	7.31E-12	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT7G27510.1	AT-NHX1,ATNHX1,ATNHX1,N	Na+/H+ exchanger 1	sodium/hydrogen exchanger
Sapur.006G000400.1	72202.89427	0.268227949	0.034867749	7.687819	1.38E-14	3.52E-14	cpen	0.514653365	1.38E-12	GO:0055114,GO:0016616	AT1G11440.1	GLYR1	glycerate/hydroxypyruvate dehydrogenase C2	glycerate/hydroxy-3-phosphate dehydrogenase
Sapur.013G107300.1	226.9300654	0.325180683	0.042269276	7.693074	1.44E-14	3.65E-14	cpen	0.496268048	7.14E-11	GO:0048544,GO:0006468,GO:0005524,GO:0004672	AT5G34300.1		lectin protein kinase family protein	Serine/Threonine-kinase
Sapur.011G062100.1	3.469165573	1.279267441	0.166259159	7.69553	1.45E-14	3.69E-14	cpen	0.517701894	1.36E-12	GO:0005515	AT4G28800.1	AtRLP43,RLP43	receptor like protein 43	NA
Sapur.018G084700.1	2797.154338	-0.300080406	0.046804077	-7.69266	1.46E-14	3.66E-14	cpen	-0.544227062	1.75E-13	GO:0008234,GO:0006508	AT4G24280.1		alpha/beta-Hydrolases superfamily protein	lysosomal pro-X carboxypeptidase
Sapur.002G013900.2	70.37595841	-0.231021205	0.030097586	7.691051	1.46E-14	3.71E-14	cpen	0.519226338	2.97E-12	GO:0016020	AT5G48140.3		Protein of unknown function (DUF3644)	DUF3644 family protein
Sapur.004G121400.1	394.1062057	-0.592974917	0.077118393	-7.68851	1.49E-14	3.79E-14	cpen	-0.535012244	5.26E-13	GO:0006508,GO:0004252	AT4G10550.1		Subtilase family protein	subtilisin-like protease
Sapur.006G230100.1	3108.489154	-0.49887934	0.064924272	7.677855	1.62E-14	4.11E-14	cpen	0.506734801	1.27E-11	GO:0005515	AT3G25490.1	EBF1,FBL6	E3ID-binding F box protein 1	E3ID-binding F-box protein
Sapur.010G053800.2	1.406092456	-1.244611259	0.241844793	-7.67487	1.63E-14	4.14E-14	cpen	-0.550649516	6.46E-14	GO:0008270,GO:0005515	AT5G08950.1		RING/U-box superfamily protein	RING-zinc finger protein, putative
Sapur.007G039900.1	48.23032879	-0.74830395	0.097407908	-7.67506	1.65E-14	4.19E-14	cpen	-0.582653092	1.19E-15		AT5G66440.1			transmembrane protein, putative
Sapur.014G117200.1	1.187410123	2.463282332	0.318561807	-7.63479	2.24E-14	5.71E-14	cpen	-0.519856521	2.31E-12		AT1G69410.1		Protein of unknown function (DUF3754)	NA
Sapur.001G121300.1	960.9604043	-0.254715142	0.032177771	-7.66804	1.75E-14	4.43E-14	cpen	-0.58229562	7.18E-16	GO:0008168	AT4G18030.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase, putative
Sapur.001G131300.1	6.721916166	1.064918282	0.138855105	7.66697	1.76E-14	4.46E-14	cpen	-0.550403872	1.63E-16	GO:0008270,GO:0005515	AT5G04790.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.009G111700.1	591.4894663	0.347680132	0.045348526	7.666845	1.78E-14	4.47E-14	cpen	-0.493003475	6.63E-11		AT5G62130.1			coiled-coil protein
Sapur.009G075000.2	22.57998663	-0.426087264	0.055608332	-7.66257	1.79E-14	4.48E-14	cpen	-0.540074174	2.30E-12	GO:0003677,GO:0005515	AT3G19530.1	HAT3.1	Homeodomain-like protein with RING/FYVE/PHD-type zinc finger domain	homeobox domain protein
Sapur.009G060500.1	494.0276025	-0.65679951	0.085684362	-7.66534	1.78E-14	4.52E-14	cpen	-0.548266107	1.07E-13	GO:0016758,GO:0008152	AT2G30140.1		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase, putative
Sapur.002G096200.1	1043.417066	0.335787192	0.043827886	7.661497	1.84E-14	4.65E-14	cpen	0.521193954	2.59E-12	GO:0016114,GO:0008685	AT5G20370.1	ISPF,MECPS	isoprenoid F	2-C-methyl-D-erythritol 2%2C4-cyclodiphosphate synthase
Sapur.003G000300.1	3.52417564	-0.52169294	0.17721	-7.65893	1.87E-14	4.73E-14	cpen	-0.521873853	2.40E-12		AT1G78850.1		Tetratricopeptide repeat (TPR)-like superfamily protein	pentatricopeptide (PPR) repeat protein, putative
Sapur.005G047900.1	1256.709166	-0.302173767	0.065658995	-7.64844	2.03E-14	5.14E-14	cpen	-0.577627204	2.36E-15	GO:0042651,GO:0015979,GO:0009522,GO:0005516	AT5G64040.1	PSAN	photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN)	photosystem I reaction center subunit N
Sapur.009G072100.1	192.1449916	-0.567004187	0.073788718	-7.6402	2.17E-14	5.48E-14	cpen	-0.513819447	1.87E-12		AT1G19540.1		Protein of unknown function (DUF620)	lipase, putative
Sapur.013G078200.1	294.5426227	0.537788757	0.070411691	7.637776	2.21E-14	5.58E-14	cpen	0.512166897	7.07E-12	GO:0005085,GO:0016020,GO:0008180,GO:0005215,GO:0006863,GO:0005345	AT3G10960.1	ATAGL1,AZG1	AZA-guanine resistant1	NA
Sapur.013G085200.1	13.27568705	-0.447282332	0.180561807	-7.63479	2.24E-14	5.71E-14	cpen	-0.496622427	3.71E-11	GO:0003723	AT4G19370.1		RNA-binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.002G204900.1	969.7909152	-0.235169181	0.030876568	-7.62864	2.37E-14	5.99E-14	cpen	-0.534442531	5.63E-13	GO:0009508,GO:0015979,GO:0006364,GO:0009523,GO:0005509	AT5G11450.1		Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein	PsbP protein
Sapur.002G045400.1	82.00864609	-0.607197208	0.076549194	-7.62519	2.43E-14	6.13E-14	cpen	-0.550043872	8.36E-14		AT5G20370.2			NA
Sapur.7135500.1	2.462882199	1.271614567	0.166758869	7.625469	2.43E-14	6.13E-14	cpen	0.587063755	6.45E-16					NA
Sapur.006G076000.1	21.94956639	-0.275164231	0.035904804	-7.62532	2.43E-14	6.14E-14	cpen	0.48268702	5.01E-10	GO:0005089	AT2G02010.1	ATRORGEF1,ROPGEF7	RhoGAP-nucleotide exchange factor 7	Rho/guanine nucleotide exchange factor
Sapur.010G113200.1	62.83992519	-0.692087291	0.090602107	-7.62525	2.43E-14	6.14E-14	cpen	-0.533347996	1.16E-12		AT5G49330.1	ATMYB113,MYB113,PFG3	myb domain protein 113	MYB-like DNA-binding domain protein
Sapur.159G115700.2	21.4868067	-0.604308596	0.07929923	-7.62061	2.52E-14	6.36E-14	cpen	-0.49408044	4.45E-11	GO:0008641	AT5G49940.1	AT-SAE1-1,ATSAE1a,SAE1a	SUMO-activating enzyme 1A	NA
Sapur.004G083600.1	137.3887425	-0.426881631	0.0466502	-7.61965	2.54E-14	6.41E-14	cpen	-0.540209039	2.82E-12	GO:0005515	AT4G17980.1		Calcium-dependent lipid-binding (CaLB domain) family protein	Arf GTPase activating protein
Sapur.019G069700.1	1237.45665	0.227131806	0.026810357	7.619228	2.55E-14	6.43E-14	cpen	0.511499638	7.02E-12		AT4G13530.1			transmembrane protein, putative
Sapur.005G104100.1	7.700012431	-0.536127888	0.123433344	-7.61723	2.58E-14	6.50E-14	cpen	-0.52049118	2.81E-12		AT4G25170.1		Uncharacterized conserved protein (UCP012943)	hypothetical protein
Sapur.7161500.1	360.3831094	0.407269728	0.053498789	7.613317	2.68E-14	6.78E-14	cpen	0.567518776	9.68E-15	GO:0005085,GO:0016020,GO:0008180,GO:0015171,GO:0003333	AT1G58330.1	CAT2	cationic amino acid transporter 2	NA
Sapur.006G169000.2	4.130718205	-0.451254704	0.059128119	-7.61016	2.73E-14	6.87E-14	cpen	-0.551832427	1.46E-14		AT1G18240.1			DUF886 domain protein
Sapur.003G143100.1	6.662216568	-1.152363771	0.151540596	-7.60432	2.86E-14	7.21E-14	cpen	-0.605166431	6.27E-17		AT5T23A,5T2A	sulfotransferase 2A	sulfotransferase family protein	flavonol 4'-sulfotransferase, putative
Sapur.001G072400.1	31.23073219	-0.591683474	0.077817433	-7.6022	2.93E-14	7.39E-14	cpen	-0.525676608	5.66E-12	GO:0008270,GO:0005515	AT5G60510.1		RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.018G114300.1	0.852514333	2.448645919	0.322286169	7.597206	3.03E-14	7.61E-14	cpen	-0.501727761	2.17E-11		AT3G22235.1			NA
Sapur.004G143900.1	172.9320858	0.445863479	0.058679029	7.59482	3.08E-14	7.75E-14	cpen	0.467573375	6.66E-10	GO:0016020	AT5G36380.1		Integral membrane Yip1 family protein	membrane protein ob40
Sapur.001G079000.1	6.614213839	1.318180789	0.172956337	7.594669	3.09E-14	7.77E-14	cpen	0.502356187	2.08E-11	GO:0005085,GO:0016021,GO:0015299,GO:0006812	AT5G41610.1	CHX18,CHX18	cation/H+ exchanger 18	cation proton exchanger
Sapur.009G019400.2	31.30353832	-0.517800185	0.068191215	-7.59365	3.11E-14	7.82E-14	cpen	-0.501227962	2.29E-11	GO:0005515	AT5G21090.1		Leucine-rich repeat (LRR) family protein	brassinosteroid insensitive 1-associated receptor kinase
Sapur.015G175700.1	2.954233808	-0.556205396	0.121510391	-7.59185	3.13E-14	7.86E-14	cpen	-0.4840036	1.81E-10	GO:0006508,GO:0004185	AT2G35770.1	scp2B	serine carboxypeptidase 10	serine carboxypeptidase
Sapur.005G142300.1	54.8230943	1.087574031	0.143361612	7.586904	3.28E-14	8.23E-14	cpen	0.479540858	2.06E-10		AT4G39400.1			DUF688 family protein
Sapur.016G251700.1	239.1438859	-0.769444136	0.10547555	-7.57968	3.46E-14	8.68E-14	cpen	-0.489401357	7.77E-11	GO:0006355,GO:0003700	AT1G01720.1	ATERF-4,ATERF4,ERF4,RAP2	ethylene responsive element binding factor 4	ethylene-responsive transcription factor, putative
Sapur.7096000.1	0.651019976	1.159847228	0.285081622	7.576242	3.56E-14	8.92E-14	cpen	0.59692736	1.57E-16		AT4G26700.2	ATFIM1,FIM1	Fimbrin 1	NA
Sapur.014G054700.1	182.7767375	-0.426497527	0.056295462	-7.57622	3.58E-14	8.97E-14	cpen	-0.553670227	1.81E-14		AT4G05600.1		alpha/beta-Hydrolases superfamily protein	phosphatidylcholine:diacylglycerol lipid transporter
Sapur.010G147300.1	21.55493948	0.802375329	0.106041797	7.566598	3.81E-14	9.60E-14	cpen	-0.685366158	8.67E-11		AT4G40330.1	PYL8,RCAR9	PYR1-like 8	polyketide cyclase/dehydrase and lipid transporter
Sapur.001G075300.1	466.0754127	-0.615617003	0.081386159	-7.56502	3.88E-14	9.75E-14	cpen	-0.542782634	1.54E-13		AT4G18840.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	transcription factor jumonji (jmj) c domain protein
Sapur.004G076100.1	16.5803041	0.661549929	0.087554411	7.555872	4.16E-14	1.04E-13	cpen	-0.466889911	7.13E-10	GO:0005515	AT5G39250.1		F-box family protein	Non-S-locus F-box protein, putative
Sapur.009G112200.2	8.613130135	-0.873132986	0.115599858	-7.55462	4.20E-14	1.05E-13	cpen	-0.536298881	4.47E-13	GO:0006468,GO:0005524,GO:0004672	AT5G23281.1	BSK1	BR-signaling kinase 1	kinase
Sapur.7039500.1	2.930600664	-0.460340102	0.085754259	-7.55321	4.25E-14	1.06E-13	cpen	-0.543978787	2.56E-13	GO:0005840,GO:0005622,GO:0003735	AT5G27481.1	RPS10-BETA	ribosomal protein S10 beta	NA
Sapur.008G190400.1	135.3071907	-0.438267662	0.058030434	-7.53288	4.27E-14	1.07E-13	cpen	-0.539279827	3.17E-13	GO:0006508,GO:0004185	AT5G15000.1	scp5D	serine carboxypeptidase-like 50	NA
Sapur.7146000.1	4.124445416	1.270164461	0.169464496	7.531765	4.29E-14	1.07E-13	cpen	0.501343058	2.36E-11					NA
Sapur.008G051000.2	53.17786615	-0.548161995	0.073179223	-7.53579	4.75E-14	1.19E-13	cpen	0.574215869	7.11E-15		AT3G39950.1			hypothetical protein
Sapur.001G079000.1	296.8865662	-0.345628284	0.046207246	-7.5274	4.79E-14	1.20E-13	cpen	-0.52407818	1.78E-12	GO:0030170,GO:0008483	AT4G00050.1	WIN1	HOPW1-1-interacting 1	acetylornithine aminotransferase
Sapur.007G063300.1	14.41693941	1.202710151	0.159565847	7.537391	4.79E-14	1.20E-13	cpen	-0.473467026	3.72E-10		AT5G66900.1		Disease resistance protein (CC-NBS-LRR class) family	CC-NBS-LRR resistance protein
Sapur.005G248800.1	272.5656211	-0.246171495	0.045486732	-7.53249	4.86E-14	1.24E-13	cpen	-0.541611481	7.37E-12	GO:0016020	AT3G04710.1	ATBSMT1,BSMT1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase
Sapur.7152700.1	3.76310126	-0.429570048	0.189854436	-7.52882	5.12E-14	1.28E-13	cpen	-0.533890516	6.02E-13	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G37340.1	RPS11-BETA	ribosomal protein S11-beta	NA
Sapur.006G071000.2	2.384658866	-1.266128337	0.319125758	-7.52178	5.17E-14	1.29E-13	cpen	-0.526364565	2.61E-12	GO:0016592,GO:0031410,GO:0005829,GO:0005819	AT5G15130.2		TPX2 (targeting protein for Xklp2) family protein	TPX2 (targeting protein for Xklp2) family protein, putative
Sapur.012G007700.9	3.063245939	-1.233615162	0.163894981	-7.52686	5.20E-14	1.30E-13	cpen	-0.534434481	5.64E-13	GO:0030881,GO:0006298,GO:0005524	AT5G54090.1		DNA mismatch repair protein MutS, type 2	DNA mismatch repair MutS family protein
Sapur.017G100400.1	1088.4065	-0.280545764	0.037286201	-7.52412	5.31E-14	1.32E-13	cpen	-0.537152588	4.10E-13	GO:0005515	AT3G17320.1	DHAR3	dehydroascorbate reductase 1	glutathione-S-transferase DHAR3
Sapur.019G009481.1	43.45207751	-0.557408716	0.069286478	-7.51836	5.51E-14	1.38E-13	cpen	-0.517803101	3.75E-12		AT5G30301.1			DUF688 family protein
Sapur.009G053800.1	826.7195001	-0.362369336	0.048097148	-7.51779	5.57E-14	1.39E-13	cpen	-0.547382874	1.12E-13		AT5G19370.1		rhodanese-like domain-containing protein / PPIC-type PPIASE domain-containing protein	peptidyl prolyl cis/trans isomerase-like protein, putative
Sapur.016G291500.1	1319.345417	-0.357469552	0.047576484	-7.51104	5.87E-14	1.46E-13	cpen	-0.532836018	9.14E-13		AT4G16660.1		heat shock protein 90 family protein	heat shock 90 kDa protein
Sapur.009G115500.1	42.52556621	-0.537564159	0.071406587	-7.50405	6.19E-14	1.54E-13	cpen	-0.5288573	1.01E-12		AT2G15510.1	AHP1	histidine-containing phosphotransmitter 1	NA
Sapur.006G000900.1	156.5461365	-0.430820974	0.054414281	-7.502828	6.25E-14	1.56E-13	cpen	-0.570321991	2.95E-15		AT5G27140.1	SWEETIE	HEAT repeat-containing protein	NA
Sapur.005G205100.1	3.509509821	-1.140788641	0.152171764	-7.49672	6.54E-14	1.64E-13	cpen	-0.550058692	8.53E-14					NA
Sapur.006G089200.1	126.9016146	-0.406289201	0.052501857	-7.49602	6.58E-14	1.64E-13	cpen	-0.513119234	5.38E-12	GO:0006468,GO:0004672	AT5G68690.1		Protein kinase superfamily protein	serine kinase domain protein
Sapur.019G050800.3	8.404443285	-0.915382466	0.121146396	-7.49414	6.67E-14	1.66E-13	cpen	-0.483234289	1.81E-10		AT5G16830.1		Protein kinase superfamily protein	ATP-binding/kinase
Sapur.002G124900.1	608.9220773	-0.243858563	0.032667852	-7.49364	6.71E-14	1.68E-13	cpen	-0.510539415	8.42E-12	GO:0000160	AT4G16130.1	ARR2,RR2	response regulator 2	PRR response regulator
Sapur.006G128000.1	26.68705581	-0.757744632	0.101269481	-7.48688	7.05E-14	1.75E-13	cpen	-0.445552009	4.99E-09		AT5G61250.1		Pentatricopeptide repeat (PPR-like) superfamily protein	PPR containing plant protein
Sapur.159G118300.1	68.02923842	-0.641232489	0.085688893	-7.4849	7.16E-14	1.78E-13	cpen	-0.536149226	4.60E-13	GO:0006355,GO:0003677	AT5G13180.1	ANAC081,NAC081,VNI2	NAC domain containing protein 83	NAC transcription factor
Sapur.013G004500.1	306.9944314	-0.198208398	0.05349322	-7.48668	7.17E-14	1.78E-13	cpen	-0.519650501	2.03E-12	GO:0006355,GO:0003700	AT5G67261.1	AT5SERAT1-1,SAT-52,SAT5,52	serine acetyltransferase 5.2	serine O-acetyltransferase
Sapur.013G089400.1	388.4682845	0.304995673	0.04078205	-7.47868	7.51E-14	1.87E-13	cpen	-0.516589429	4.34E-12	GO:0006276,GO:0005685,GO:0003729	AT5G03340.1	UNE6	LUC7 related protein	RNA-binding LUC7-like protein, putative
Sapur.013G130800.1	0.680269823	-0.551896454	0.341146858	-7.47338	7.87E-14	1.97E-13	cpen	-0.489504948	1.31E-11		AT5G18150.1		RNI-like superfamily protein	F-box protein
Sapur.010G084000.2	6.106468948	-0.869802788	0.11634027	-7.47637	7.64E-14	1.90E-13	cpen	-0.513723851	5.96E-12		AT3MKK2,MK1,MKK2	MAP kinase kinase 2	MAP kinase kinase	MAP kinase kinase
Sapur.013G100500.1	3.984073514	-0.614149822	0.191861487	-7.47484	7.73E-14	1.92E-13	cpen	-0.457752995	1.66E-09	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G37570.1		Leucine-rich repeat protein kinase family protein	receptor kinase, putative
Sapur.006G053600.2	26.6234928	0.515257776	0.068595205	7.472945	7.85E-14	1.95E-13	cpen	-0.543941198	1.81E-13		AT5G25180.1		RabGAP/TBC domain-containing protein	RabGAP/TBC domain protein
Sapur.010G147600.1	51.63897105	-0.402266551	0.054000117	-7.4708	7.98E-14	1.98E-13	cpen	-0.482843604	5.06E-10		AT5G20760.1			NA
Sapur.012G062300.1	27.6864604	-1.561446002	0.209057653	-7.46763	8.17E-14	2.03E-13	cpen	-0.536212684	4.57E-13		AT3G15130.1		Tetratricopeptide repeat (TPR)-like superfamily protein	ankyrin repeat family protein
Sapur.005G042900.1	608.9220773	-0.243858563	0.03266762	-7.46484	8.34E-14	2.07E-13	cpen	-0.517824072	3.78E-12	GO:0005515	AT5G04710.3		ankyrin repeat family protein	ankyrin-1 protein
Sapur.016G099500.2	18.07157504	-0.502606204	0.064056412	-7.46439	8.38E-14	2.08E-13	cpen	-0.51861186	5.37E-12	GO:0005975,GO:0003824	AT3G01200.1		Carbohydrate-binding-like fold	carbohydrate-binding module family 20 protein
Sapur.013G051800.1	51.11591242	-0.625835893	0.083862538	-7.46253	8.49E-14	2.10E-13	cpen	-0.514145251	6.68E-12	GO:0005515	AT4G03790.2		ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein	ankyrin repeat and regulator of chromosome condensation (RCC1) domain protein
Sapur.001G052200.1	43.50993214	-0.732973233	0.098212364	-7.46242	8.49E-14	2.11E-13	cpen	-0.550042008	8.55E-14	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G07930.1		Ribosomal protein L7 family protein	ribosomal protein L7
Sapur.005G051100.1	1222.190896	-0.292910726	0.039253749	-7.46198	8.52E-14	2.11E-13	cpen	-0.507810208	1.13E-11	GO:0009088,GO:0003852,GO:0003824	AT1G74040.1	IMS1,IPMS2,MAM1,-3	2-isopropylmalate synthase 1	2-isopropylmalate synthase
Sapur.002G056600.1	16.42052646	-0.726272835	0.097342585	-7.46097	8.56E-14	2.12E-13	cpen	-0.524152293	1.81E-12	GO:0005515	AT4G20220.1	MEE50	ARM repeat superfamily protein	NA
Sapur.018G023300.1	91.78648372	-0.690911913	0.092605158	-7.457182	8.84E-14	2.19E-13	cpen	-0.483709378	1.36E-10	GO:0006468,GO:0005524,GO:0004672	AT4G23300.1	SD2-5	S-domain-2 5	G-type lectin S-receptor-like Serine/Threonine-kinase SD2-5
Sapur.008G000800.1	27.07974116	-0.827436161	0.110968381	-7.45628	8.87E-14	2.20E-13	cpen	-0.516681013	4.30E-12					NA
Sapur.001G180500.1	3.405417809	-1.343068553	0.180119813	-7.45653	8.88E-14	2.20E-13	cpen	-0.6729536	5.09E-22					kinesin-like protein, putative
Sapur.006G084900.1	35.33319729	-0.508885123	0.068250414	-7.45163	9.21E-14	2.28E-13	cpen	0.563704098	7.30E-15		AT5G27140.3	SWEETIE	HEAT repeat-containing protein	NA
Sapur.004G095300.1	0.41313309	2.294063388	0.307987035	7.448571	9.44E-14	2.34E-13	cpen	-0.634662216	4.45E-19	GO:0005681,GO:0000398,GO:0000187	AT5G54385.2		ARM repeat superfamily protein	NA
Sapur.013G182000.3	8.832315293	-0.825088437	0.110876974	-7.44617	9.61E-14	2.38E-13	cpen	-0.529210363	1.04E-12		AT1G22700.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR protein
Sapur.001G063200.1	21.30438764	-0.608868898	0.081782746	-7.44496	9.76E-14	2.40E-13	cpen	-0.500803005	4.01E-11	GO:0005515	AT3G14110.2	ATNIJ/SGT2,NIJ/SGT2,SAR1	Protein SGT2/SGT2 homologs RESISTANCE	suppressor of auxin resistance 1 protein
Sapur.010G117700.1	2.974954117	1.382416581	0.172228785	7.444438	9.74E-14	2.41E-13	cpen	-0.495280769	6.23E-11		AT4G30230.1			hypothetical protein
Sapur.006G079100.1	518.1072502	0.253112605	0.031875568	7.442314	9.89E-14	2.44E-13	cpen	-0.524817838	1.73E-12	GO:0016020,GO:0008417,GO:0006486	AT1FUT1,FUCT1,FUCTA,FU	fucosyltransferase 11	fucosyltransferase 11	glycoprotein 3-alpha-L-fucosyltransferase, putative
Sapur.010G052800.1	985.4219939	-0.370010763	0.049727034	-7.44084	1.00E-13	2.47E-13	cpen	-0.542807871	2.06E-13	GO:0006418,GO:0005524,GO:0004812,GO:0000166	AT5G26880.1		glycyl-tRNA synthetase / glycine--tRNA ligase	glycyl-tRNA synthetase
Sapur.006G071500.1	656.8456157	-0.365027291	0.123430355	-7.44041	1.00E-13	2.48E-13	cpen	-0.515317388	4.97E-12	GO:0006412,GO:0003824	AT2G45400.1	BEN1	NAD(P)-binding Rossmann-fold superfamily protein	NA
Sapur.012G237000.1	124.9901645	-0.360950209	0.052560612	-7.43722	1.03E-13	2.54E-13	cpen	-0.523388013	7.17E-13		AT5G55840.1		Pentatricopeptide repeat (PPR) superfamily protein	NA
Sapur.013G089700.1	2.308840281	-1.555813291	0.20619154	-7.43478	1.05E-13	2.59E-13	cpen	-0.528819905	1.98E-12	GO:0008270,GO:0003677	AT2G19810.2	AZM4	AZM4/Mi-like zinc finger family protein	zinc finger AZD and ANU domain stress-associated protein, putative
Sapur.010G049200.2	11.90704227	-0.626484275	0.084305042	-7.43116	1.08E-13	2.66E-13	cpen	-0.528591932	1.07E-12		AT2G39980.1	BLI,HDS1	BLISTER	hypothetical protein
Sapur.008G195700.1	682.7636399	-0.209251857	0.028164734	-7.429571	1.09E-13	2.69E-13	cpen	-0.51073515	8.26E-12	GO:0005515	AT5G55040.1	GSTL2	glutathione transferase lambda 2	glutathione-S-transferase
Sapur.005G238100.1	143.3195517	-0.648888288	0.085459238	-7.42911	1.09E-13	2.70E-13	cpen	-0.536412249	4.62E-13		AT5G54680.1		Glycoprotein membrane GPI-anchored	NA
Sapur.005G168700.1	14.14397655	-0.869677018	0.114438277	-7.42489	1.13E-13	2.79E-13	cpen	-0.535811773	4.87E-13					NA
Sapur.010G184000.1	4.398851185	-1.811247129	0.239448605	-7.42372	1.14E-13	2.81E-13	cpen	-0.51197126	7.20E-14		AT5G04330.1		Pectin lyase-like superfamily protein	pectate lyase, putative
Sapur.001G155400.1	31.96262662	-0.726318582	0.097839684	-7.42356	1.14E-13	2.81E-13	cpen	-0.524579024	1.77E-12	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT5G34110.1		Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.005G208100.1	28.87169944	-0.580160411	0.078204923	-7.41888	1.18E-13	2.92E-13	cpen	-0.497925317	2.56E-11	GO:0003677,GO:0000786	AT4G40030.2		Histone superfamily protein	histone H3
Sapur.010G141100.1	601.2117979	0.293107943	0.039512993	7.418014	1.19E-13	2.93E-13	cpen	-0.499505925	2.73E-11		AT4G16230.1	E-COAH-2,ECHA	enoyl-CoA hydratase/isomerase A	hypothetical protein
Sapur.007G060700.1	10.28515132	-0.821813287	0.110761262	-7.41674	1.19E-13	2.94E-13	cpen	-0.537976452	2.71E-13		AT5G48860.1			NA
Sapur.018G209800.1	14.90994663	-0.958665271	0.129236127	-7.41447	1.22E-13	3.01E-13	cpen	-0.488989223	8.14E-11	GO:0005634	AT4G14070.1		Polynucleotidyl trans

Sapur.03G0230300.1	10.83349006	0.10083406	0.130014387	6.986777	2.83E-12	6.62E-12	ppm	0.492984393	5.41E-11	GO:0008652;GO:0008270;GO:0003871;GO:0009086	ATCMS,ATMETS,ATMS1	Cobalamin-independent synthase family protein			S-methylthetrahydropteroylhiglutamate-homocysteine methyltransferase
Sapur.15WG1003300.1	69.8710702	0.890365941	0.127444535	-6.9863	2.83E-12	6.65E-12	ppm	-0.472420182	4.19E-10		SIP1	Raffinose synthase family protein			NA
Sapur.09G0249700.1	107.2696002	0.612281518	0.087634264	-6.98589	2.83E-12	6.66E-12	ppm	-0.42420782	7.08E-10	GO:0016758;GO:0008152	UGT5BA1	UDP-glucuronosyltransferase 88A1			NA
Sapur.03G0286600.1	138.1643514	0.946815293	0.135658833	6.979489	2.96E-12	6.97E-12	ppm	-0.46496035	8.74E-10	GO:0006468;GO:0006472;GO:0005975;GO:0004553		S-lacus lectin protein kinase family protein			receptor-like kinase
Sapur.07G0133600.1	1.038835567	1.495067844	0.531230262	6.974734	3.06E-12	7.19E-12	ppm	-0.41836675	5.04E-08	GO:0003700;GO:0003677	ANAC055,ATNAC3,NACOS5	NAC domain containing protein 3			NAC domain transcription factor, putative
Sapur.05G0261100.1	48.39992298	1.68901302	0.242383358	6.968356	3.21E-12	7.54E-12	ppm	-0.55407271	1.69E-11	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP76G1	cytochrome P450, family 76, subfamily G, polypeptide 1			NA
Sapur.01G0320700.1	122.259573	0.32273477	0.046315426	6.968162	3.21E-12	7.55E-12	ppm	-0.48581273	1.12E-10		ATH1	alpha/beta-Hydrolases superfamily protein			X-pro dipeptidyl-peptidase, S15 family protein
Sapur.01G0257900.1	28.527605	0.547317433	0.078576607	-6.96563	3.27E-12	7.68E-12	ppm	-0.49392099	1.66E-10	GO:0000160	ARR12,RR2	response regulator 2			PRR response regulator
Sapur.09G0129400.1	402.1485302	0.28322893	0.040676675	6.962735	3.34E-12	7.84E-12	ppm	0.50898326	2.35E-11		ELM1	Protein of unknown function (DUF3022)			fission ELM1 protein
Sapur.09G0266700.1	1023.389832	0.38622502	0.057776759	6.962407	3.35E-12	7.86E-12	ppm	0.47461607	1.07E-10		ATCCD1,ATNCED3,CCD1,NC	carotenoid cleavage dioxygenase			carotenoid cleavage
Sapur.05G0219200.1	4970.813513	0.36234570	0.052058822	6.96058	3.39E-12	7.96E-12	ppm	0.50991308	2.37E-11	GO:0055114;GO:0016490;GO:0016209;GO:0006976;GO:0004602	ATGPX1,GPX1	glutathione peroxidase 1			glutathione peroxidase
Sapur.04G0270300.1	17.43946513	1.173606409	0.169866204	6.95365	3.47E-12	8.16E-12	ppm	-0.49551831	1.97E-10	GO:0055114;GO:0000337;GO:0016705;GO:0005506	BRG5CO2,CYP85A2	brassinosteroid-C-6 oxidase 2			cytochrome P450 family protein
Sapur.05G0691600.1	1.668806129	2.199078022	0.316388977	6.950554	3.64E-12	8.53E-12	ppm	-0.46858126	6.07E-10						NA
Sapur.03G0267100.1	12.33457369	0.814997241	0.117242268	6.942669	3.84E-12	8.99E-12	ppm	-0.45650984	8.15E-10	GO:0008152;GO:0003824	LACS9	long chain acyl-CoA synthetase 9			long-chain-fatty-acid-CoA ligase
Sapur.09G0116600.1	151.7078754	0.237712982	0.034295082	-6.9314	4.17E-12	9.75E-12	ppm	-0.47404261	5.58E-10	GO:0009058;GO:0004161	ATIPT2,IPT1,IPT2	tRNAisopentenyltransferase 2			tRNA isopentenyltransferase
Sapur.01G0279900.1	43.89629605	0.495023664	0.05675104	-6.93664	4.29E-12	9.94E-12	ppm	-0.46484004	7.95E-10		PRA1.H	prenylated RAB acceptor 1.H			PRA1 family protein
Sapur.01G0091500.1	21.5638231	0.863765548	0.124678621	-6.92831	4.26E-12	9.96E-12	ppm	-0.48596391	1.11E-10			Tetratricopeptide repeat (TPR)-like superfamily protein			PPR containing plant protein
Sapur.T03.T00.1	16.60771719	0.695204753	0.100442133	6.927618	4.28E-12	1.00E-11	ppm	0.42482208	2.92E-08			Tetratricopeptide repeat (TPR)-like superfamily protein			NA
Sapur.09G0267600.1	10.26468727	-0.575165594	0.111183941	-6.92695	4.28E-12	1.00E-11	ppm	-0.47735226	4.70E-10	GO:0055085;GO:0046873;GO:0030001;GO:0016020	MGT6,MRS2-3	magnesium transporter 6			magnesium transporter
Sapur.01G0269200.1	706.3953091	0.191515452	0.027700081	6.913895	4.73E-12	1.10E-11	ppm	-0.45202872	1.78E-09	GO:0005515		UBX domain-containing protein			Fas-associated factor-like protein
Sapur.01G0207500.1	948.9762072	0.12506733	0.018106489	6.913189	4.75E-12	1.12E-11	ppm	-0.51489862	2.02E-10			peptidyl-Pro cis-trans isomerase 1			peptidyl-Pro cis-trans isomerase
Sapur.03G0137700.1	7.138832036	-1.45690561	0.210891533	-6.90858	4.90E-12	1.14E-11	ppm	-0.47869479	2.24E-10	GO:0004857		Plant invertase/pectin methylesterase inhibitor superfamily protein			plant invertase/pectin methylesterase inhibitor
Sapur.01G0286600.1	427.2514164	0.180288403	0.04386287	6.897919	4.92E-12	1.15E-11	ppm	0.48512589	1.72E-10		TIC1	TIG-linked interacting protein 1			MFB DNA-binding domain protein, putative
Sapur.01G0250800.1	619.4308113	0.310708089	0.045037511	6.901379	5.15E-12	1.20E-11	ppm	-0.47016632	5.22E-10	GO:0008430	SBP1	selenium-binding protein 1			S6 kDa selenium-binding protein (SBP56)
Sapur.03G0417200.1	33.03402723	0.514499341	0.074656549	6.89277	5.22E-12	1.22E-11	ppm	-0.51581221	1.16E-10	GO:0008152;GO:0003824		AMP-dependent synthetase and ligase family protein			4-coumarate-CoA ligase
Sapur.01G0264900.1	38.4904296	-0.52437372	0.076031716	-6.89078	5.32E-12	1.24E-11	ppm	-0.47762592	2.45E-10						hypothetical protein
Sapur.01G0295300.1	74.19518808	0.315851566	0.04577528	-6.89863	5.33E-12	1.24E-11	ppm	-0.57143276	5.48E-15	GO:0034968;GO:0018024;GO:0008270;GO:0005634;GO:0005515	SDG20,SUVR3	SET domain protein 20			histone-lysine N-methyltransferase
Sapur.09G0260800.1	242.4888113	0.260376146	0.042447214	6.89497	5.38E-12	1.25E-11	ppm	-0.47774883	2.50E-10						hypothetical protein
Sapur.01G0300400.1	236.0915618	0.346131707	0.050214382	-6.89309	5.46E-12	1.27E-11	ppm	-0.48152974	1.91E-10	GO:0016021;GO:0015031					secretory carrier-associated membrane protein
Sapur.09G0251900.1	334.0179911	0.164166164	0.024562584	-6.89112	5.54E-12	1.29E-11	ppm	-0.49501876	7.21E-11		SC3	secretory carrier 3			sphingolipidosis-beta-1,3/2-glucosyltransferase
Sapur.05G0145800.1	19.2928984	0.827106991	0.120099991	-6.88682	5.71E-12	1.33E-11	ppm	-0.44302743	6.23E-09	GO:0005515		Exostosin family protein			F-box protein SKP2A
Sapur.01G0240700.1	948.9762072	-0.12506733	0.018166749	-6.88395	5.86E-12	1.37E-11	ppm	-0.48771802	1.36E-10		CYP708A2	RNA-binding (RRM/RBD/RNP motifs) family protein			peptidyl-Pro cis-trans isomerase
Sapur.03G0184900.1	170.8546635	-0.3702671	0.053820507	-6.87967	6.02E-12	1.40E-11	ppm	-0.46705963	6.99E-10	GO:0006355		Far-red impaired response (FAR1) family protein			Far-red impaired response-like protein
Sapur.01G0261700.1	838.8318314	0.214042607	0.031187223	-6.87918	6.02E-12	1.40E-11	ppm	-0.5180406	3.56E-13						SnRK1-interacting protein, putative
Sapur.04G0257000.2	20.3601588	0.501562363	0.072974274	-6.8731	6.28E-12	1.46E-11	ppm	-0.47518874	3.20E-10						anaphase-promoting complex subunit 5
Sapur.01G0244100.1	311.0403029	0.127114461	0.018494181	-6.87184	6.34E-12	1.47E-11	ppm	-0.77927219	2.06E-12	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871					NA
Sapur.01T0272800.2	57.94526023	0.42268178	0.061538666	-6.86967	6.43E-12	1.50E-11	ppm	-0.49166661	6.20E-11	GO:0043565;GO:0003700;GO:0003700	WRKY40	P-loop containing nucleoside triphosphate hydrolases superfamily protein			WRKY transcription factor, putative
Sapur.01G0203500.1	191.2248644	-0.30251798	0.044084791	-6.86779	6.52E-12	1.52E-11	ppm	-0.51690585	3.07E-12		MEE9	WRKY transcription factor 40			maternal effect embryo arrest 9
Sapur.03G0147300.1	105.4979934	-0.154847216	0.077816602	-6.86777	6.52E-12	1.52E-11	ppm	-0.51581221	1.16E-10	GO:0055114;GO:0016491		Glycosyltransferase family 61 protein			maternal effect embryo arrest 9 protein, putative
Sapur.08G0171300.1	363.9108118	0.330059886	0.048078011	-6.86509	6.64E-12	1.54E-11	ppm	-0.47618881	2.91E-10			Dehydroquinate/shikimate dehydrogenase family protein			NA
Sapur.09G0193200.1	56.01527259	0.561287564	0.078833369	-6.86321	6.73E-12	1.56E-11	ppm	-0.54287557	2.46E-11						hypothetical protein
Sapur.01G0279900.1	630.5462205	0.29505409	0.042954521	-6.862689	6.76E-12	1.57E-11	ppm	-0.47067652	4.96E-10	GO:0016020;GO:0008417;GO:0006486		BGD domain containing protein			NA
Sapur.01G0321400.1	884.4412256	0.16266145	0.023681028	-6.862418	6.77E-12	1.57E-11	ppm	-0.47404267	3.46E-10	GO:0005515	CYP81D11	cytochrome P450, family 81, subfamily D, polypeptide 11			NA
Sapur.09G0230800.1	83.95727449	0.392725688	0.057237964	-6.86128	6.82E-12	1.58E-11	ppm	-0.47739102	2.64E-10		MEE66	F-box family protein			F-box protein PP2-B1
Sapur.01G0280200.1	1021.102057	0.388361822	0.056637969	-6.85813	6.98E-12	1.62E-11	ppm	-0.47579935	3.02E-10	GO:0016020;GO:0008185;GO:0005215	GAMMA-TIP;GAMMA-TIP1	gamma tonoplast intrinsic protein			tonoplast intrinsic protein bdTIP24-protein
Sapur.01G0289300.2	5.107939178	1.771868588	0.258398537	-6.857115	7.03E-12	1.63E-11	ppm	-0.54389596	1.23E-13	GO:0005085;GO:0016020;GO:0051297;GO:0051328;GO:0006855		MATE efflux family protein			MATE efflux family protein
Sapur.01G0264900.1	7.0354583	1.48025386	0.216082147	-6.84768	7.46E-12	1.74E-11	ppm	-0.49392604	3.46E-11			S-adenosyl-L-methionine-dependent methyltransferases superfamily protein			NA
Sapur.04G0864600.1	45.19562303	0.408798279	0.059714878	-6.845308	7.60E-12	1.76E-11	ppm	-0.52953458	9.52E-13		SWEETIE	HEAT repeat-containing protein			NA
Sapur.09G0231100.1	279.6262511	-0.487182541	0.071182469	-6.84414	7.68E-12	1.78E-11	ppm	-0.52989389	9.58E-13	GO:0005525	BPG2	P-loop containing nucleoside triphosphate hydrolases superfamily protein			SDS-ribosome-binding GTPase
Sapur.09G0288800.1	186.6049511	-0.327008592	1.85E-11	6.12278587	7.84E-12	1.81E-11	ppm	-0.49992801	2.74E-11			Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein			NA
Sapur.01G0250700.1	14.80188069	0.706587072	0.10328821	-6.83431	8.24E-12	1.91E-11	ppm	-0.48402435	1.34E-10			Tetratricopeptide repeat (TPR)-like superfamily protein			NA
Sapur.01G0188300.1	1684.393962	0.093411156	0.013661156	-6.83429	8.24E-12	1.91E-11	ppm	-0.47842868	2.50E-10	GO:0016853;GO:0009507	AOC3	allene oxide cyclase			allene oxide cyclase
Sapur.01G0288800.1	8.664881853	0.877308417	0.128575339	6.823302	8.90E-12	2.06E-11	ppm	0.50516782	1.51E-11						NA
Sapur.09G0117500.1	2.2215461	2.359266145	0.317188824	6.820674	9.04E-12	2.08E-11	ppm	0.54754705	2.2E-12		emb2234	ARM repeat superfamily protein			NA
Sapur.05G0248800.2	22.62491576	-0.694879411	0.101903612	-6.81887	9.17E-12	2.12E-11	ppm	-0.4580449	1.92E-10		ATHDA14,hda14	histone deacetylase 14			histone deacetylase family protein
Sapur.09G0238300.1	5.088939964	-0.9113388	0.13360612	-6.81896	9.17E-12	2.12E-11	ppm	-0.48175208	1.70E-10						hypothetical protein
Sapur.03G0139600.1	53.0576662	-0.447039145	0.065596068	-6.81503	9.42E-12	2.18E-11	ppm	-0.53209205	8.33E-13			C2H2-like zinc finger protein			zinc finger protein, putative
Sapur.08G0166600.1	195.9983617	-0.015823769	0.09044112	-6.80911	9.82E-12	2.27E-11	ppm	-0.48839122	8.51E-11			Uncharacterized protein family (UPF0497)			plant integral membrane protein
Sapur.09G0288500.4	3.469571959	-0.551752752	0.101642299	-6.80386	1.02E-11	2.35E-11	ppm	-0.42357662	2.02E-08						hypothetical protein
Sapur.05G0124200.1	204.3552063	0.702777631	0.10342192	6.793917	1.09E-11	2.51E-11	ppm	-0.42314276	3.38E-08	GO:0006508;GO:0004252	XSP1	xylem serine proteinase 1			xylem serine proteinase
Sapur.15WG0241900.1	70.46870023	-1.74988197	0.257622385	-6.79246	1.10E-11	2.54E-11	ppm	-0.64313832	5.64E-14			DEAD(Asp-Glu-His-Asp) box helicase family protein			NA
Sapur.15WG0247300.1	510.6456132	0.198892584	0.029274829	-6.76275	1.18E-11	2.71E-11	ppm	-0.49459718	4.61E-11	GO:0031683;GO:0019001;GO:0007186;GO:0004871;GO:0003924	XLG3	extra-large GTP-binding protein 3			GTP-binding protein alpha subunit, gna protein3XL
Sapur.05T0260100.1	35.82315158	0.468138279	0.073615176	-6.77618	1.23E-11	2.81E-11	ppm	-0.47478518	1.51E-11	GO:0004852;GO:0005515		Protein kinase family protein			Serine/Threonine-kinase, G2E, putative
Sapur.09G0219300.1	466.8124235	0.175326272	0.025911346	6.774109	1.25E-11	2.88E-11	ppm	-0.50024915	2.54E-11			MIF4G domain-containing protein / MA3 domain-containing protein			NA
Sapur.01G0233500.1	13.40253896	-0.84428788	0.125195427	-6.76266	1.28E-11	2.94E-11	ppm	-0.45890604	3.30E-09	GO:0006468;GO:0005524;GO:0004672		Phosphoserine/threonine-protein kinase family protein			calcium-dependent kinase
Sapur.01G0285500.1	119.2295746	-0.401461358	0.059306959	-6.77224	1.29E-11	2.91E-11	ppm	-0.46654321	7.34E-10	GO:0055114;GO:0016491	HEMG1,PPO1,PPOX	Flavin containing amine oxidoreductase family			NA
Sapur.01G0132300.1	151.1138218	0.204511249	0.03025146	6.765574	1.31E-11	2.96E-11	ppm	-0.48868318	3.36E-11	GO:0004852;GO:0005515	ATNAK3	Acyl-CoA N-acyltransferase family superfamily protein			N-acetyltransferase Nak3-like protein
Sapur.01G0268700.1	36.1128872	-0.973570676	0.144082255	-6.7577	1.40E-11	3.21E-11	ppm	-0.49764544	3.33E-11			Transmembrane amino acid transporter family protein			lysine/histidine transporter
Sapur.01G0250400.1	3.2398395	1.114268861	0.165056767	6.75081	1.47E-11	3.37E-11	ppm	-0.49401416	4.87E-11		ATCRM1,ATXPO1,HET2,XPO	exportin 1A			NA
Sapur.09G0249500.1	2.320420918	-1.251892679	0.179978813	-6.74485	1.53E-11	3.51E-11	ppm	-0.54379528	8.82E-14	GO:0016020;GO:0005215	ATCNX2,CNX2,ER1;ER1	calnexin/calreticulin family protein			NA
Sapur.09G0113900.1	10.82655632	0.583637097	0.086564727	-6.7422	1.56E-11	3.57E-11	ppm	-0.45601254	1.95E-09		ATKAG2,FAB1,KAS2	fatty acid biosynthesis 1			beta-ketoacyl-acyl-carrier synthase II
Sapur.09G0137500.1	295.4128853	0.170067186	0.025221461	-6.68806	2.14E-11	4.88E-11	ppm	-0.61577161	1.87E-09	GO:0005515		Galactose oxidase/kelch repeat superfamily protein			kelch repeat F-box protein
Sapur.09G0092000.1	574.0203084	-0.337051528	0.050038338	-6.73633	1.62E-11	3.71E-11	ppm	-0.51735293	1.99E-12	GO:0045454;GO:0015035;GO:0006662	ATHB7HD,TRX H9	thioredoxin H-type 9			thioredoxin H- protein
Sapur.09G0238300.1	191.0554751	0.532575517	0.079754088	-6.72788	1.73E-11	3.88E-11	ppm	-0.44724209	4.30E-09		PSC52	delta 1-pyrroline 5-carboxylate synthase 2			delta-pyrroline-5-carboxylate synthetase
Sapur.01G0192600.1	617.3743803	0.289774099	0.043110379	6.723129	1.78E-11	4.06E-11	ppm	-0.48938618	7.82E-11			heat shock protein 70 (Hsp 70) family protein			heat shock 70 kDa protein
Sapur.01G0192300.1	1.051126218	0.350207417	0.053074147	6.719325	1.81E-11	4.17E-11	ppm	-0.65651605	8E-21			Nucleoporin, Nup133/Nup155-like			nucleoporin
Sapur.01G0148400.1	26.76289003	-0.743674792	0.110759381	-6.71433	1.89E-11	4.31E-11	ppm	-0.51374267	5.94E-12						transmembrane protein, putative
Sapur.09G0242800.1	0.96402939	2.033907677	0.303885514	6.710651	1.94E-11	4.42E-11	ppm	-0.45123715	2.78E-09						NA
Sapur.09G0249500.1	70.85667503	-0.438477412	0.065388879	-6.70589	2.05E-11	4.56E-11	ppm	-0.47263663	4.11E-10			Uncharacterized protein family (UPF0497)			pepsinian strip membrane protein, putative
Sapur.01G0215500.1	5.740692291	0.861097589	0.128540702	6.699027	2.10E-11	4.78E-11	ppm	0.43605788	1.94E-08		RGLG2	RING domain ligase 2			E3 ubiquitin-protein ligase RGLG2
Sapur.T17B00.1	0.472687938	2.288071641	0.341177792	6.689401	2.11E-11	4.80E-11	ppm	0.53264507	4.1E-13						NA
Sapur.07G0087500.1	167.0896652	0.263187229	0.039682814	6.693548	2.18E-11	4.96E-11	ppm	0.49108717	1.30E-11	GO:0005515	ATXR5,SDG15	ARABIDOPSIS TRITHORAX-RELATED PROTEIN 5			histone-lysine N-methyltransferase ATXR5, putative
Sapur.09G0247600.1	78.25951663	0.370067686	0.055322651	-6.68856	2.26E-11	5.14E-11	ppm	-0.48831664	1.61E-10	GO:0005515;GO:0009165;GO:0006455;GO:0004146	THY-1	thymidylate synthase 1			dihydrofolate reductase-thymidylate synthase
Sapur.01G0254500.1	52.57023515	0.648881765	0.097117529	6.68175	2.36E-11	5.37E-11	ppm	-0.45874935	5.12E-09	GO:0016567;GO:0006842		Armadillo/beta-catenin-like repeat family protein			U-box protein, putative
Sapur.01G0159600.1	11.08173497	0.622560924	0.09114379	-6.68041	2.38E-11	5.42E-11	ppm	-0.50508861	2.33E-11			Predicted AT-hook DNA-binding protein			AT-hook DNA-binding protein
Sapur.09G0921000.1	16039.55111	-0.402224153	0.06037879	-6.66168	2.71E-11	6.15E-11	ppm	-0.45746381	1.71E-09	GO:0003676		cold, circadian rhythm, and RNA binding 1	ATGRP8,CCR1,GR-RBP8,GRI		RNA recognition motif, a.k.a. RRM/RNC RBD protein
Sapur.01G0288800.4	23.78218374	-0.614141388	0.093166154	-6.65784	2.78E-11	6.31E-11	ppm	-0.45498878	1.62E-09			Uncharacterized BCR, YbaK family COG2718			NA
Sapur.01G0211600.2	0.56209529	-0.663791566	0.099737314	-6.65577	2.82E-11	6.39E-11	ppm	-0.48229908	1.60E-10	GO:0005515		F-box/RNI-like/FBD-like domains-containing protein			F-box/LRR protein
Sapur.01G0282400.1	2.338879944	1.361768517	0.189664722	6.653624	2.88E-11	6.53E-11	ppm	-0.45752874	1.70E-09	GO:0004857;GO:0042545;GO:0030599;GO:0005618		Plant invertase/pectin methylesterase inhibitor superfamily			pectinesterase/pectinesterase inhibitor, putative
Sapur.01G0261300.1	1.452931884	1.878303383	0.262328552	6.651285	2.89E-11	6.55E-11	ppm	-0.47869312	2.28E-10			DOT domain-containing protein			NA
Sapur.03G0242600.1	139.6397262	-0.487406431	0.072081646	-6.65119	2.93E-11	6.59E-11	ppm	-0.45393937	2.36E-09	GO:0046983		basic helix-loop-helix (bHLH) DNA-binding family protein	BHLH62,TT8		BHLH transcriptor factor
Sapur.09G0283500.1	4.276089053	-0.754192274	0.108309506	-6.68112	2.97E-11	6.75E-11	ppm	-0.52829892	1.12E-12		CDS1,PDS1	CTC interacting domain 1			hypothetical protein
Sapur.01G0210200.1	213.231882	-0.597113047	0.08695077	-6.64233	3.09E-11	6.99E-11	ppm	-0.49526847	4.07E-11						Sof1-related ribosome biogenesis protein SKI2, putative
Sapur.01G0188000.1	338.7866179	-0.52239164	0.08017461	-6.64058	3.11E-11	7.07E-11	ppm	-0.56052224	2.9E-14	GO:0006412;GO:0005840;GO:0003735;GO:0015934		Ribosomal protein L13 family protein			60S ribosomal protein L13a
Sapur.01G0198500.1	124.5237062	0.194192013	0.029257501	-6.63725	3.20E-11	7.23E-11	ppm	-0.52190896	2.07E-12		TBL35	TRICHOME BIREFRINGENCE-LIKE 35			trichome birefringence-like protein
Sapur.01G0239100.1	694.9867867	-0.203182224	0.03068188	-6.6344	3.26E-11	7.37E-11	ppm	-0.47617303	8.10E-10	GO:0003676		RNA binding (RRM/RBD/RNP motifs) family protein			RNA recognition motif protein
Sapur.01G0160600.1	94.11328888	0.353507559	0.053388272	-6.62145	3.56E-11	8.04E-11	ppm	-0.49967762	2.70E-11			Protein of unknown function (DUF565)			transmembrane protein, putative
Sapur.09G0416100.2	16.08872728	-0.642000422	0.097017519	-6.61968	3.58E-11	8.11E-11	ppm	-0.46303822	1.29E-09						hypothetical protein
Sapur.03G0260000.1	26.75544648	-0.66105763	0.099876438	-6.61888	3.62E-11	8.18E-11	ppm	-0.4630522	1.22E-09						DUF740 family protein
Sapur.01G0195200.1	180.7472881	0.272539393	0.041198852	6.615218	3.73E-11	8.38E-11	ppm	0.46882098	5.39E-10	GO:0005515	ATBPM2,BPM3	BTB/POZ/MATH-domain containing protein			speckle-type POZ protein, putative
Sapur.01G0160600.1	515.6588979	0.262572019	0.039713019	6.611751	3.88E-11	8.57E-11	ppm	0.46389476	9.46E-10		TAAC	thylakoid ATP/ADP carrier protein			ADP/ATP carrier protein, putative
Sapur.09G0234700.2	3.79743529	1.005809673	0.152335588	6.603025	4.03E-11	9.09E-11	ppm	0.49389109	4.91E-11	GO:0046872;GO:0000166	AHA5,HA6	H(+)-ATPase 5			plasma membrane H+-ATPase
Sapur.09G0137500.1	0.93779756	-0.873464342	0.131331343	-6.59708	4.18E-11	9.42E-11	ppm	-0.45752576	1.78E-09			ELMO/CED-12 family protein			ELMO/CED-12 family protein
Sapur.03G0265300.1	134.9883868	-0.347906154	0.052771492	-6.59269	4.32E-11	9.71E-11	ppm	-0.47657534	2.80E-10	GO:0016829;GO:0010332;GO:0008152;GO:0000287	ATKL4,ATKS1,GA2,KS,KS1	Terpenoid cyclases/Protein prenyltransferases superfamily protein			Ent-kaurene synthase
Sapur.09G0151500.1	20.67617869	-0.332282491	0.050265837	-6.54242	4.63E-11	1.04E-10	ppm	-0.50349403	1.30E-11			Galactose oxidase/kelch repeat (PPR) superfamily protein			NA
Sapur.09G0269900.1	8629.522148	-0.196435021	0.04035754	-6.58014	4.70E-11	1.06E-10	ppm	-0.47586974	3.00E-10	GO:0005524		chaperonin-60alpha	CH-CPN60A,CPN60A,SLP		RuBisCO large subunit-binding protein subunit alpha, putative
Sapur.03G0175300.1	28.41337224	0.165396395	0.090205454	6.570849	4.90E-11	1.10E-10	ppm	-0.42635033	2.01E-08						transmembrane protein, putative
Sapur.03G0150700.1	47.4857661	-0.754655506	0.114814904	-6.57106	5.00E-11	1.12E-10	ppm	-0.46759189	6.65E-10	GO:0009611;GO:0004867		Serine protease inhibitor, potato inhibitor I-type family protein			protease inhibitor 1
Sapur.01G0285300.1	139.5807177	-0.589709763	0.089746839	-6.57089	5.08E-11	1.12E-10	ppm	-0.53879571	8.15E-13	GO:0003676			ATSC1,ATSC1,ATSC1,ATSC1		serine/arginine-rich splicing factor 10 (SRS10)-like RNA recognition motif protein
Sapur.01G0188300.1	178.7516688	0.157456897	0.064437813	6.564791	5.21E-11	1.17E-10	ppm	0.41950652	2.54E-08	GO:0005515		BTB/POZ domain containing protein, putative			potassium channel tetramerization-dependent protein, putative
Sapur.T17J00.1	0.47451244	2.063843336	0.316814526	6.562078	5.31E-11	1.19E-10	ppm	0.52834986	1.15E-12						NA
Sapur.09G0214000.6	1.585905261	1.408142224	0.214879129	6.546115	5.86E-11	1.40E-10	ppm	-0.61112897	9.61E-23	GO:0034968;GO:0018024;GO:0008270;GO:0005634;GO:0005515;GO:0042393	SUVH1	SuVH[4/5]-9 homolog 1			histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3 protein, putative
Sapur.03G0172500.1	522.7347374	0.240208511	0.036825556	6.512795	7.38E-11	1.65E-10	ppm	-0.45007237	3.07E-09	GO:0055114;GO:0016491		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein			prolyl 4-hydroxylase alpha subunit, putative
Sapur.09G0161600.1	104.6878974	0.261461637	0.04075319	6.51157	7.44E-11	1.66E-10	ppm	-0.52482118	1.7E-12			Plant protein of unknown function (DUF247)			DUF868 family protein
Sapur.01G0169800.1	2.52397558	-1.06765991	0.164000494	-6.5101	7.51E-11	1.68E-10	ppm	-0.51947203	3.15E-12						NA
Sapur.04G0268700.1	10.12546279	-0.746748648	0.122682671	-6.50452	7.76E-11	1.74E-10	ppm	-0.52288621	2.12E-12			Plant protein of unknown function (DUF247)			NA
Sapur.05G0260900.1	18.94116133	-0.603412243	0.092920487	-6.49386	8.37E-11	1.87E-10	ppm	-0.46130938	1.20E-09						NA
Sapur.03T0260100.1	306.7384107	0.564013624	0.086845003	6.492432	8.45E-11	1.89E-10	ppm	0.50456821	2.88E-11						NA
Sapur.01G0240400.1	469.0156228	0.181259057	0.027923893	-6.49118	8.52E-11	1.90E-10	ppm	-0.46394265	9.38E-10			Exostosin family protein			NA
Sapur.09G0137700.1	371.3974865	0.302168891	0.046100774	-6.47863	9.26E-11	2.06E-10	ppm	-0.48973807	5.44E-10			Emsy N Terminus (ENT)/ plant Tudor-like domains-containing protein			Hop-interacting protein THI115, putative
Sapur.09G0270200.1	3.458607692	-0.393993566	0.121234608	-6.47684	9.38E-11	2.08E-10	ppm	-0.47269158	4.08E-10	GO:0008080		Protein of unknown function (DUF680 and DUF632)			BZIP transcription factor bZIP107, putative
Sapur.15WG0271300.1	143.7657593	0.593412193	0.091689819	6.471953	9.67E-11	2.15E-10	ppm	-0.45246358	2.69E-09	GO:0071805;GO:0016020;GO:0015079		Arginyl-Cys N-acyltransferase (NAT) superfamily protein			tyrosine N-fenylalanine/tyrosine, putative
Sapur.09G0285100.1	86.43625254	0.162204	0.025147464	6.46889	9.88E-11	2.19E-10	ppm	-0.45821847	1.58E-09		ATKT2,ATKUP2,KT2,KUP2.5I

Sapur.05W053900.1	0.434503238	1.869261861	0.326676206	5.757346	8.54E-09	1.76E-08	cpm	0.46079711	1.26E-09				NA
Sapur.003G105200.1	526.1206736	2.293372341	0.051113426	7.73963	9.49E-09	1.96E-08	cpm	0.44193745	6.88E-09	GO:0016810;GO:0008807	ATSG15590.1	carbon-nitrogen hydrolase family protein	glutamine-dependent NAD(+) synthetase, putative
Sapur.005G069600.1	871.7930539	2.191610246	0.033447719	5.72869	1.01E-08	2.07E-08	cpm	0.42311809	5.07E-10	GO:0005515	ATSG20675.1	BTB/POZ domain-containing protein	BTB/POZ domain protein
Sapur.012G029100.1	646.7915389	2.322429934	0.058031942	5.72836	1.01E-08	2.08E-08	cpm	0.38586073	6.01E-07	GO:0008270;GO:0006355;GO:0005634;GO:0003700	ATMYB6.1;NFXL1	NF-X-like 1	NF-X1 type zinc finger protein
Sapur.T025200.3	1.461164001	2.328328753	0.214484446	5.72689	1.02E-08	2.09E-08	cpm	0.48268333	1.51E-10		ATSG18740.1	F-box containing nucleotide triphosphate hydrolases superfamily protein	NA
Sapur.017G113300.1	68.0673789	1.09161384	0.190955808	5.716602	1.09E-08	2.22E-08	cpm	0.533892233	6.01E-13	GO:0005852;GO:0005737;GO:0003743	ATG66070.1	Translation initiation factor eIF3 subunit	NA
Sapur.003G169700.1	17.43349303	0.422480595	0.073960657	-5.7123	1.13E-08	2.38E-08	cpm	-0.445140542	5.18E-09	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATSG15592.1	F-box containing nucleotide triphosphate hydrolases superfamily protein	Kinesin motor domain protein
Sapur.016G088900.1	1.645585181	3.170682076	0.241318104	-5.70584	1.16E-08	2.37E-08	cpm	-0.770745404	3.75E-32		ATSB18145.1	plastid-specific ribosomal protein 4	hypothetical protein
Sapur.012G008700.1	13.60018891	0.596759069	0.104642283	-5.70285	1.18E-08	2.41E-08	cpm	-0.400661139	2.00E-07		ATSG54165.1		Ar4/JC7-9 rapidly elicited protein, putative
Sapur.019G141600.1	17.98042534	-1.031231553	0.181528249	-5.68083	1.34E-08	2.73E-08	cpm	-0.532191332	5.18E-09	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATMG00490.1	CYP86A10	cytochrome P450, family 86, subfamily A, polypeptide 10
Sapur.009G073700.1	48.82973899	0.840269118	0.147955075	-5.67922	1.35E-08	2.76E-08	cpm	-0.482467557	1.57E-10		ATSG19508.1		complex 1 protein, LYR family protein
Sapur.T025900.1	2.557934207	3.168404262	0.190216026	5.677276	1.37E-08	2.79E-08	cpm	-0.409028236	1.02E-07				NA
Sapur.015W041400.1	34.960065	0.865578425	0.152875563	-5.66197	1.52E-08	3.09E-08	cpm	-0.461689528	1.16E-09	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATSG22330.1	ERL1	ERECTA-like 1
Sapur.004G046100.1	291.5403016	2.139145	0.473604669	5.65408	1.64E-08	3.37E-08	cpm	-0.412131439	1.20E-08		ATSG46170.1		F-box family protein
Sapur.T003500.1	377.4854862	2.294066422	0.052131618	5.621329	1.89E-08	3.83E-08	cpm	-0.386439813	5.77E-07	GO:0033179;GO:0015991;GO:0015078	ATPinx_V0 complex, subunit E		ATPinx_V0 complex, subunit E
Sapur.005G081800.1	855.1369322	2.054819349	0.045682516	5.61604	1.94E-08	3.94E-08	cpm	-0.385693471	1.06E-08		ATSB28525.1	Transmembrane amino acid transporter family protein	aromatic and neutral amino acid transporter
Sapur.011G046900.2	0.46919709	1.117727888	0.178833187	5.589209	2.28E-08	4.60E-08	cpm	-0.455132614	2.11E-09	GO:0005515;GO:0006468;GO:0004672	ATSG45840.2	Leucine-rich repeat protein kinase family protein	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.012G042900.3	3.672237054	0.992328826	0.177892799	5.579364	2.41E-08	4.87E-08	cpm	-0.395248002	3.01E-07	GO:0006629	ATSG73920.1	alpha/beta-hydrolases superfamily protein	alpha/beta hydrolase family protein
Sapur.007G067205.1	606.4446314	2.000481062	0.061179225	-5.57821	2.48E-08	4.90E-08	cpm	-0.460272249	2.97E-08	GO:0005509;GO:0004185	ATSG28260.1	serine carboxypeptidase 35	serine carboxypeptidase
Sapur.008G033800.1	14.62645688	0.516197505	0.092658837	5.570959	2.53E-08	5.10E-08	cpm	-0.429488992	1.99E-08		ATSG37060.1	NF-YB8	nuclear factor Y, subunit B8
Sapur.002G017700.1	494.6842295	0.915164597	0.164364507	5.568655	2.57E-08	5.16E-08	cpm	-0.475789166	1.68E-07	GO:0042347;GO:0030904;GO:0015031;GO:0008565	ATSG7450.1	VPS18	VPS18 homologs
Sapur.006G089500.3	9.940713869	0.591565526	0.106507884	-5.54951	2.88E-08	5.76E-08	cpm	-0.419187126	4.05E-08	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATSG13130.1	CYP97C7;LUT1	Cytochrome P450 family 97 monooxygenase
Sapur.T026800.1	2.768827447	5.822327927	0.148240803	5.544669	2.93E-08	5.86E-08	cpm	-0.559394999	2.63E-14		ATSG27143.3	SWEET16	HLAT repeat-containing protein
Sapur.002G065000.2	1.084423669	-5.683237477	0.303416109	-5.54465	2.95E-08	5.92E-08	cpm	-0.481324973	1.77E-10	GO:0055114;GO:0010277;GO:0051537;GO:0016491	ATSG44646.1	ATCAO;CAO;CHQ	Phosphorbidate a oxygenase family protein with Rieske [2Fe-2S] domain
Sapur.T006207.1	20.41055325	-0.473604669	0.085628995	-5.5314	3.14E-08	6.37E-08	cpm	-0.434447683	1.61E-08		ATSG41060.1	TRY	Tryptophan biosynthesis protein
Sapur.012G048900.1	223.386105	0.195032635	0.035498879	5.521299	3.17E-08	6.75E-08	cpm	-0.410645536	9.20E-08	GO:0005515	ATSG45760.1	transducin/WD40 domain protein	transducin/WD40 domain protein
Sapur.018G052100.1	3.628035718	1.045576116	0.189455815	-5.51896	3.41E-08	6.80E-08	cpm	-0.493951604	4.90E-11	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATSG26710.1	CYP97A3;CYP77A4;L	Cytochrome P450 superfamily protein
Sapur.006G137005.1	276.9602104	0.912242359	0.163813576	-5.48129	4.21E-08	8.40E-08	cpm	-0.392908671	3.58E-07	GO:0055114;GO:0016614;GO:0005840	ATMAD1;FAD3	fatty acid desaturase 3	long-chain-alcohol oxidase FAD1
Sapur.018G025300.1	2.297837338	-2.352394895	0.228519397	-5.47644	4.34E-08	8.66E-08	cpm	-0.509726461	9.22E-12		ATSG50660.2	alpha/beta-hydrolases superfamily	acyl protein thioesterase
Sapur.T017700.1	12.61181206	0.404591623	0.075957793	5.470579	4.49E-08	8.94E-08	cpm	-0.439638129	8.38E-09		ATCIMS1;ATKPOL;HET2;XPO1	exportin 1A	NA
Sapur.009G029900.1	531.5836967	2.091028317	0.036994648	5.456487	4.80E-08	9.56E-08	cpm	-0.436791609	1.07E-08	GO:0006367;GO:0005672	ATSG07480.2	Transcription factor IIA, alpha/beta subunit	transcription factor/transcription initiation factor
Sapur.017G092500.1	0.551617206	2.248283832	0.412863137	5.45129	5.17E-08	1.03E-07	cpm	-0.418508883	4.88E-08		ATSG45890.1	Pectin lyase-like superfamily protein	pectinesterase family protein
Sapur.010G065600.3	0.878183969	0.658026148	0.305082369	-5.43764	5.40E-08	1.07E-07	cpm	-0.7715267	2.31E-12		ATSG22810.1	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region	auxin-correlation protein
Sapur.T026200.1	126.3924248	0.363774146	0.067007364	-5.42312	5.86E-08	1.16E-07	cpm	-0.441124222	7.26E-09		ATSG32031.1		transmembrane protein, putative
Sapur.014G111400.3	4.86647807	0.757813377	0.139775247	-5.42166	5.90E-08	1.17E-07	cpm	-0.545098722	2.58E-13	GO:0006355;GO:0005739;GO:0003690	ATSG62990.1	Mitochondrial transcription termination factor family protein	transcription termination factor family protein
Sapur.003G089300.2	0.819038893	-0.552238502	0.139775522	-5.41137	6.21E-08	1.23E-07	cpm	-0.730257976	2.57E-26	GO:0003676	ATSG19830.1	Nucleic acid-binding, OB-fold-like protein	heat shock factor protein hsf8, putative
Sapur.T009300.1	0.362641818	1.76875734	0.326956167	5.409769	6.31E-08	1.25E-07	cpm	-0.491682242	6.19E-11		ATSG26380.1	Meltdase family protein	NA
Sapur.005G112800.1	252.8039362	0.248840565	0.045881791	-5.40736	6.40E-08	1.27E-07	cpm	-0.399464255	2.19E-07		ATSG50010.1	sequence-specific DNA binding transcription factors;transcription regulators	transcription factor, putative
Sapur.005G185200.1	392.2727532	0.651454193	0.02898005	-5.38802	7.12E-08	1.41E-07	cpm	-0.430331061	1.85E-08		ATSG18530.1	Protein of unknown function (DUF707)	transmembrane protein, putative
Sapur.003G137600.1	77.28999525	1.250972992	0.247528829	5.372888	7.75E-08	1.53E-07	cpm	-0.492267628	5.77E-11				hypothetical protein
Sapur.T008200.1	42.31617685	-0.864955158	0.181027648	-5.3551	8.51E-08	1.68E-07	cpm	-0.478177999	2.60E-10				NA
Sapur.009G108700.7	2.114694985	1.060008962	0.198163728	5.349157	8.84E-08	1.76E-07	cpm	-0.621583834	1.73E-18		ATSG15130.3	Arabidopsis phospholipase-like protein (PLAIs); 4] family	phospholipase-like protein (patatin-6), putative
Sapur.009G023100.1	144.8070621	-1.149173502	0.216113378	-5.34769	8.94E-08	1.76E-07	cpm	-0.386791244	9.50E-07	GO:0005515	ATSG35;SGS3	XS domain-containing protein; Tudor domain-containing protein-related	hypothetical protein
Sapur.003G111700.2	30.97132919	-0.420144117	0.078782068	-5.33299	9.60E-08	1.90E-07	cpm	-0.451930974	1.89E-07		ATSG19003.2	VPS25	C2H2/DP family winged-helix DNA-binding domain
Sapur.003G032000.4	0.977898322	-0.455601249	0.168660605	-5.32105	1.03E-07	2.03E-07	cpm	-0.828936884	5.98E-41	GO:0006457	ATSG45640.1	FKBP-like peptidyl-prolyl cis-trans isomerase	peptidyl-prolyl cis-trans isomerase FKBP16-3
Sapur.018G091600.1	0.45971563	2.465638269	0.462356415	5.314509	1.07E-07	2.10E-07	cpm	-0.423710682	1.21E-08	GO:0015151;GO:0030488;GO:0016429	ATSG14600.1	S-adenosyl-L-methionine-dependent methyltransferases superfluorin protein	NA
Sapur.006G212000.1	2.032955551	0.488387969	0.091513178	5.308137	1.08E-07	2.12E-07	cpm	-0.408204746	1.16E-07	GO:0008270;GO:0005622;GO:0005515	ATSG49381.1	CONSTANS-like 4	constans-like zinc finger protein
Sapur.016G154300.1	69.32550009	-0.488879969	0.092462172	-5.29973	1.16E-07	2.27E-07	cpm	-0.417235589	4.50E-10		ATSG7635.1	NIT;WIP2	C2H2-type zinc finger family protein	transparent TESTA 1 protein, putative
Sapur.003G173900.2	5.203563085	-0.677092103	0.128092235	-5.29065	1.23E-07	2.39E-07	cpm	-0.643845261	9.43E-20		ATSG40880.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/lipid transfer family protein
Sapur.014G044800.1	2.368624249	-0.770082963	0.146087872	-5.27488	1.32E-07	2.60E-07	cpm	-0.612621447	1.51E-17		ATSG20160.1	C2H2-like zinc finger protein	nucleic acid-binding protein, putative
Sapur.010G041200.1	244.0429243	0.257874192	0.048909119	5.263585	1.41E-07	2.76E-07	cpm	0.408613808	1.12E-07		ATSG23280.2	XBAT35	RING-H2 ortholog 5 in Arabidopsis thaliana	E3 ubiquitin-protein ligase XBAT34, putative
Sapur.006G119100.1	121.4860024	0.644381844	0.122063369	5.23577	1.64E-07	3.20E-07	cpm	-0.386274656	5.79E-07		ATSG7210.1	Protein of unknown function (DUF231)	NA
Sapur.008G041800.4	3.886156952	0.736084448	0.140968387	5.221061	1.78E-07	3.46E-07	cpm	0.810362497	8.16E-18		ATSG59300.1	ubiquitin carrier protein 7	ubiquitin-conjugating enzyme E2
Sapur.015G017000.1	55.58694917	0.320187005	0.062613378	-5.18763	2.15E-07	4.21E-07	cpm	-0.382627955	3.26E-06		ATSG13120.1	Pentatricopeptide repeat (PPR) superfamily protein	NA
Sapur.003G080800.1	338.5056259	0.241113368	0.046296536	5.207979	1.91E-07	3.71E-07	cpm	0.365026995	2.50E-06	GO:0005085;GO:0016021	ATSG54115.1	ATCCA;CCM4	calcium calcium exchanger 4	calcium/cation exchanger
Sapur.006G046500.1	853.7154473	0.215318344	0.041577582	5.184004	2.17E-07	4.21E-07	cpm	0.373857298	5.04E-06	GO:0004872	ATSG20110.1	RING/FYVE/PHD zinc finger superfamily protein	zinc finger protein, putative
Sapur.006G057700.1	16.53867744	-0.814093363	0.157461413	-5.17077	2.33E-07	4.51E-07	cpm	-0.413241065	7.49E-08				NA
Sapur.012G190400.1	105.9549367	-0.384913758	0.074577568	-5.14779	2.64E-07	5.09E-07	cpm	-0.438380845	1.40E-08		ATSG22120.1	ATGT18;GT18	galactosyltransferase 18	galactosyltransferase family
Sapur.010G181800.1	6863.010499	0.172364188	0.033632202	5.122007	3.02E-07	5.81E-07	cpm	0.363192647	2.30E-06	GO:0006508;GO:0004185	ATSG10410.1	CPY;ECA4	SERINE CARBOXYPEPTIDASE-LIKE 49	serine carboxypeptidase
Sapur.008G113300.1	687.3213576	0.173731362	0.033931815	5.120014	3.06E-07	5.87E-07	cpm	-0.402238857	1.77E-07		ATSG10930.1	ATBHLL88;BPE;1	basic pentacysteine1	GAGA-binding transcriptional activator
Sapur.T010600.1	0.303826119	0.597239207	0.192061319	5.115685	3.13E-07	6.00E-07	cpm	0.550718449	7.86E-14					NA
Sapur.005G163000.4	12.49699572	-0.585815902	0.114430642	-5.11048	3.21E-07	6.17E-07	cpm	-0.512869769	6.52E-12		ATSG10260.3		Reticulon family protein	reticulon-like protein
Sapur.T018800.1	3.454079911	1.602771294	0.227249591	5.104966	3.26E-07	6.26E-07	cpm	0.393727392	3.46E-07		ATSG10582.3	LHY;LHY1	Histone/histone fold-containing protein	late elongated hypocotyl and circadian clock associated-like protein
Sapur.006G206200.1	791.1606918	0.392038382	0.076788255	5.105447	3.30E-07	6.33E-07	cpm	-0.385482514	6.18E-07	GO:0016747;GO:0008610;GO:0016020;GO:0006633	ATSG36640.1	KCS11	3-ketoacyl-CoA synthase 11	3-ketoacyl-CoA synthase
Sapur.008G046600.1	809.7152503	-0.405600869	0.078000617	-5.10126	3.30E-07	6.33E-07	cpm	-0.460800869	1.81E-10		ATSG20250.1		NADP(H)-binding Rossmann-fold superfamily protein	tropinone reductase, putative
Sapur.010G104000.1	312.1321183	0.266941447	0.052358387	5.098741	3.42E-07	6.55E-07	cpm	-0.335629504	1.73E-05		ATSG37035.1			transmembrane protein, putative
Sapur.003G053000.1	265.0029216	0.313321157	0.061456457	5.098103	3.46E-07	6.68E-07	cpm	-0.336429797	1.32E-06	GO:0006468;GO:0004672	ATSG74740.1	ATCPK30;CDPK14;CPK30	calcium-dependent protein kinase 30	calcium-dependent kinase
Sapur.006G001500.1	101.1362881	-0.777654112	0.153425148	-5.06862	4.01E-07	7.66E-07	cpm	-0.436756604	1.07E-08					transmembrane protein, putative
Sapur.010G097200.1	113.5732626	-0.385501855	0.076106322	-5.03961	4.68E-07	8.88E-07	cpm	-0.432924045	1.49E-08		ATSG8585.1			hypothetical protein
Sapur.016G198800.1	488.9802786	0.251789079	0.049925242	5.039404	4.67E-07	8.89E-07	cpm	0.403572023	6.68E-07		ATSG45490.1			hypothetical protein
Sapur.15W0139500.1	175.1848536	0.360707142	0.052073773	5.006496	5.54E-07	1.05E-06	cpm	0.402265326	1.77E-07	GO:0003676	ATSG44730.1		RNA-binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.018G091800.1	0.453224614	0.287387855	0.042861379	4.964613	6.21E-07	1.18E-06	cpm	0.420713134	1.76E-08	GO:0015151;GO:0030488;GO:0016429	ATSG14600.1	S-adenosyl-L-methionine-dependent methyltransferases superfluorin protein	S-adenosyl-L-methionine-dependent methyltransferases
Sapur.002G079400.1	27.0880791	0.342124285	0.068767628	-4.93653	6.47E-07	1.22E-06	cpm	-0.492000113	1.29E-11		ATSG89980.1	FBW2	F-BOX WITH WD-40 2	F-box protein, putative
Sapur.005G146500.1	1.205230793	-0.361231282	0.280006268	-4.86697	1.13E-06	2.14E-06	cpm	-0.654557657	5.61E-22		ATSG78430.1	AKR2	ROP interactor kinase 2	interactor of constitutive active ROPs protein, putative
Sapur.005G183700.1	460.0501457	0.494728594	0.096656021	-4.964213	6.90E-07	1.30E-06	cpm	-0.365192983	2.56E-06	GO:0005975;GO:0004553	ATSG66460.1	Glycosyl hydrolase superfamily protein	mannan endo-1|3|4-beta-mannosidase
Sapur.006G075300.2	14.8016769	0.510192663	0.127588223	-4.95152	7.36E-07	1.39E-06	cpm	-0.378600394	2.01E-06	GO:0005739;GO:0016021	ATSG9520.1	ATUPS2;UPS2	mitochondrial prohibitin complex protein	ATP-dependent zinc metalloprotease FtsH
Sapur.017G104000.1	0.962964678	-1.417833276	0.286632311	-4.91299	9.01E-07	1.69E-06	cpm	0.6455774	7.00E-20	GO:0008270	ATSG20175.1	RING/FYVE/PHD zinc finger superfamily protein	RING/FYVE/PHD zinc finger superfamily protein	zinc finger protein
Sapur.15W0251400.1	7.755879806	0.862842311	0.135231861	4.901887	9.48E-07	1.78E-06	cpm	0.553615284	5.48E-14	GO:0003824;GO:0006470;GO:0004722	ATSG31481.1	Protein phosphatase 2C family protein	protein phosphatase 2C	protein phosphatase 2C
Sapur.005G121200.1	0.39968577	-1.924457785	0.197073	-4.847091	1.26E-06	2.36E-06	cpm	-0.692570845	1.27E-09	GO:0007165	ATSG18290.1	REN1	Rho GTPase activating protein (RhoGAP) with PH domain	Rho-GTPase-activating protein, putative
Sapur.008G170600.1	166.1123635	0.220197221	0.045499118	4.840438	1.30E-06	2.41E-06	cpm	0.327922188	2.76E-05	GO:0005515	ATSG23880.1		F-box and associated interaction domains-containing protein	F-box protein interaction domain protein
Sapur.011G040500.1	84.63616139	0.531828922	0.110753137	4.80165	1.57E-06	2.91E-06	cpm	-0.378192023	9.90E-07	GO:0003824;GO:0006508	ATSG45580.1	Grantalin repeat protein family	Grantalin repeat protein family	cysteine protease
Sapur.014G069500.1	726.4293718	0.145978853	0.030443885	4.795014	1.63E-06	3.02E-06	cpm	-0.351862158	5.45E-06	GO:0005515;GO:0051287	ATSG15510.1	AN	NADP(H-binding Rossmann-fold superfamily protein	NA
Sapur.005G048200.1	67.58639797	0.517368623	0.107806124	4.75605	1.97E-06	3.65E-06	cpm	-0.302095568	7.01E-06		ATSG7670.1	TWI;WIP2	C2H2-type zinc finger family protein	transparent TESTA 1 protein, putative
Sapur.006G067100.2	0.507164822	1.627178558	0.342433823	4.751804	2.02E-06	3.72E-06	cpm	0.623703063	2.68E-18	GO:0006796;GO:0005737;GO:0004427;GO:0000287	ATSG3620.1	AtPPA4;PPa4	pyrophosphorylase 4	inorganic pyrophosphatase
Sapur.T031500.1	1.138969222	1.06861337	0.2250574	4.665316	3.08E-06	5.62E-06	cpm	0.458189137	1.31E-08		ATSG60860.1	SEC7-like guanine-nucleotide exchange family protein	SEC7-like guanine-nucleotide exchange family protein	NA
Sapur.016G050800.2	0.4623389	1.807056186	0.389760288	4.636258	3.51E-06	6.48E-06	cpm	0.667031218	1.47E-21	GO:0043562;GO:0009744	ATSG16360.3	5';-AMP-activated protein kinase beta-2 subunit	SNF1-related kinase regulatory beta subunit 1	SNF1-related kinase regulatory beta subunit 1
Sapur.006G184500.1	11.58363686	0.472008457	0.102472867	4.604743	3.58E-06	6.53E-06	cpm	0.365408803	1.53E-06		ATSG20550.1	Ypt/Rab-GAP domain of gyp1p superfamily protein	Rab5A/Y7/RC domain protein	Rab5A/Y7/RC domain protein
Sapur.002G189900.1	102.7592766	0.736085112	0.159760573	4.607427	4.08E-06	7.42E-06	cpm	0.335767694	5.61E-05		ATSG7260.1	Tetratricopeptide repeat (TPR)-like superfamily protein	Tetratricopeptide repeat (TPR)-like superfamily protein	chloroniperoxidase reduction protein, putative
Sapur.016G182700.1	0.962926106	-1.292026875	0.270738847	-4.54426	5.51E-06	9.96E-06	cpm	-0.6327214	5.80E-17	GO:0005515;GO:0003677	ATSG62700.1	zinc ion binding;DNA binding	zinc finger CCCH domain protein, putative	zinc finger CCCH domain protein, putative
Sapur.013G144000.1	347.4682022	-0.307793822	0.068208785	-4.51305	6.26E-06	1.13E-05	cpm	-0.439132658	1.30E-19	GO:0015031;GO:0006457	ATSG8695.2			hypothetical protein
Sapur.010G130500.4	1.400471959	-0.052461391	0.233266899	-4.51261	6.40E-06	1.15E-05	cpm	-0.737995847	2.87E-28		ATSG16146.1		cyMAP-regulated phosphoprotein/endosulfine motif protein	cyMAP-regulated phosphoprotein/endosulfine motif protein
Sapur.002G020400.4	11.01211119	0.387817284	0.087716586	-4.42187	9.78E-06	1.74E-05	cpm	0.737943477	3.60E-20	GO:0003824;GO:0006508	ATX87;SDG25	SET domain protein 25	SET domain protein	SET domain protein
Sapur.002G052300.1	20.14015682	0.50001047	0.113657956	4.400074	1.08E-05	1.92E-05	cpm	0.330768024	2.32E-05	GO:0005515	ATSG43640.1	ATLP5;TLP5	tubby like protein 5	tubby-like 5 box protein
Sapur.016G132200.1	0.983090588	-0.566892019	0.265408774	-4.39637	1.10E-05	1.96E-05	cpm	-0.456529104	9.60E-10	GO:0005737;GO:0005457	ATFABP42;FABP42;TWD1.LI	FABP domain-containing protein	FABP domain-containing protein	peptidyl-prolyl cis-trans isomerase family
Sapur.005G113300.1	89.01617162	0.251175003	0.057816305	4.344363	1.40E-05	2.47E-05	cpm	0.379341201	9.61E-07		ATSG45630.1	SUV2	protein dimerizations	NA
Sapur.003G147400.1	189.3878863	0.323396662	0.07560923	4.3418	1.41E-05	2.49E-05	cpm	-0.388182834	3.96E-07	GO:0005085;GO:0046875;GO:0003051;GO:0016020	ZIP1	zinc transporter 1 precursor	zinc transporter 1 precursor	ZIP zinc/iron transport family protein
Sapur.004G070900.1	0.812742077	1.319457823	0.305189504	4.321277	1.54E-05	2.71E-05	cpm	0.596602449	1.65E-16		ATSG6580.1			MYB DNA-binding domain protein, putative
Sapur.007G138900.3	16.86878177	0.370352949	0.086091145	4.302286	1.64E-05	2.87E-05	cpm	0.582450099	2.15E-16		ATSG49370.1		RNA-binding protein	LA-related protein 6 LA RNA-binding domain protein
Sapur.012G161500.1	35.15154779	1.909595812	0.45087426	4.235318	2.28E-05	3.98E-05	cpm	0.410013831	9.67E-08	GO:0007165;GO:0005515	ATSG2900.1	Toll-interleukin-Resistance (TIR) domain family protein		
Sapur.008G166500.1	152.3928283	0.929892076	0.121125682	-4.20961	2.58E-05	4.45E-05	cpm	-0.337987263	1.50E-05		ATSG15630.1	Uncharacterized protein family (UPF0497)	Uncharacterized protein family (UPF0497)	plant integral membrane protein
Sapur.005G007100.1	355.8748716	-0.449383297	0.106937662	-4.2026	2.64E-05	4.59E-05	cpm	-0.396247561	4.60E-07		ATSG15260.2	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/lipid transfer family protein
Sapur.006G068400.1	92.20152894	0.581619211	0.138646845	-4.19497	2.73E-05	4.74E-05	cpm	-0.775617761	3.90E-32	GO:0016491;GO:0008152	ATSG0540.1	NADP(H-binding Rossmann-fold superfamily protein	NADP(H-binding Rossmann-fold superfamily protein	short chain dehydrogenase
Sapur.11W0289400.1	49.1106169	1.343461337	0.082436091	4.16265	3.16E-05	5.27E-05	cpm	-0.759007181	4.30E-27		ATSG7910.2	ATGMS1;GMS1	ADP-glucose pyrophosphorylase family protein	mannose-1-phosphate guanyltransferase
Sapur.013G029600.2	0.391853512	1.890609006	0.459381715	-4.11632	3.85E-05	6.63E-05	cpm	-0.857646652	1.36E-46	GO:0004871;GO:0000160	ATSG29150.1	AHP2	histidine-containing phosphotransmitter 2	histidine phosphotransfer protein
Sapur.008G108500.1	588.5923603	0.108021241	0.05555175	4.11618	3.90E-05	6.71E-05	cpm	-0.315980247	1.57E-05	GO:0005872	ATSB19190.1	ULT;ULT1	Development and cell fate specifier protein	transcription factor, putative
Sapur.017G024000.1	108.5869645	0.175921993	0.043644806	-4.03056	5.61E-05	9.50E-05	cpm	-0.429320035	1.81E-07	GO:0016021	ATSB38630.1	ACYB-1;CYB-1	cytochrome b561 family protein	cytochrome protein b561
Sapur.016G092600.1	4.78027563	0.860107698	0.173143843	4.013233	5.96E-05	1.00E-04	cpm	0.296421468	2.00E-03	GO:0005488;GO:0004872	ATSB51130.1	chaperonin-like protein	chaperonin-like protein	glycogen synthase kinase 3 MAK-3 protein
Sapur.016G089100.1	0.42051929	-1.775069133	0.446743592	-3.97537	7.03E-05	1.00E-04	cpm	0.837853451	1.36E-42	GO:0006457	ATSG10060.1	FKBP-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase FKBP16-4	peptidyl-prolyl cis-trans isomerase FKBP16-4
Sapur.012G019700.1	0.800390365	1.390410357	0.353395183	3.912296	9.14E-05	1.00E-03	cpm	0.6250616	2.14E-18	GO:0003824;GO:0006470;GO:0004722	ATSG29380.1	HAK3	highly ABA-induced PP2C gene 3	protein phosphatase 2C
Sapur.016G055100.1	0.686687673	1.123216616	0.320797974	3.506019	0.00045	0.00221	cpm	-0.723470271	1.27E-26	GO:0003723	ATSG4610.2	APO1	Arabidopsis thaliana protein of unknown function (DUF794)	APO RNA-binding protein
Sapur.015G168200.2	0.560664721	1.417605088	0.370403382	3.820597	0.00013927	0.00216064	cpm	0.585904418	4.57E-16		ATSG35540.1			DUF3741 family protein
Sapur.016G247700.1	47.43867686	0.252192224	0.071083479	3.547489	0.00054193	0.00429912	cpm	-0.479887974	1.97E-10		ATSG14830.1			hypothetical protein
Sapur.017G081800.1	8.421016648	-0.497879442	0.133336378	3.734031	0.00018845	0.00331445	cpm	-0.49485814	8.31E-10		ATSB9500.1		Thioredoxin superfamily protein	DiSulfo oxidoreductase family protein
Sapur.T024800.1	-2.033650353	0.615175364	0.163848487	-3.72	0.00019	0.00359984	cpm	-0.532464354	1.55E-14		ATSG9740.1		P-loop containing nucleotide triphosphate hydrolases superfamily protein	NA
Sapur.003G170400.1	0.566642711	1.417605088	0.370403382	3.820597	0.00013927	0.00216064	cpm	0.585904418	4.57E-16		ATSG35540.1			DUF3741 family protein
Sapur.T026300.1	47.43867686	0.252192224	0.071083479	3.547489	0.00054193	0.00429912	cpm	-0.479887974	1.97E-10		ATSG14830.1			hypothetical protein
Sapur.017G081800.1	8.421016648	-0.497879442	0.133336378	3.734031	0.00018845	0.00331445	cpm	-0.49485814	8.31E-10		ATSB9500.1		Thioredoxin superfamily protein	DiSulfo oxidoreductase family protein
Sapur.T024800.1	-2.033650353	0.615175364	0.163848487	-3.72	0.00019	0.00359984	cpm	-0

Sapur.T073800.1	76.14622759	1.34231773	0.156431778	8.583497	9.20E-18	2.57E-17	darkgreen	0.513719953	5.96E-12	GO:0003968	ATG2G19910.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T150900.1	31.59626017	0.80976888	0.118763539	6.818329	9.21E-12	2.13E-11	darkgreen	0.449161458	3.64E-09	GO:0003968	ATG2G19920.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T0G6134700.1	2.23605131	1.29957762	0.129614189	5.682224	1.43E-08	2.92E-08	darkgreen	0.160318023	1.93E-06				NA
Sapur.0G6134300.1	23.9916064	0.88919423	0.168736155	5.269525	1.37E-07	2.67E-07	darkgreen	0.404534973	1.48E-07				NA
Sapur.0G6134100.1	16.4008175	1.38802487	0.191709899	4.61429	1.01E-05	1.79E-05	darkgreen	0.307704309	2.32E-07				NA
Sapur.0G5117200.1	14.48881783	0.66991304	0.162248345	4.128925	3.64E-05	6.29E-05	darkgreen	0.336140424	1.68E-05				NA
Sapur.0G6120100.1	169.4730994	0.28107303	0.088246132	3.148825	0.001639283	0.002539231	darkgreen	0.235405949	0.002992906		AT5G20520.1	WAV2	alpha/beta-Hydrolases superfamily protein	NA
Sapur.T087400.1	3.477643903	0.62318055	0.228538803	2.726792	0.006395918	0.009469147	darkgreen	0.243873691	0.002084149				NA
Sapur.0G6120200.1	265.2076054	0.16816227	0.061920185	2.718278	0.006562269	0.009887145	darkgreen	0.13971265	0.0132049		AT5G20520.1	WAV2	alpha/beta-Hydrolases superfamily protein	alpha/beta hydrolase family protein
Sapur.0G6137100.1	14.58364861	0.5224667	0.240764542	2.169227	0.0137146	0.016829768	darkgreen	0.253113676	0.00105097		AT2G30200.3	VEL1	vernalization5/VIN3-like	protein vernalization insensitive protein
Sapur.0G6145400.1	91.57608018	0.20609185	0.085185136	2.520268	0.012317768	0.017752966	darkgreen	0.195880563	0.013956797	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T087300.1	76.62763884	0.19175368	0.078207793	2.451126	0.016214602	0.023576572	darkgreen	0.257646015	0.00113843	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.0G6143400.1	136.6307394	0.38504905	0.176044479	2.161618	0.030647436	0.042401068	darkgreen	0.206283854	0.009541583	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T087700.1	4.162953128	0.31335231	0.145179325	2.159104	0.030845267	0.042663267	darkgreen	0.196236209	0.013726654				NA
Sapur.T087600.1	56.18949257	0.46835259	0.22659932	2.06644	0.03878697	0.053080116	darkgreen	0.224823046	0.006424566	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.0G6132500.1	13.93765369	0.39235521	0.192656227	2.036563	0.04178968	0.056812667	darkgreen	0.208654823	0.013742559		ATG2G27810.1	Protein of unknown function (DUF2361)	transmembrane protein, putative
Sapur.T147100.1	14.56638011	0.38852884	0.191402866	2.029901	0.042366619	0.057764727	darkgreen	0.189512961	0.017446679	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T072800.1	11.88868825	0.41520117	0.206303582	2.012583	0.044158466	0.060078037	darkgreen	0.192469664	0.015735728	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T074400.1	132.0800765	0.34349624	0.172134147	1.993896	0.046270425	0.064070628	darkgreen	0.186335168	0.021231012	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T087800.1	5.651524521	0.49840685	0.250776696	1.918576	0.055030867	0.074060378	darkgreen	0.194846613	0.014469304				NA
Sapur.T073100.1	4.902618206	0.56175513	0.293129504	1.916574	0.055239943	0.074351969	darkgreen	0.18220569	0.022491468				NA
Sapur.0G6144900.1	22.78242296	0.52138836	0.297740496	1.750768	0.079885853	0.105442708	darkgreen	0.231127242	0.003579707				NA
Sapur.0G6144000.1	15.58833599	0.28178378	0.162460566	1.734383	0.082832216	0.109231517	darkgreen	0.157037879	0.049458785	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T146700.1	2.479933566	0.32690758	0.209592239	1.570162	0.11627744	0.15201649	darkgreen	0.138875115	0.087387143	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.0G6126100.1	99.73945518	0.26155224	0.166817145	1.567664	0.116959126	0.153052387	darkgreen	0.138547061	0.08545824		ATG2G19930.1		NA
Sapur.T072900.1	27.50747277	0.37854359	0.245726472	1.539738	0.123424258	0.159309585	darkgreen	0.181414693	0.022974759	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T088100.1	34.99621156	0.25482979	0.16677076	1.526885	0.126785583	0.162802588	darkgreen	0.142845516	0.074318586	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T087900.1	9.521661173	0.37267666	0.250262276	1.489584	0.136319192	0.174473658	darkgreen	0.154456959	0.053433604	GO:0003968			NA
Sapur.0G6145000.1	76.21622113	0.29684526	0.20132902	1.460414	0.144176357	0.183827924	darkgreen	0.15438216	0.053454569	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.0G6144200.1	83.48016257	0.28235752	0.207570184	1.360221	0.173878204	0.220219944	darkgreen	0.138729204	0.101232012	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T072600.1	9.026976949	0.37778293	0.273868187	1.379435	0.167702752	0.211708894	darkgreen	0.154667916	0.052094435				NA
Sapur.T072200.1	8.125410026	0.34238667	0.252927735	1.353327	0.187993767	0.235367586	darkgreen	0.138128562	0.094623713				NA
Sapur.T146800.1	41.70668906	0.30568888	0.239634338	1.275197	0.202239672	0.251887588	darkgreen	0.153806405	0.055602627	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.0G6144700.1	11.97166669	0.34465144	0.283600205	1.213622	0.224888108	0.278220581	darkgreen	0.140248435	0.074609941				NA
Sapur.T073500.1	22.81758005	0.36479936	0.301587588	1.209431	0.226497397	0.280002552	darkgreen	0.168072889	0.015368833				NA
Sapur.T073000.1	64.96573866	0.25661204	0.213024811	1.182157	0.237366557	0.291895256	darkgreen	0.179164517	0.024788089				NA
Sapur.T153600.1	27.2383478	0.27164815	0.232862908	1.166558	0.243388833	0.2991717	darkgreen	0.13257572	0.091175591	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.0G6144400.1	34.12739264	0.28444703	0.257253417	1.105707	0.268852191	0.32885729	darkgreen	0.141499387	0.077107811	GO:0003968	ATG2G19930.1	RNA-dependent RNA polymerase family protein	NA
Sapur.T087500.1	22.54868655	0.25485815	0.285718108	0.891669	0.321820304	0.38172027	darkgreen	0.124993026	0.138816399				NA
Sapur.0G6142300.1	492.4991306	0.12235312	0.139109651	-0.97383	0.330143303	0.39659922	darkgreen	-0.092290035	0.250306474		AT4G30410.2	sequence-specific DNA binding transcription factors	transcription factor, putative
Sapur.T073700.1	17.18414727	0.29229884	0.377510313	0.946025	0.343216625	0.410202046	darkgreen	0.114663016	0.175198855				NA
Sapur.0G6145100.1	14.86314979	0.24097434	0.268226898	0.898398	0.368973152	0.43801107	darkgreen	0.108164141	0.177958228				NA
Sapur.T087500.1	24.14288223	0.19386247	0.330925667	0.586421	0.557663402	0.612202077	darkgreen	0.109134403	0.227230103		AT3G18660.1	PNP-A	plant ratiurietic peptide A	NA
Sapur.T150700.1	12.26998148	0.16021668	0.283313391	0.565175	0.571954414	0.64729282	darkgreen	0.068251892	0.395886118				NA
Sapur.0G6144300.1	0.82122663	0.14852318	0.262026664	0.56642	0.572097548	0.64844042	darkgreen	-0.005168856	0.947691794				NA
Sapur.T087100.1	3.394772887	0.12009609	0.233627092	0.517647	0.604704778	0.67861404	darkgreen	0.03493757	0.663997323				NA
Sapur.T146900.1	15.70180761	0.13748763	0.287282255	0.478624	0.632205868	0.70499589	darkgreen	0.068247763	0.396489032				NA
Sapur.0G6123500.1	0.08313304	0.46560278	1.217708962	0.38782	0.69059325	0.75956776	darkgreen	-0.118793975	0.138382344	GO:0030145;GO:0004177	AT4G29490.1	Metallopeptidase M24 family protein	lea-pro dipeptidase
Sapur.0G6138500.1	124.3752364	-0.13622713	0.393622310	-0.34684	0.729717272	0.79479816	darkgreen	-0.057533816	0.47415887				NA
Sapur.T150600.1	7.506664717	0.13581242	0.362925252	-0.31088	0.755809401	0.81847949	darkgreen	-0.031838532	0.688263038				NA
Sapur.0G6144200.1	6.984535642	-0.07891693	0.267310925	-0.29522	0.767823182	0.82910735	darkgreen	-0.030205925	0.708924655				NA
Sapur.0G6144700.1	4.547334229	-0.06241763	0.266004111	-0.2346	0.814523134	0.86760821	darkgreen	-0.023520397	0.769574455				NA
Sapur.0G6144800.1	3.481606707	-0.05185284	0.23964478	-0.21632	0.828374465	0.87934739	darkgreen	-0.024279774	0.651933474				NA
Sapur.T153800.1	3.394839976	-0.04227627	0.231549102	-0.18295	0.873138281	0.91304887	darkgreen	-0.028363936	0.618322245				NA
Sapur.T152500.1	3.786649511	0.03610731	0.229681344	0.158963	0.873884819	0.91417997	darkgreen	0.016149225	0.843897732				NA
Sapur.0G6144600.1	10.07406024	0.03255184	0.230488305	-0.02502	0.980038013	0.98711409	darkgreen	0.005041213	0.946076093				NA
Sapur.0G3G103500.1	26.03577715	-1.65208569	0.1101075	-15.0043	6.89E-51	3.84E-50	darkgreen	-0.330328842	2.39E-05	GO:0016787;GO:0005634;GO:0003677	ATG3G35530.2	DEAD/DEAH box RNA helicase family protein	NA
Sapur.0G8296700.3	12.65854996	-0.59045998	0.094189676	-6.26884	3.64E-10	7.80E-10	darkgreen	-0.114726415	0.152957724	GO:0005525	ATG2G30300.2	Avirulence induced gene (AIG2) family protein	import component Tic56/159, G and M domain protein
Sapur.0G5G800001.2	0.865916641	-0.07806886	0.1251865	-0.6003	5.64E-07	1.07E-06	darkgreen	-0.329842162	2.52E-05	GO:0004408;GO:0005634;GO:0004177	ATG2G18500.2	Protein kinase superfamily protein	receptor-like kinase, putative
Sapur.0G4G137300.3	9.970211791	0.44562339	0.115080326	3.867677	0.000108877	0.000184247	darkgreen	-0.054281829	0.499540909		ATG2G37500.1	Protein kinase superfamily protein	ABC1 family protein
Sapur.0G3G300001.3	14.24268849	0.29182182	0.093171283	3.130488	0.004659348	0.007029863	darkgreen	-0.124420498	0.105305078	GO:0005515	ATG2G35090.1 LRS1	Transducin/WD40 repeat-like superfamily protein	ssh-induced WD protein
Sapur.0T0G5100.3	0.75809186	0.91329254	0.308196864	3.023487	0.002498797	0.00382033	darkgreen	-0.081608864	0.309509942	GO:0005634		ARM repeat superfamily protein	condensin-2 complex subunit G2
Sapur.0T0G5120.3	0.75809186	0.91329254	0.308196864	3.023487	0.002498797	0.00382033	darkgreen	-0.081608864	0.309509942	GO:0005634		ARM GTPase domain family protein	ADP-ribosylation factor GTPase-activating protein AGD3
Sapur.0T0G5120.3	295.7354755	-1.00787164	0.276981176	-1.75369	0.079483872	0.10484364	darkgreen	-0.155613439	0.015179328		AGD3,SFC,VAN3 ATG2G19200.1	Stigma-specific Stig1 family protein	Stig1 stigma-specific protein
Sapur.0T0G5160.3	1.013654147	-0.28788267	0.269171283	-1.07002	0.284966468	0.36147667	darkgreen	-0.137172164	0.080457018		ATG2G19325.1	Stigma-specific Stig1 family protein	Stig1 stigma-specific protein
Sapur.0G6G284000.5	8.816305254	-0.11802552	0.106032352	-1.13458	0.256532245	0.31498767	darkgreen	-0.122261207	0.171915563		ATG2G19370.1	Ankyrin repeat family protein	ankyrin repeat protein 13C-B
Sapur.0G6G500001.3	1.152905093	-0.46180278	1.217708962	-0.38782	0.69059325	0.75956776	darkgreen	-0.118793975	0.138382344	GO:0030145;GO:0004177	ATG2G19440.1	Metallopeptidase M24 family protein	lea-pro dipeptidase
Sapur.0T0G5200.3	2.184812351	-0.52683585	0.62044667	-0.87008	0.384258785	0.45436631	darkgreen	-0.136038473	0.08934881		ATG2G19440.1	ATNSPN13,NPSN13	novel plant SNARE protein	novel plant SNARE protein
Sapur.0G6148800.1	0.167092617	-0.84667626	0.978801932	-0.86501	0.387031729	0.45767468	darkgreen	-0.240205806	0.00189734		ATG2G17650.1	Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator RCC1 repeat protein
Sapur.0T0G5280.3	2.385318888	-0.43377575	0.511859187	-0.85224	0.42809271	0.49248354	darkgreen	-0.029059553	0.717888801		ATG2G17670.1	Protein of unknown function (DUF1278)	Egg cell-secreted protein, putative
Sapur.0G3G130800.1	0.300314653	-0.60706093	1.06812794	-0.56838	0.569743207	0.64516563	darkgreen	-0.107745761	0.179210073		ATG2G30555.3	PLACZA family protein	PLACZA family protein
Sapur.0G6G501500.5	0.174653454	-0.37388324	0.73537882	-0.51014	0.609234556	0.68110076	darkgreen	-0.130593954	0.150484979	GO:0003723	ATG2G69310.2 APO1	Arabidopsis thaliana protein of unknown function (DUF794)	APO RNA-binding protein
Sapur.0T0G6G700.1	0.252204348	-0.29593694	0.688077361	-0.47901	0.631933833	0.70417679	darkgreen	-0.089503337	0.264957259				NA
Sapur.0G6G684000.6	0.127947344	-0.18532627	0.752294515	-0.24663	0.805169819	0.86067274	darkgreen	-0.100684419	0.180557723	GO:0019239;GO:0032264;GO:0003876	ATG3G18280.1 ATAMPD,FAC1	AMP deaminase, putative / myoadenylate deaminase, putative	AMP deaminase
Sapur.0G3G180000.2	0.2599326	-0.08205957	0.624004056	-0.13151	0.895375588	0.92955162	darkgreen	-0.039426644	0.623911763		ATG3G17230.1	RNI-like superfamily protein	F-box/LRR protein
Sapur.0T0G6G900.2	0.181416277	-0.06629830	0.2	0.331218	0.918446855	0.94731751	darkgreen	-0.027212764	0.735127409	GO:0016020;GO:0008378;GO:0006486	ATG3G17710.1	Galactosyltransferase family protein	beta-1\3\2-galactosyltransferase, putative
Sapur.0G3G191000.2	0.00865734	-0.13774771	1.513276235	-0.091	0.927889108	0.95427185	darkgreen	-0.114010754	0.155091502		ATG3G21295.1	Tudor/PWWP/MBT superfamily protein, putative	tudor/PWWP/MBT superfamily protein, putative
Sapur.0G6G900.2	0.051104224	0.04968021	1.512988932	0.019884	0.984135599	0.99027495	darkgreen	-0.020609568	0.908888307	GO:0005085	ATG3G3590.1 ATOPT5,OPT5	oligopeptide transporter 5	NA
Sapur.0T0G6G800.1	0.044979945	0.24503975	1.689528879	0.144988	0.884720081	NA	darkgreen	0.077939907	0.131938345				hypothetical protein
Sapur.0G3G141000.2	0.064363835	0.16592503	2.037931614	-0.08312	0.933756269	NA	darkgreen	-0.189828804	0.017259521		ATG4G06330.1	Uncharacterized conserved protein (UCP030365)	hypothetical protein
Sapur.0G3G640000.1	0.044957224	0.09626788	2.031081822	0.047442	0.962832836	NA	darkgreen	-0.145203386	0.06399284	GO:0016020;GO:0008381;GO:0005215	ATG4G08470.1 ATNRAMP1,NRAMP1,PMT7	natural resistance-associated macrophage protein 1	nramp metal transporter
Sapur.T168800.1	0.013293476	0.12680929	2.904823183	0.046355	0.965179652	NA	darkgreen	0.01454169	0.856555663				NA
Sapur.1H5G6G28800.4	0.013869549	0.09118603	2.904823183	0.031302	0.97495456	NA	darkgreen	-0.008455564	0.916294947	GO:0004648;GO:0005634;GO:0004672	ATG5G00000.1	Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.0T0G6G740.1	0.037669087	-0.05877365	1.302716134	-0.02552	0.979637355	NA	darkgreen	-0.132702286	0.097559233		ATG5G17370.1		NA
Sapur.0T0G6G800.1	0.027564234	0.05188425	2.709186407	0.019117	0.984716147	NA	darkgreen	-0.067341654	0.556846653	GO:0005886;GO:0031072	ATG1,U2	DNAJ homologue 2	DnaJ central domain protein
Sapur.0G3G630400.2	0.006764801	0.05557053	2.904834396	0.01913	0.984737169	NA	darkgreen	-0.081608864	0.309509942	GO:0004064;GO:0016762;GO:0006073;GO:0005618;GO:0005975;GO:0004553	ATG1G12730.1 ATH10,XTR4	xyloglucan endotransglucosylase/hydrolase 30	xyloglucan endotransglucosylase/hydrolase
Sapur.0G6G7100.4	0.006764801	0.05557053	2.904834396	0.01913	0.984737169	NA	darkgreen	-0.081608864	0.309509942		ATG1G15100.1	DNAse I-like superfamily protein	beta-1\3\2-galactosyltransferase, putative
Sapur.0G6G630500.2	0.006764801	0.05557053	2.904834396	0.01913	0.984737169	NA	darkgreen	-0.081608864	0.309509942		ATG1G43490.1	Ribosomal protein L1p/L10e family	50S ribosomal protein L1
Sapur.0T0G6G400.2	0.006764801	0.05557053	2.904834396	0.01913	0.984737169	NA	darkgreen	-0.081608864	0.309509942		ATG1G86481.1 CID1	Chlorophyl-I-like domain 1	heat shock protein-binding protein
Sapur.0T0G6G400.6	0.006764801	0.05557053	2.904834396	0.01913	0.984737169	NA	darkgreen	-0.081608864	0.309509942		ATG1G51520.1	RING/U-box superfamily protein	RING-finger protein
Sapur.0G6G298100.1	0.006764801	0.05557053	2.904834396	0.01913	0.984737169	NA	darkgreen	-0.081608864	0.309509942	GO:0008270;GO:0003676;GO:0006355;GO:0003677	ATG1G7870.1 ATCSP1/CSP3	cold shock domain protein 3	NA
Sapur.0T0G6G750.1	0.006764801	0.05557053	2.904834396	0.01913	0.984737169	NA	darkgreen	-0.081608864	0.309509942		ATG1G8150.1 ZW18	Putative serine esterase family protein	serine esterase family protein, putative
Sapur.0T0G6H300.1	0.030468061	-0.02136925	2.668491224	-0.00796	0.993646414	NA	darkgreen	-0.009078861	0.211779282		ATG2G3370.1		NA
Sapur.0G6G480200.1	0.028837619	-0.02116449	2.667645434	-0.00788	0.993719334	NA	darkgreen	-0.109604576	0.175426361	GO:0055114;GO:0008630	ATG2G5160.1	Glyceraldehyde-3-phosphate dehydrogenase-like family protein	hydroxyisomer dehydrogenase
Sapur.0G6G527000.5	0.029547811	-0.02122675	2.904832276	-0.00731	0.994149578	NA	darkgreen	-0.082119992	0.306607623		ATG2G3270.4	Small nuclear RNA activating complex (SNAPC), subunit SNAP43 protein	small nuclear RNA activating complex (SNAPC), subunit SNAP43
Sapur.0G6G417000.1	0.020440234	-0.03329124	2.904834395	-0.00667	0.994678445	NA	darkgreen	-0.112237652	0.16932315	GO:0003723	ATG2G8610.1	RNA-binding KH domain-containing protein	KH domain protein
Sapur.0T0G6G500.2	0.018644087	-0.01927434	2.904834395	-0.00667	0.994678445	NA	darkgreen	-0.10513336	0.188362456		ATG2G8370.1	IQ calmodulin-binding motif family protein	calmodulin-binding family protein, putative
Sapur.T136000.1	0.015318269	-0.01972034	2.904834395	-0.00667	0.994678445	NA	darkgreen	-0.113762008	0.085450474		ATG3G2710.1	F-box/ galactinol/sucrose/raffinose hydrolases superfamily protein	NA
Sapur.0G2G81000.1	0.01210157	0.01808053	2.904834395	0.00623	0.995028949	NA	darkgreen	-0.115140166	0.151015538		ATG4G7010.1		hypothetical protein
Sapur.0G3G133300.1	0.019874799	0.01431942	2.315104654	0.006185	0.995609944	NA	darkgreen	-0.058683568	0.481341874				NA
Sapur.0G3G250600.3	0.015562258	0.01432787	2.3409852	0.006121	0.995616164	NA	darkgreen	-0.066850867	0.455478707	GO:0005515	ATG4G11740.1 SAY1	Ubiquitin-like superfamily protein	Ave4-interacting protein, putative
Sapur.0T0G6L800.1	0.067316612	-0.00873884	2.025720958	-0.00431	0.996539954	NA	darkgreen	-0.054662812	0.4953308				NA
Sapur.0T0G6M200.1	0.025165848	0.40820431	0.508838663	0.802325	4.54E-18	1.29E-17	darkgreen	2.27618669	0.00042038				NA
Sapur.0T0G6P300.1	10.08709764	2.60299655	0.390778587	7.42875	1.10E-13	2.71E-13	darkgreen	0.252826541	0.051399968		ATG4G5760.1 ATGDU2,GDU2	glutamine dumper 2	transmembrane protein, putative
Sapur.0G6G738000.1	0.717439047	2.42194182	0.665301817	3.557766	1.95E-07	3.76E-07	darkgreen	0.202661833	0.020911676	GO:0004648;GO:0005634;GO:0004672	ATG4G6840.1	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.0G6G125400.1	2.236562387	0.91774368	0.230364939	3.834077	0.000126037	0.000210638	darkgreen	-0.19492112	0.034601302	GO:0009731	ATG4G8840.1	SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.0G6G810300.2	1.553465263	0.83238537	0.238668208	3.71344	0.000209463	0.000337009	darkgreen	0.014168873	0.860195266	GO:0016829;GO:0005634;GO:0005524;GO:0003824;GO:0003677;GO:0008737	ATG4G9960.1 SPO11-2	operation 11-2	meiotic recombination protein SPO11, putative
Sapur.0G6G600500.1	0.412899717	2.09432825	0.736105031	2.845141	0.004439172	0.006685657	darkgreen	2.288911714	0.000242838	GO:0046983;GO:0003677	ATG2G46840.1 AGLG1,DLA	AGAMOUS-like 61	NA
Sapur.0G6G231800.1	378.3014439	-0.41640987	0.167148933	-2.49138	0.012736906	0.018280312	darkgreen	-0.151179526	0.058756013		ATG1G3130.1		hypothetical protein
Sapur.0T0G6J500.1	0.420264672	0.07165188	0.464164217	0.154439	0.877048224	0.91629168	darkgreen	-0.163920165	0.041667514	GO:0016740	ATG4G8930.1	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase
Sapur.0G6G154500.2	0.212591309	1.01459986	0.574318952	1.767036	0.077222256	0.10202728	darkgreen	0.145547934	0.079137837	GO:0046872;GO:0000166	ATG4G6640.1 AHAB,HAB	H(+)-ATPase B	plasma membrane H+ ATPase
Sapur.0G5G140000.1	0.528488955	0.79395546	0.394862348	1.737318	0.082217547	0.10360868	darkgreen	-0.123620008	0.882963133	GO:0008652;GO:0046746;GO:0003951	ATG2G6410.1 ATNAD2,NAD2	NAD kinase	NAD kinase
Sapur.1H5G0G14000.1	0.367635138	0.85763876	0.528846935	1.621856	0.104825637	0.136066269	darkgreen	0.138794683	0.082990242		ATG5G4530.1	Calcium-binding EF-hand family protein	NA
Sapur.0G6G115000.1	0.398283528	0.52747231	0.91783834	1.02	0.310976526	0.37503267	darkgreen	0.078458236	0.318214887	GO:0016787	ATG4G8230.2	Peptidase M20/M25/M40 family protein	N-acyl-L-amino-acid amidohydrolase
Sapur.0T0G6J700.1	0.732854698	0.49662613	0.423994101	1.169975	0.242019922	0.29756758	darkgreen	0.069919668	0.184233804		ATG4G5680.1	Arabidopsis protein of unknown function (DUF241)	DUF241 domain protein
Sapur.0T0G6J800.1	0.056719737	0.04133789	0.235446486	0.866059	0.386475209	0.45696281	darkgreen	0.064506329	0.482302124	GO:0055515;GO:0006468;GO:0004672	ATG4G7530.1	Leucine-rich repeat family protein	NA
Sapur.0T0G6J900.1	37.79343954	0.06337896	0.125372726	0.425126	0.673371149	0.74366554	darkgreen	0.026201187	0.938595927	GO:0016788	ATG4G7690.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.0T0G6P500.1	0.127573333	0.04000000	0.734268514	0.054485	0.956734989	0.97638679	darkgreen	0.038610104	0.635888396		ATG4G9320.1	O-Fucosyltransferase family protein	growth regulator, putative
Sapur.0G6G481800.4	0.14703573	0.10962462	0.784308145	0.140303	0.888849495	0.92555138	darkgreen	0.04889614	0.54208	GO:0008270;GO:0005515	ATG4G6790.1	RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.0G6G250900.1	4.58279221	0.02435275	0.287377374	0.105527	0.915858039	0.94152463	darkgreen	0.011377878	0.887530471	GO:0008152;GO:0005524	ATG6G6120.1	AMP-dependent synthetase and ligase family protein	acyl-CoA synthetase
Sapur.0G6G180800.1	0.107950241	0.06174892	1.13875721	-0.01546	0.987462293	0.99261496	darkgreen	-0.004872025	0.951763078	GO:0016887;GO:0005524	ATG6G6790.1 ATGCN1,GCN1	AAC transporter family protein	AAC transporter family protein
Sapur.0G4G138600.1	0.059498839	-0.02524777	1.631078718	-0.01527	0.987815421	0.9920597	darkgreen	-0.062230956	0.438770301		ATG6G8240.1		NA
Sapur.0T0G6J600.1	56.73424828	0.00600284	0.117904873	0.050911	0.959425968	0.97371568	darkgreen	-0.005766008	0.872772507		ATG2G2140.1		Ar5972-P rapidly elicited protein, putative
Sapur.0G6G118800.1	0.026650002	0.27107688	2.388068881	0.113512	0.909624529	NA	darkgreen	0.155095826	0.052493374	GO:0007264;GO:0005525	ATG1G6230.1 ARIA1F,ATARIA1F	ADP-ribosylation factor A1F	ADP-ribosylation factor
Sapur.0T0G6K100.1	0.010188443	0.23552643	2.904832057	0.018979	0.919379974	NA	darkgreen	0.078436136	0.32814487		ATG1G1390.1	Protein kinase family protein	Ax6F domain kinase
Sapur.0G2G317000.2	0.018896542	0.09900829	2.904831116	0.068857	0.945135354	NA	darkgreen	0.095895857	0.212194379	GO:0016020;GO:0008381;GO:0005215	ATG4G6550.1 ATPTR3,PTR3	peptide transporter 3	peptide transporter PTR3-A
Sapur.0G3G080000.2	0.015000919	0.16428147	2.904831116	0.035653	0.954899498	NA	darkgreen	0.111441607	0.36407555		ATG1G7160.1	RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.0G4G298900.1	0.029161809	0.12493885	2.681261075	0.046561	0.962863245	NA	darkgreen	0.029315179	0.715513633				NA
Sapur.0G2G280400.1	0.007596602	0.12861759	2.904832276	0.064292	0.964671295	NA	darkgreen	0.078458531	0.32814487	GO:0004672;GO:0006468	ATG2G2750.1	Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.0G3G870005.1	0.007596602	0.12861759	2.904832276	0.064292	0.964671295	NA	darkgreen	0.078458531	0.32814487	GO:0004648;GO:0004672	ATG4G3050.1	PAS domain-containing protein tyrosine kinase family protein	tyrosine kinase domain protein
Sapur.0G5G182800.2	0.007596602	0.12861759	2.904832276	0.064292	0.964671295	NA	darkgreen	0.078458531	0.32814487	GO:0005515	ATG5G8540.2	transducin family protein / WD-40 repeat family protein	transducin/WD40 domain protein
Sapur.0T0G6N200.1	0.007596602	0.12861759	2.904832276	0.064292	0.964671295	NA	darkgreen	0.078458531	0.32814487				NA
Sapur.0G6G1B7000.1	0.007596602	0.12861759	2.904832276	0.064292	0.964671295	NA	darkgreen	0.078458

Sapur.T158100.1	14.1916397	1.18748503	0.18298423	10.03805	1.04E-23	3.37E-23	darkturquoise	0.593296543	2.66E-16					NA
Sapur.T148100.1	8.646962613	1.164656473	0.16863455	9.964248	2.19E-23	7.06E-23	darkturquoise	0.619185395	5.46E-18					NA
Sapur.T111500.1	18.9072212	1.03779351	0.15253803	9.859148	6.26E-23	1.98E-22	darkturquoise	0.568834791	6.65E-16	GO:0005524;GO:0003676	ATSG08110.1		nucleic acid binding;ATP-dependent helicases;ATP-binding;helicases;ATP-dependent helicases	NA
Sapur.T165600.1	188.242798	1.051536673	0.10674752	9.850853	6.80E-23	2.17E-22	darkturquoise	0.572342045	4.91E-15		ATSG08110.1		nucleic acid binding;ATP-dependent helicases;ATP-binding;helicases;ATP-dependent helicases	NA
Sapur.T157500.1	10.09168683	1.1213439	0.11388587	9.84624	7.12E-23	2.27E-22	darkturquoise	0.572343882	4.59E-15					NA
Sapur.T111400.1	12.3207825	1.072975801	0.10913149	9.700255	3.01E-22	9.46E-22	darkturquoise	0.607238657	3.42E-17					NA
Sapur.T165800.1	79.6844279	1.102320684	0.11453725	9.626185	6.20E-22	1.93E-21	darkturquoise	0.562354199	1.80E-14					NA
Sapur.T136600.1	27.44423816	0.999531131	0.10493935	9.525061	1.65E-21	5.08E-21	darkturquoise	0.562329171	1.84E-14	GO:0005524;GO:0003676	ATSG08110.1		nucleic acid binding;ATP-dependent helicases;ATP-binding;helicases;ATP-dependent helicases	NA
Sapur.T173200.1	6.20257826	1.080154485	0.10608353	9.070435	1.19E-19	3.48E-19	darkturquoise	0.588404691	5.16E-16					NA
Sapur.T165900.1	31.95576283	1.034139606	0.11542228	8.961383	2.44E-19	7.11E-19	darkturquoise	0.542836701	2.04E-13					NA
Sapur.T173300.1	16.12803625	1.054918806	0.11597181	8.751382	2.11E-18	5.99E-18	darkturquoise	0.543101033	2.00E-13					NA
Sapur.T136800.1	10.54027728	0.9207276	0.11128338	8.632984	5.98E-18	1.68E-17	darkturquoise	0.57272111	8.68E-15					NA
Sapur.T136200.1	56.31812	0.961578271	0.11522839	8.345082	7.12E-17	1.93E-16	darkturquoise	0.522202587	2.31E-12					NA
Sapur.T165100.1	65.46388303	0.95129184	0.11288499	8.152139	3.58E-16	9.51E-16	darkturquoise	0.500324240	2.55E-11		ATSG10820.2		Transcription elongation factor (TFIIS) family protein	NA
Sapur.T148300.1	13.46869199	0.961204312	0.10631969	7.159585	8.09E-13	1.94E-12	darkturquoise	0.475569835	3.09E-10	GO:0005524;GO:0003676	ATSG08110.1		nucleic acid binding;ATP-dependent helicases;ATP-binding;helicases;ATP-dependent helicases	NA
Sapur.T136700.1	4.867968933	0.863364563	0.12588554	6.731846	1.68E-11	3.83E-11	darkturquoise	0.465555493	1.56E-10					NA
Sapur.T148200.1	4.76163006	0.843023037	0.12603761	6.693452	2.18E-11	4.96E-11	darkturquoise	0.487245853	9.72E-11					NA
Sapur.T173000.1	24.08869963	0.679731927	0.11400596	6.101597	1.05E-09	2.36E-09	darkturquoise	0.412082622	7.59E-08		ATSG10820.2		Transcription elongation factor (TFIIS) family protein	NA
Sapur.T152514.1	16.83890494	0.667097986	0.11651214	5.68077	1.21E-08	2.46E-08	darkturquoise	0.412491962	2.01E-08					NA
Sapur.T157900.1	24.88663261	0.618271605	0.11229157	5.505773	3.68E-08	7.35E-08	darkturquoise	0.36830975	2.08E-06		ATSG10820.2		Transcription elongation factor (TFIIS) family protein	NA
Sapur.T162000.1	20.7145266	0.596205167	0.11029136	5.362816	8.16E-08	1.62E-07	darkturquoise	0.374051517	1.32E-06		ATSG10820.2		Transcription elongation factor (TFIIS) family protein	NA
Sapur.T110600.1	1.757787238	1.039659119	0.19648005	5.291425	1.21E-07	2.38E-07	darkturquoise	0.412773255	7.78E-08		ATSG10820.2		Transcription elongation factor (TFIIS) family protein	NA
Sapur.T112500.1	11.63849322	0.521177407	0.09951926	5.257049	1.46E-07	2.86E-07	darkturquoise	0.414270549	6.90E-08					NA
Sapur.T173100.1	17.22833947	0.538131757	0.10470637	4.871265	1.11E-06	2.07E-06	darkturquoise	0.357176939	4.35E-06	GO:0005524;GO:0003676	ATSG08110.1		nucleic acid binding;ATP-dependent helicases;ATP-binding;helicases;ATP-dependent helicases	NA
Sapur.T152681.1	26.76008849	0.513167317	0.10543582	4.866129	1.14E-06	2.12E-06	darkturquoise	0.350021884	6.00E-06	GO:0005524;GO:0003676	ATSG08110.1		nucleic acid binding;ATP-dependent helicases;ATP-binding;helicases;ATP-dependent helicases	NA
Sapur.T152047500.1	33.60050407	0.216414818	0.08495361	2.50204	0.01234801	0.017774214	darkturquoise	0.201726784	0.011291935		ATSG08110.1		nucleic acid binding;ATP-dependent helicases;ATP-binding;helicases;ATP-dependent helicases	NA
Sapur.T136900.1	0 NA	NA	NA	NA	NA	NA	darkturquoise	0.695132344	5.52E-24					NA
Sapur.B036101.T05	262.3571311	3.454037064	0.18471927	18.70064	4.89E-78	4.14E-77	greenyellow	0.493818072	5.07E-11		AT4G17030.1	AT-EXPR,ATEXB21,ATEXPR1	expansin-like B1	NA
Sapur.B170208500.1	23.19982874	3.376642793	0.18634574	18.12034	2.20E-73	1.74E-72	greenyellow	0.435604586	1.09E-08	GO:0055114;GO:0020037;GO:0004879;GO:0004601	AT5G13930.1	RC1,RC1A	Peroxidase superfamily protein	NA
Sapur.B142806300.1	199.5478897	2.322000213	0.12633845	18.69175	1.78E-73	3.92E-72	greenyellow	0.591832923	3.40E-16		AT4G01575.1		serine protease inhibitor, Kazal-type family protein	NA
Sapur.B076111400.1	6.701887776	1.467916416	0.24367599	17.02352	5.50E-65	3.86E-64	greenyellow	0.659519524	5.88E-21	GO:0020347;GO:0006468;GO:0005524;GO:0004672	ATSG38260.1		Protein kinase superfamily protein	NA
Sapur.B162354000.1	41.43254721	2.388892849	0.19034736	16.71131	2.68E-62	1.88E-61	greenyellow	0.670001132	1.38360231	GO:0005515	ATSG27150.1		Galactose mutarotase/aldose 1-epimerase family protein	NA
Sapur.B162399900.1	45.20898155	3.28013371	0.19818037	16.55062	1.58E-61	1.05E-60	greenyellow	0.424219911	3.08E-08	GO:0055114;GO:0005506;GO:0016491	AT4G20820.1		FAD-binding Berberine family protein	NA
Sapur.B142500200.1	106.3327045	2.396408479	0.14527926	16.51582	2.82E-61	1.86E-60	greenyellow	0.61682807	7.87E-18	GO:0016887;GO:0005524;GO:0016833;GO:0008810;GO:0005215	AT4G27780.1	AAC2	homolog 6	AAC transporter family, cholesterol/phospholipid flippase/K,ZC pative
Sapur.B152682900.1	34.24799844	4.356262058	0.26463098	16.46165	6.92E-61	4.53E-60	greenyellow	0.331620897	2.21E-05		AT5G61820.1			stress up-regulated Nod 19 protein
Sapur.B152649600.1	103.705642	2.182385802	0.14968038	15.76164	3.52E-56	2.26E-55	greenyellow	0.515762906	2.32E-14		AT4G37420.1	ATEXT2,EXT1,RSH	extensin 3	hypothetical protein
Sapur.B042147400.1	64.28580632	4.508015783	0.28617564	15.75268	6.58E-56	3.88E-55	greenyellow	0.439858345	2.92E-09	GO:0055114;GO:0020037;GO:0004879;GO:0004601	AT5G05340.1		Peroxidase superfamily protein	cationic peroxidase
Sapur.B162622900.1	35.84049717	2.103443358	0.13450205	15.64023	3.87E-55	2.31E-54	greenyellow	0.58920971	4.77E-16		AT5G46830.1	DTA2	downstream target of AGL15 2	glycosyl transferase family 90 protein
Sapur.B162398800.1	68.00231332	2.117631317	0.17435832	15.57518	1.07E-54	6.37E-54	greenyellow	0.444712095	1.37E-09	GO:0055114;GO:0005506;GO:0016491	AT4G20820.1		FAD-binding Berberine family protein	NA
Sapur.B150431300.1	13.88162601	2.056875517	0.13274386	15.49209	3.92E-54	2.31E-53	greenyellow	0.538937229	5.31E-16	GO:0008270;GO:0055115	AT5G42360.1		RING/U-box superfamily protein	RING/U-box superfamily protein
Sapur.B152012000.1	134.7911338	2.288485647	0.14867685	15.3926	1.84E-53	1.07E-52	greenyellow	0.51126218	3.16E-14	GO:0004866	AT5G7260.1	ATKTI1,ATI1	kunitz trypsin inhibitor 1	kunitz-type trypsin inhibitor C8
Sapur.B070205100.1	6.539843809	3.709148591	0.24282487	15.275	1.12E-52	6.45E-52	greenyellow	0.542203373	2.23E-13		AT5G26320.1	ATMES1,MES1	methyl esterase 1	polyneuridine-aldehyde esterase, putative
Sapur.B070204900.1	6.186772029	3.588925194	0.23209836	15.21161	2.86E-52	1.64E-51	greenyellow	0.534511173	3.81E-13		AT5G26320.1	ATMES1,MES1	methyl esterase 1	NA
Sapur.B150670500.1	5.586730865	5.084456538	0.33471824	15.19046	4.09E-52	2.33E-51	greenyellow	0.34878974	7.58E-06	GO:0005975;GO:0004553	AT4G44480.1	BGLU17	beta glucosidase 17	NA
Sapur.B162322000.1	23.63973833	4.056082102	0.26736183	15.0905	1.67E-51	1.05E-50	greenyellow	0.432152239	1.54E-08	GO:0016829;GO:0010333;GO:0016987;GO:0000287	AT3G26960.1		terpene synthase family protein	sesquiterpene synthase
Sapur.B070204600.1	7.997926276	3.850627792	0.25458847	15.07109	2.42E-51	1.36E-50	greenyellow	0.38837843	5.58E-07		AT5G26320.1	ATMES1,MES1	methyl esterase 1	NA
Sapur.B162621100.1	241.3128241	3.172814479	0.21047215	14.9384	3.83E-50	2.01E-49	greenyellow	0.534214799	5.78E-13	GO:0005975;GO:0004866	AT5G7260.1	ATKTI1,ATI1	kunitz trypsin inhibitor 1	NA
Sapur.B162300200.1	19.62784926	1.173943479	0.10779486	14.57217	4.22E-48	2.24E-47	greenyellow	0.385172452	6.32E-07	GO:0055114;GO:0005506;GO:0016491	AT4G20820.1		FAD-binding Berberine family protein	NA
Sapur.B162086200.1	122.892963	1.899786444	0.13101729	14.49989	1.21E-47	6.39E-47	greenyellow	0.522060504	2.35E-12		AT4G01575.1		serine protease inhibitor, Kazal-type family protein	NA
Sapur.B070200200.1	17.49924968	1.509231634	0.17507614	14.33268	1.37E-46	7.07E-46	greenyellow	0.505231676	1.50E-11	GO:0004866	AT5G7260.1	ATKTI1,ATI1	kunitz trypsin inhibitor 1	kunitz-type trypsin inhibitor C4
Sapur.B151117700.1	98.09548008	2.061654239	0.29405628	13.74244	5.65E-43	2.74E-42	greenyellow	0.382578328	7.62E-07	GO:0055114;GO:0005506;GO:0016491	AT5G44440.1		FAD-binding Berberine family protein	NA
Sapur.T107900.1	2.238713293	1.304000204	0.32747248	13.62147	2.98E-42	1.40E-41	greenyellow	0.522692929	2.20E-12		AT4G05950.1		RmlC-like cupins superfamily protein	NA
Sapur.B070100100.1	19.1654784	2.429565558	0.25201916	13.6081	3.58E-42	1.72E-41	greenyellow	0.342633909	1.12E-05	GO:0004866	AT5G7260.1	ATKTI1,ATI1	kunitz trypsin inhibitor 1	kunitz-type trypsin inhibitor C4
Sapur.B151177500.1	19.46002266	2.388892849	0.26760219	13.50858	4.08E-42	1.95E-41	greenyellow	0.447594174	4.86E-09	GO:0055114;GO:0005506;GO:0016491	AT5G44440.1		FAD-binding Berberine family protein	cellobiose dehydrogenase
Sapur.T107900.1	2.24606623	4.463952039	0.32912935	13.56291	6.64E-42	3.17E-41	greenyellow	0.519230324	2.24E-12		AT4G05950.1		RmlC-like cupins superfamily protein	NA
Sapur.B170208500.1	2.24606523	4.463952039	0.32912935	13.56291	6.64E-42	3.17E-41	greenyellow	0.519230324	2.24E-12		AT4G05950.1		RmlC-like cupins superfamily protein	NA
Sapur.B162303300.1	19.38921101	2.941736077	0.21898295	13.37783	8.15E-41	3.82E-40	greenyellow	0.391600423	1.95E-07	GO:0055114;GO:0005506;GO:0016491	AT5G44440.1		FAD-binding Berberine family protein	reticuline oxidase
Sapur.B170245800.1	6.627555874	3.319833088	0.24844072	13.36253	1.00E-40	4.68E-40	greenyellow	0.544692955	1.38E-14	GO:0055115	AT5G26420.1	ATGSTU7,GSTZ5,GSTU7	glutathione S-transferase tau 7	tau class glutathione transferase GSTU37
Sapur.B162600000.1	16.65890561	2.776477926	0.22235246	13.34687	1.24E-40	5.79E-40	greenyellow	0.392180997	7.84E-07	GO:0055114;GO:0005506;GO:0016491	AT5G44440.1		FAD-binding Berberine family protein	NA
Sapur.B162188200.1	720.1214148	2.175788556	0.16340832	13.31526	1.88E-40	8.77E-40	greenyellow	0.28762851	0.00325922		AT1G50030.2		Pathogenesis-related thaumatin superfamily protein	allergen Pru ds, putative
Sapur.B162686700.1	1.940351957	2.263000143	0.33070247	13.2008	2.47E-38	6.58E-38	greenyellow	0.535450337	1.46E-11	GO:0005975;GO:0004553	AT4G44480.1	BGLU17	beta glucosidase 17	NA
Sapur.B162079500.1	6.316308084	3.340428784	0.41488289	12.97833	1.62E-38	7.26E-38	greenyellow	0.433517646	1.41E-08	GO:0016567;GO:0008842	AT1G61930.1	PUB23	plant U-box 23	E3 ubiquitin-protein ligase PUB22, putative
Sapur.B162342100.1	5.908633374	3.597018814	0.28201749	12.7573	2.90E-37	1.27E-36	greenyellow	0.514429882	2.45E-08	GO:0016788	AT4G26960.1	GLIP1	GDSL lipase 1	GDSL esterase/lipase
Sapur.B070205300.1	9.072862334	3.345761167	0.26126168	12.61281	1.79E-36	7.70E-36	greenyellow	0.373171143	1.68E-06		AT3G26320.1	ATMES1,MES1	methyl esterase 1	NA
Sapur.B162301200.1	10.73122644	3.192248964	0.24611646	12.56443	3.31E-36	1.42E-35	greenyellow	0.362769417	5.51E-06					hypothetical protein
Sapur.B062157300.1	12.49030794	2.051062918	0.16452538	12.46885	1.10E-35	4.68E-35	greenyellow	0.568524275	2.28E-14	GO:0006468;GO:0005524;GO:0004672;GO:0030246	AT5G07460.1		Concanavalin A-like lectin protein kinase family protein	lectin domain receptor kinase
Sapur.B162342200.1	4.857018845	2.661908655	0.33426042	12.44811	1.61E-35	6.61E-35	greenyellow	0.471308764	4.66E-10	GO:0005975;GO:0004553	AT4G44480.1	BGLU17	beta glucosidase 17	NA
Sapur.B062015600.1	13.71314652	1.486163957	0.19884739	12.39868	2.68E-35	1.12E-34	greenyellow	0.562879175	1.68E-14	GO:0006468;GO:0004672	AT4G05200.1	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	NA
Sapur.B062150100.1	17.61293019	1.920061912	0.15730875	12.20594	2.88E-34	1.19E-33	greenyellow	0.454236423	2.30E-09	GO:0003700;GO:0000958	AT3G51510.1	ACS1,AT-ACS1	ACC synthase 1	1-aminocyclopropane-1-carboxylate synthase
Sapur.B162261100.1	8.463897523	1.921443872	0.17790832	12.05755	1.77E-33	7.38E-33	greenyellow	0.554271137	7.08E-14	GO:0055114;GO:0016491	AT5G05020.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	aminocyclopropanecarboxylate oxidase, putative
Sapur.B062189600.1	4.420519819	2.895077208	0.24215817	11.95935	5.80E-33	2.33E-32	greenyellow	0.544553947	1.68E-13		AT3G02645.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.B062139300.1	13.41768822	2.857102206	0.23892617	11.9582	5.88E-33	2.35E-32	greenyellow	0.411163127	8.70E-08	GO:0016887;GO:0005524;GO:0016020	AT5G15120.1	ABCG40,ATABCG40,ATPDR1	pleiotropic drug resistance, ABC transporter family protein, putative	pleiotropic drug resistance, ABC transporter family protein, putative
Sapur.B162842000.1	14.42768815	4.033571273	0.34047424	11.84692	2.23E-32	8.86E-32	greenyellow	0.243192292	0.00147396	GO:0005975;GO:0004553	AT5G42260.1	BGLU12	beta glucosidase 12	NA
Sapur.B162347500.1	4.385544838	4.42161622	0.37184643	11.82907	2.93E-32	1.16E-31	greenyellow	0.318260651	0.00425	GO:0055114;GO:0005506;GO:0016491	AT5G05690.1	CYP705A30	cytochrome P450 family 705, subfamily A, polypeptide 30	cytochrome P450 family protein
Sapur.B162151500.1	41.60075389	1.869175821	0.15898801	11.75667	6.53E-32	2.56E-31	greenyellow	0.408834379	1.08E-07	GO:0055114;GO:0016491;GO:0008270	AT4G37980.1	ATCAD7,CAD7,ELI1,ELI3-1	elicitor-activated gene 3-1	cinnamyl alcohol dehydrogenase
Sapur.B162277100.1	297.3844692	1.550973884	0.13316684	11.71416	1.08E-31	4.21E-31	greenyellow	0.486681174	4.21E-10	GO:0005975;GO:0004553	AT4G45680.1		Glycosyl hydrolase family protein	potato inhibitor I family protein
Sapur.B162276600.1	18.22115076	2.028169164	0.17060457	11.6893	1.45E-31	5.62E-31	greenyellow	0.442428373	6.57E-09	GO:0016758;GO:0008152	AT2G28110.1	GT72B,UGT72B1	UDP-Glycosyltransferase superfamily protein	UDP-Glycosyltransferase
Sapur.B156018900.1	323.0808604	1.331823425	0.11432075	11.64988	2.30E-31	8.91E-31	greenyellow	0.497282815	3.47E-11	GO:0005975;GO:0004553	AT5G42690.1	ATCHIA,CHIA	chitinase A	acidic class III chitinase
Sapur.B162311005.1	33.29608904	1.614719153	0.13547632	11.56662	6.08E-31	2.34E-30	greenyellow	0.292695792	0.00318302		AT5G49130.1		RmlC-like cupins superfamily protein	rhizaffinin receptor, putative
Sapur.B036101500.1	75.16368814	1.569382264	0.13595628	11.54481	7.84E-31	3.01E-30	greenyellow	0.5863809	1.33E-11		AT5G51911.1		cryptdin protein-related	hypothetical protein
Sapur.B162580400.1	2.188894932	1.827087076	0.33780649	11.32928	9.48E-30	3.51E-29	greenyellow	0.462230161	1.92E-09		AT4G05950.1		RmlC-like cupins superfamily protein	rhizaffinin receptor, putative
Sapur.B070209900.1	10.58254886	2.392535966	0.38261879	11.11302	1.08E-28	3.97E-28	greenyellow	0.325202874	1.28E-05	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT5G36300.1	CYP71B34	cytochrome P450, family 71, subfamily B, polypeptide 34	cytochrome P450 family protein
Sapur.B162070200.1	88.90054441	1.668328984	0.15053445	11.07892	1.56E-28	5.76E-28	greenyellow	0.508575371	1.01E-11	GO:0005524;GO:0016887;GO:0016020	AT4G05480.1		Serine protease inhibitor, potato inhibitor I-type family protein	potato inhibitor I family protein
Sapur.B151151700.1	48.8857649	2.147775809	0.19115788	11.00567	3.59E-28	1.30E-27	greenyellow	0.374291142	1.37E-06	GO:0055114;GO:0005506;GO:0016491	AT4G20860.1		FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.B162058200.1	1.986605254	2.902318897	0.33790561	10.94882	4.73E-28	2.42E-27	greenyellow	0.448884822	3.72E-09		AT5G05690.1		RmlC-like cupins superfamily protein	NA
Sapur.B156060700.1	4.802877166	2.529076225	0.23144363	10.92739	8.53E-28	3.06E-27	greenyellow	0.476730977	2.76E-10		AT5G18810.1		phytochrome kinase substrate-related	phytochrome kinase substrate protein, putative
Sapur.B162581000.1	3.302940791	3.506409209	0.33122629	10.71645	8.52E-27	2.98E-26	greenyellow	0.456681466	3.16E-09		AT5G45580.1		Serine protease inhibitor, potato inhibitor I-type family protein	NA
Sapur.B151157000.1	8.786048877	2.940861561	0.2862505	10.27366	9.26E-25	3.10E-24	greenyellow	0.389290295	4.08E-07	GO:0055114;GO:0020037;GO:0004867	AT5G45580.1		Serine protease inhibitor, potato inhibitor I-type family protein	cysteine proteinase inhibitor 2, putative
Sapur.B096112200.1	6.091659984	2.306127645	0.20650549	10.19889	2.01E-24	6.65E-24	greenyellow	0.45782182	1.64E-09		AT4G37630.1		Transmembrane amino acid transporter family protein	lysine/histidine transporter
Sapur.B050217200.1	25.67748804	1.654735513	0.32476832	9.965995	2.21E-23	8.45E-23	greenyellow	0.212997625	0.02738861					NA
Sapur.B162404000.1	9.168556671	4.292125182	0.42275516	9.918817	3.45E-23	1.11E-22	greenyellow	0.29019132	0.00327164	GO:0005975;GO:0004553	AT5G44480.1	BGLU17	beta glucosidase 17	NA
Sapur.B162640000.1	46.21054513	2.380667491	0.23663025	9.743383	1.67E-22	5.26E-22	greenyellow	0.318176245	9.8E-05	GO:0009507;GO:0009532	AT2G42620.1	MLP423	MLP-like protein 423	Bet v 1 allergen protein
Sapur.B162432300.1	7.970562528	1.831042288	0.18776248*	9.751868	1.81E-22	5.72E-22	greenyellow	0.519883339	2.97E-12	GO:0016020;GO:0009570	AT2G29120.1	ATGLR2,7,GLR2.7	glutamate receptor 2.7	glutamate-gated kainate-type ion channel receptor subunit GluR5
Sapur.B162600400.1	18.20225553	1.910907932	0.20884183	9.740519	2.08E-22	6.56E-22	greenyellow	0.294663794	0.00132665	GO:0055114;GO:0005506;GO:0016491	AT5G07020.1		FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.B162237000.1	5.43684782	2.027334777	0.20859184	9.706939	2.82E-22	8.85E-22	greenyellow	0.417875692	5.17E-08	GO:0006629	AT5G26580.1	PLA IIA,PLA2A,PLP2	phospholipase 2A	patatin-like phospholipase
Sapur.B162037200.1	15.22774425	1.591346218	0.16568852	9.610237	7.24E-22	2.25E-21	greenyellow	0.427205489	6.90E-10	GO:0006661;GO:0004867	AT2G38870.1		Serine protease inhibitor, potato inhibitor I-type family protein	protease inhibitor 1, putative
Sapur.B162037900.1	2.403472621	3.27366274	0.34050265	9.601001	7.92E-22	2.46E-21	greenyellow	0.38469218	5.78E-07					hypothetical protein
Sapur.B062806300.1	6.769523884	2.384568486	0.23968319	9.536905	1.67E-21	5.15E-21	greenyellow	0.244873662	0.00384646		AT5G07460.1		Concanavalin A-like lectin protein kinase family protein	NA
Sapur.B171261500.1	3.30669764	1.049897812	0.43483686	9.313832	1.23E-20	3.71E-20	greenyellow	0.382721192	5.74E-07		AT4G37150.1			NA
Sapur.B162070800.1	7.672851002	1.364642277	0.14734713	9.261415	2.02E-20	6.06E-20	greenyellow	0.48364372	1.40E-10	GO:0016567;GO:0006462	AT5G27490.1	ARM repeat superfamily protein	ArgN/CT-9 rapidly elicited protein	ArgN/CT-9 rapidly elicited protein
Sapur.B151051200.1	6.087995632	1.819696315	0.41624687	9.17702	4.43E-20	1.31E-19	greenyellow	0.32603727	3.06E-05	GO:0005507;GO:0009532	AT5G42620.1	MLP423	MLP-like protein 423	Bet v 1 allergen protein
Sapur.B050208500.1	14.03148651	1.393621509	0.15253046	9.136676	6.44E-20	1.90E-19	greenyellow	0.501609976	1.31E-11	GO:0005515	AT4G26110.1	ARIP11,RLP11	receptor like protein 11	Serine/Threonine-kinase, plant-type protein,N,ZC pative
Sapur.B156079500.1	5.252583019	1.270610315	0.22880293	9.11395	8.06E-20	2.37E-19	greenyellow	0.483467655	5.41E-10	GO:0005524;GO:0004674;GO:0006468	AT5G67340.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like Ser/Thr/Tyrosine-kinase, putative
Sapur.B152697200.1	10.85835565	2.811233811	0.31022994*	9.064676	1.25E-19	3.66E-19	greenyellow	0.226786613	0.00428701	GO:0005487;GO:0005488;GO:0003959;GO:0005618	AT4G45220.1		Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.B162640100.1	4.428166384	4.067370701	0.44941454	9.06953	1.43E-19	4.16E-19	greenyellow	0.254728793	0.01284072	GO:0005975;GO:0004553	AT4G44480.1	BGLU12	beta glucosidase 12	NA
Sapur.B036101400.1	6.668212047	2.141661212	0.23723161	9.025781	1.78E-19	5.21E-19	greenyellow	0.368507118	2.05E-06		AT5G51915.1		cryptdin protein-related	NA
Sapur.B162173300.1	7.724641081	3.443063011	0.45276925	9.015884	1.94E-19	5.65E-19	greenyellow	0.209866642	0.03834949					NA
Sapur.B051177900.1	23.68513202	2.001465414	0.22133453	9.010106	2.06E-19	6.01E-19	greenyellow	0.464112924	9.23E-10	GO:0005885;GO:0016021	AT3G18940.1	ATPT2,PHT1;4	phosphate transporter 1;4	inorganic phosphate transporter, putative
Sapur.B162432800.1	7.56231062	1.790750002	0.19988788	8.95909	3.27E-19	9.50E-19	greenyellow	0.4848175	1.24E-10	GO:0016020;GO:0009570	AT2G29120.1	ATGLR2,7,GLR2.7	glutamate receptor 2.7	glutamate receptor 2.7
Sapur.B151081100.1	2.390245927	2.764727211	0.31246738	8.912662	4.97E-19	1.45E-18	greenyellow	0.466317668	7.47E-10	GO:0016020;GO:0008320;GO:0005215	AT3G02040.1	ATPTR2,ATPTR2-B,NTR1.PT	peptide transporter 2	peptide transporter
Sapur.T007700.1	2.110068881	3.759725066	0.42123268	8.906634	5.26E-19	1.52E-18	greenyellow	0.38183786	8.04E-07		AT5G39160.1		RmlC-like cupins superfamily protein	NA
Sapur.B062169800.1	6.620824671	2.118887561	0.23897319	8.874665	7.02E-19	2.01E-18	greenyellow	0.324882645	2.22E-06		AT5G07020.1		Glycosyl hydrolase family protein 2	glycosyltransferase family 2 protein
Sapur.B162600600.1	8.806567235	1.063869643	0.13470449	8.834052	1.01E-18	2.89E-18	greenyellow	0.477167669	2.64E-10	GO:0005975;GO:0004553	AT5G60130.1	BGLU16	beta glucosidase 16	NA
Sapur.B162600100.1	10.79528697	1.163645331	0.18527786	8.724176	1.17E-18	3.35E-18	greenyellow	0.416764256	2.29E-08	GO:0016567;GO:0006462	AT5G61390.1	ATPBR1,PPR1	pinoresinol-lariciresinol reductase 1	phenylcoumaran benzylic ether reductase-like protein
Sapur.B150207500.1	246.1849971	1.073572568	0.12202874	8.767686	1.40E-18	3.99E-18	greenyellow	0.442157351	6.50E-09	GO:0005975;GO:0004553	AT4G38870.1		Serine protease inhibitor, potato inhibitor I-type family protein	inhibitor of trypsin and hagemann factor
Sapur.B162600500.1	4.452060794	2.854182894	0.29712448	8.753294	1.85E-18	5.29E-18	greenyellow	0.228573276	0.00261165		AT5G07460.1			NA
Sapur.B162660500.1	8.860812047	3.028378726	0.34143219	8.775281	1.70E-18	4.85E-18	greenyellow	0.277385664	4.21E-10	GO:0005975;GO:0004553	AT3G60130.1	BGLU16	beta glucosidase 16	NA
Sapur.B162070600.1	2.362211005	2.670327864	0.30440025	8.77008	1.75E-18	4.99E-18	greenyellow	0.368630347	2.02E-06		AT5G23270.1			NA
Sapur.B151100000.1	15.38279855	1.360126359	0.15569107	8.755945	2.42E-18	6.85E-18	greenyellow	0.49351349	1.02E-07	GO:0006629	AT2G26560.1	PLA IIA,PLA2A,PLP2	phospholipase 2A	patatin-like phospholipase
Sapur.B151101000.1	11.40706428	1.493721968	0.17224023	8.673168	4.24E-18	1.20E-17	greenyellow	0.443041348	7.42E-09

Sapur.01G2693400.1	5.219140088	6.930460946	6.26207886	3.503309	0.000384779	0.000022612	greenyellow	0.27016985	0.000621154	GO:0005515;GO:0006468;GO:0005524;GO:0004672	AT4G08510.1	Leucine-rich repeat receptor-like protein kinase family protein	receptor kinase, putative
Sapur.01G0413700.1	1.708134607	0.984264948	0.277258866	1.549985	0.000381552	0.000023317	greenyellow	0.226828236	0.006252954	GO:0008152;GO:0003824	AT1G65520.1	ATECH1,ECHC,ECI1,PEC11	delta(3), delta(2)-enoyl-CoA isomerase 1
Sapur.01G1311800.1	23.45016013	0.398984631	0.115232266	3.545455	0.000393198	0.000023727	greenyellow	0.225457354	0.006428072		AT2G47354.1	late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.01G1104900.1	0.47028677	1.982891008	0.57839423	3.428269	0.000607441	0.000970231	greenyellow	0.269464564	0.000643107	GO:0016787	AtNUDT7,ATNUDX7,GFG1.9	Mut7/nudix family protein	nudix hydrolase
Sapur.01G0267400.1	2.110516363	0.756241256	0.221053889	3.421451	0.000622878	0.000994928	greenyellow	0.206437907	0.009488851				hypothetical protein
Sapur.01G2105500.1	22.11975483	0.318358896	0.093735384	3.396368	0.000682864	0.00108676	greenyellow	0.243620952	0.02107639	GO:0005515	AT5G68550.1	MAPKKK5	mitogen-activated protein kinase kinase kinase 5
Sapur.01W2019000.1	60.83978584	0.47523188	0.141305879	3.363143	0.000776604	0.001221693	greenyellow	0.198936584	0.012606659	GO:0005975;GO:0004553	AT1H04,CHIA	chitinase A	acidic endochitinase
Sapur.01W2024800.1	0.837450251	0.782667781	0.233946556	3.118612	0.00309531	0.001427926	greenyellow	0.161821823	0.041910742			Hotsecret dehalogenase-like hydrolase (HAD) superfamily protein	hotsecret dehalogenase-like hydrolase
Sapur.01T0117700.1	0.332120168	1.64375988	0.495627613	3.31652	0.000911459	0.001437148	greenyellow	0.29435646	0.000182522				NA
Sapur.01W2167200.1	63.38474554	0.447866864	0.135066008	3.26363	0.001312777	0.001727806	greenyellow	0.195458821	0.014512339	GO:0055114;GO:0020037;GO:0006979;GO:0004601	AT5G05340.1	Peroxidase superfamily protein	peroxin 11 peroxidase
Sapur.01G1195900.1	2.062292277	0.035621934	0.324898892	3.18663	0.001439407	0.002208642	greenyellow	0.143185324	0.027940289	GO:0005515	AT5G55470.1	Calcium-dependent lipid-binding (CaLB domain) family protein	elicitor-responsive protein
Sapur.01G0267100.1	14.04691928	0.010207116	0.003149293	3.12611	0.001467038	0.002280451	greenyellow	0.169604282	0.033611069	GO:0055114;GO:0010572;GO:0018131	AT4G39080.1	GAD4	glutamate decarboxylase 4
Sapur.01G1155600.1	0.648137005	1.174417173	0.384505154	3.176643	0.001489901	0.002314996	greenyellow	0.193824813	0.015032328	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT1G27240.1	CYP87A2	cytochrome P450, family 87, subfamily A, polypeptide 2
Sapur.01W2000900.1	0.505822259	0.627627623	0.205962404	3.108989	0.001533019	0.002382623	greenyellow	0.231318228	0.033048851	GO:0006457;GO:0006532	AtLRA23	MLP-like protein 23	Ile/Val tRNA synthetase
Sapur.01G1385000.1	7.396634679	0.565573153	0.176143708	3.157116	0.001593379	0.002470556	greenyellow	0.201137204	0.01153786			VQ motif-containing protein	VQ motif protein
Sapur.01G1328000.1	0.280317687	0.968585254	0.310168117	3.123683	0.001638808	0.002541861	greenyellow	0.193920553	1.361E-05	GO:0055114;GO:0050660;GO:0016491		FAD-binding Berberine family protein	NA
Sapur.01G2299600.1	0.311209511	1.586132379	0.507456619	3.125664	0.001776044	0.002761682	greenyellow	0.327213985	2.88E-05	GO:0055114;GO:0050660;GO:0016491		FAD-binding Berberine family protein	NA
Sapur.01G0205500.1	0.424887756	1.27665506	0.409020973	3.121246	0.001880876	0.002781719	greenyellow	0.214917066	0.006870745				NA
Sapur.01T0047200.1	0.641293881	1.255720721	0.402041018	3.121503	0.002249296	0.003509169	greenyellow	0.224605485	0.005197249	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT3G13730.1	cytochrome P450, family 81, subfamily D, polypeptide 8	cytochrome P450 family protein
Sapur.01G6300100.1	0.473125255	1.483376325	0.491562724	3.017268	0.002550545	0.003897437	greenyellow	0.189288859	0.015759943		AT5G36430.1	FAD-binding Berberine family protein	NA
Sapur.01G0196400.1	0.503944483	0.444881389	0.146756056	2.968063	0.003299047	0.004996101	greenyellow	0.161664823	0.043926455		AT4G14010.1	RALR1,S2	ralf-like 22
Sapur.01T0247100.1	5.548579771	0.77616181	0.262035826	2.962052	0.003059959	0.004646676	greenyellow	0.143315098	0.07335115	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT5G62230.1	CYP81D1,CYP81A1	cytochrome P450 family protein
Sapur.01G0387600.1	0.563879594	1.470232705	0.51246916	2.886315	0.003809575	0.005809872	greenyellow	0.163402547	0.048267227				NA
Sapur.01G0899600.1	12.94885939	0.334432308	0.116335349	2.874974	0.004040613	0.006078378	greenyellow	0.207003171	0.009048729	GO:0004674;GO:0048544;GO:0006468;GO:0004672	AT5G27260.1		S-locus lectin protein kinase family protein
Sapur.01G0225300.1	10.83683017	0.467861227	0.163000173	2.869502	0.004070102	0.006086252	greenyellow	0.209133072	0.008585159	GO:0055114;GO:0016758;GO:0008152	AT5T5800.1	UDP-glucosyltransferase superfamily protein	UDP-glucosyltransferase, putative
Sapur.01T0229600.1	0.393549277	1.525969969	0.541041552	2.820571	0.004793826	0.007171657	greenyellow	0.257179158	0.001013193	GO:0006468;GO:0004672	CRK23	cysteine-rich RLK (RECEPTOR-like protein kinase) 23	Serine/Threonine kinase receptor-like protein, putative
Sapur.01G0299800.1	33.15805505	0.357281263	0.126757158	2.732403	0.006287425	0.009295115	greenyellow	0.159347965	0.046215579	GO:0016758;GO:0008152	UGT73D1	UDP-glucosyl transferase 73D1	UDP-glucosyltransferase, putative
Sapur.01G1327000.1	0.446076215	1.083366031	0.536056882	2.432608	0.014578122	0.021378684	greenyellow	0.162083221	0.042546897				transmembrane protein, putative
Sapur.01G1161700.1	8.823358095	0.452760192	0.188897135	2.396755	0.01654097	0.023479659	greenyellow	0.151796287	0.057720308	GO:0006355;GO:0003677	AT4G33000.1	anac042,NAC042	NAC domain containing protein 42
Sapur.01G0209900.1	0.323157245	0.898000223	0.378709226	2.371668	0.016771988	0.023796351	greenyellow	0.224504003	0.010373941	GO:0055114;GO:0020037;GO:0004688;GO:0004672	AT3G23791.1	WAK2	wall-associated kinase 2
Sapur.01G2039100.1	25.36342565	0.669725504	0.286026485	2.341481	0.019207417	0.027112207	greenyellow	0.139318665	0.081778725	GO:0008152;GO:0042742	AT5G47230.1	HEL,PR-4,PR4	pathogenesis-related 4
Sapur.01G6250200.1	27.08876104	0.386641259	0.173745639	2.225329	0.026107969	0.036324874	greenyellow	0.114841105	0.123828874	GO:0016567	AT5G26040.1	HXXXD-type acyl-transferase family protein	benzylalcohol acetyltransferase,
Sapur.01W5136500.1	2.550173837	0.769904561	0.369818123	2.081861	0.037156494	0.051220717	greenyellow	0.1168701	0.149298803	GO:0004857;GO:0042545;GO:0030599;GO:0005618	AT4G15230.1	Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.01T0232200.1	3.469318817	0.500008223	0.242751746	2.062632	0.039057171	0.053809872	greenyellow	0.10704586	0.182838103	GO:0005524	AATP1	AAA-ATPase 1	cell division cycle AATPase
Sapur.01G6298900.1	0.419149958	0.899306233	0.445143931	2.020369	0.043155519	0.059026898	greenyellow	0.122411085	0.126585579	GO:0055114;GO:0050660;GO:0016614	AT5G14185.1	Glucose-methanol-choline (GMC) oxidoreductase family protein	NA
Sapur.01G1170300.1	1.331496188	0.556371005	0.276133466	2.013267	0.044173836	0.060303264	greenyellow	0.109622051	0.183368526		AT5R1,PR_LPR1	pathogenesis-related gene 1	pathogenesis-related protein 1a, putative
Sapur.01G0986600.1	140.8843827	0.321887895	0.168015124	1.915827	0.055287131	0.074527013	greenyellow	0.109813669	0.170571121		AT5G64160.1	Disease resistance-responsive (dirigent-like protein) family protein	plant disease resistance response protein, putative
Sapur.01G6235200.1	0.90949994	0.684274984	0.362570202	1.887285	0.059127973	0.079268694	greenyellow	0.135278758	0.090206646	GO:0006355;GO:0003700	AT5T6P8.1	ethylene response element binding factor 1	ERF2 transcription factor
Sapur.01G1184800.1	2.234028953	0.464966157	0.246864625	1.882602	0.061878122	0.082885159	greenyellow	0.097533002	0.234383919		AT5T5800.1	Pathogenesis-related thaumatin family protein	NA
Sapur.01W2081700.1	32.66349612	0.236573918	0.131895185	1.776219	0.075696772	0.100315791	greenyellow	0.096201886	0.230703182			alpha/beta-hydrolases superfamily protein	NA
Sapur.01G1928000.1	30.20615597	0.237466144	0.138247852	1.718404	0.088969229	0.116856021	greenyellow	0.078019142	0.317881626	GO:0008061;GO:0050832;GO:0042742	HEL,PR-4,PR4	pathogenesis-related gene 4	wound-induced protein W14
Sapur.01G6285900.1	0.19664456	0.895372967	0.682875154	1.311181	0.1897966	0.237453955	greenyellow	0.201608806	0.011341603	GO:0055114;GO:0050660;GO:0016491		FAD-binding Berberine family protein	reticuline oxidase
Sapur.01G6201200.1	1.973287037	0.189909134	0.158037314	-1.20186	0.191336177	0.239208646	greenyellow	0.074478574	0.332932276	GO:0016567	AT4G27450.1	HXXXD-type acyl-transferase family protein	9-hydroxycinnamoyl/benzoyltransferase
Sapur.01G6201700.1	0.854978043	0.189909134	0.158037314	-1.20186	0.229416775	0.2832934	greenyellow	0.104678863	0.192003336	GO:0006468;GO:0004672	AT4G23180.1	CRK10,RLK4	cysteine-rich RLK (RECEPTOR-like protein kinase) 10
Sapur.01G6270300.1	19.61127968	0.133682486	0.129024474	-1.205899	0.300249184	0.36153831	greenyellow	0.051306535	0.523868886	GO:0016020;GO:0008378;GO:0006486	AT5G27500.1	Galactosyltransferase family protein	galactosyltransferase family protein
Sapur.01G2051100.1	0.23926794	0.646364363	0.67804266	0.95328	0.34048833	0.4071527	greenyellow	0.101329007	0.198685167				NA
Sapur.01T0127100.1	2.837272883	0.192144389	0.28707524	-0.66932	0.503282874	0.5782345	greenyellow	-0.056813807	0.48095644				NA
Sapur.01G0609600.1	0.153192866	0.455579659	0.964751584	0.573806	0.566099318	0.645155975	greenyellow	0.110748577	0.112812523		AT4G27485.1		hypothetical protein
Sapur.01G6254100.1	0.124306112	0.556231933	1.025257284	0.54251	0.587447486	0.682097037	greenyellow	0.13776471	0.085315902	GO:0016757	AT4G14640.1	Glycosyltransferase family 61 protein	glycosyltransferase
Sapur.01G0561400.1	0.149219133	0.477867227	0.906386015	0.526	0.58621	0.679095452	greenyellow	0.169318378	0.043570516		AT1G08490.1	DNA-lite 20	DNA-lite 20
Sapur.01G2305500.1	4.885336415	0.112114353	0.247396112	-0.45318	0.650418286	0.72261798	greenyellow	-0.031934208	0.694459702	GO:0005515	AT5G29430.1	ATGSTU7,GSTZ5,GSTU7	glutathione S-transferase tau 7
Sapur.01G1313200.1	0.367914628	0.557513026	1.319167476	0.418673	0.660869419	0.731638288	greenyellow	0.242796139	0.020277192				transmembrane protein, putative
Sapur.01G2299700.1	0.075100191	0.52325408	1.308331327	0.39984	0.689200682	0.758859572	greenyellow	0.190090414	0.0171499				NA
Sapur.01G5289300.1	0.101459661	0.786648891	1.212266463	0.369822	0.689207779	0.758801981	greenyellow	0.131772573	0.099905072	GO:0055114;GO:0020037;GO:0006979;GO:0004601	AT5G15180.1	Peroxidase superfamily protein	NA
Sapur.01G0994600.1	4.685491812	0.353651921	0.159756845	0.33763	0.735641795	0.800612594	greenyellow	-0.023694416	0.768337259		AT5G68450.1	VQ motif-containing protein	VQ motif protein
Sapur.01G6284300.1	0.055239868	0.811632281	1.822266576	0.271369	0.815018515	0.871803629	greenyellow	0.18323616	0.023232233				NA
Sapur.01G1138900.2	0.728183811	0.068898655	0.323836295	0.213699	0.837821127	0.880597627	greenyellow	0.026109542	0.745489373	GO:0055114;GO:0050660;GO:0016491	AT2G34790.1	EDA28,MEC23	FAD-binding Berberine family protein
Sapur.01G6123900.2	0.08821225	0.364962793	1.295468859	0.25152	0.83745375	0.885937353	greenyellow	0.079718419	0.330969573	GO:0010207	LPA19,PsbP2-H2	photosystem II 33 kDa protein-related	photosystem II 33 kDa protein-related
Sapur.01G2329700.1	34.96077353	0.250750001	0.152376622	0.151769642	0.911659119	0.91266012	greenyellow	-0.039609949	0.621630647	GO:0055114;GO:0016491;GO:0080270	AT4G03010.1	Oxidoreductase, zinc-binding dehydrogenase family protein	quinone-oxidoreductase-like protein
Sapur.01G0419300.1	6.001012078	0.037776593	0.152464958	0.149623	0.881057571	0.919476112	greenyellow	0.00841405	0.916703446	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT5G15160.1	ATRACYP3B3,LRE1,RNT1;	cytochrome P450, family 83, subfamily B, polypeptide 1
Sapur.01G6117700.1	0.262617701	0.118449491	0.184649	0.166664	0.927933187	0.95469999	greenyellow	0.087654123	0.279496208	GO:0009773	SAUR-like auxin-responsive family protein		auxin responsive protein
Sapur.01W2004200.1	0.552154892	0.276147848	1.676278284	0.223127	0.923428879	NA	greenyellow	0.164246634	0.074186643	GO:0005576	CID10	CTC-interacting domain 10	RNA recognition motif 2 in RNA-binding protein 34 (RBM34)-like protein
Sapur.01G0728300.1	0.062615103	0.355802011	1.723251549	0.205407	0.934577	NA	greenyellow	0.204205918	0.010347558	GO:0005515;GO:0005576	BGLU41	beta glucosidase 41	NA
Sapur.01B0613200.1	0.031477757	0.271140152	2.904819061	0.093341	0.925622248	NA	greenyellow	0.12119403	0.130513625				NA
Sapur.01G1347700.1	0.023873162	0.220360075	2.782212871	0.084648	0.932541146	NA	greenyellow	0.14934968	0.061348314	GO:0005975;GO:0004553	AT5G18070.1	BGLU43	beta glucosidase 43
Sapur.01G1784000.2	0.033188338	0.160452641	2.090383263	0.076757	0.938815129	NA	greenyellow	0.04886946	0.559988338		AT4G34160.3	ENTH/VHS family protein	clathrin interactor epsin 2
Sapur.01B0...1	0.033344697	0.109900883	2.904821116	0.068857	0.945135353	NA	greenyellow	0.136245006	0.088882887				NA
Sapur.01G2645200.1	0.023302383	0.109900883	2.904821116	0.068857	0.945135353	NA	greenyellow	0.135576906	0.09045073	GO:0046983;GO:0003677;GO:0006355;GO:0005634;GO:0003700	AT5G09910.1	AGL8,FUL	MADS-box transcription factor
Sapur.01W2139600.2	0.018056689	0.099908029	2.904821116	0.068857	0.945135353	NA	greenyellow	0.133369792	0.10346613		AT5G07600.1	Heavy metal transport/detoxification superfamily protein	ATPTM-like protein, putative
Sapur.01G7286102.1	0.017266102	0.099908029	2.904821116	0.068857	0.945135353	NA	greenyellow	0.128613039	0.108425146				hypothetical protein
Sapur.01W2035100.1	0.013085884	0.18585145	2.904821534	0.06398	0.948985886	NA	greenyellow	0.105200276	0.189765258	GO:0005515	AT5G20480.1	EFR	EF-Tu receptor
Sapur.01B6264400.1	0.014041274	0.178648895	2.904821749	0.06261	0.950860094	NA	greenyellow	0.13177573	0.155830051	GO:0055114;GO:0020037;GO:0006979;GO:0004601	AT5G47810.1	PER1 helicase	NA
Sapur.01G0960200.1	0.023156335	0.182451285	2.761513265	0.058814	0.953100331	NA	greenyellow	-0.072098875	0.365487703		AT5G28130.1		hypothetical protein
Sapur.01W2034700.1	0.011569154	0.164281247	2.904822183	0.058057	0.954899498	NA	greenyellow	0.111417813	0.164704424				hypothetical protein
Sapur.01T0207000.2	0.014424396	0.164281247	2.904822183	0.056555	0.954899498	NA	greenyellow	0.10796267	0.178336163	GO:0008152;GO:0003824	AT5G31880.1	AMP-dependent synthetase and ligase family protein	4-coumarate-CoA ligase
Sapur.01G2270000.1	0.009656263	0.123861759	2.904822276	0.046262	0.96471296	NA	greenyellow	0.078548131	0.32814987		CLAVATA2,RLK,RLE1E.5	Leucine-rich repeat protein kinase family protein	CLAVATA2 RLK
Sapur.01G0320100.1	0.014074271	0.091189602	2.904823276	0.031392	0.974956514	NA	greenyellow	0.026156622	0.745046229	GO:0005524	AT4G24480.1	STI	AAA-type ATPase family protein
Sapur.01B2678000.3	0.014812356	0.091189602	2.904823276	0.031392	0.974956514	NA	greenyellow	0.020502261	0.788816585	GO:0016491;GO:0008152	AT2G42550.1	NADP5-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase family protein
Sapur.01G6288300.2	0.014177994	0.091189602	2.904823276	0.031392	0.974956514	NA	greenyellow	-0.028372015	0.736650018	GO:0009085;GO:0008837	AT5G15180.1	diaminopimelate epimerase family protein	diaminopimelate epimerase
Sapur.01G6132300.1	0.01549138	0.091189602	2.904823276	0.031392	0.974956514	NA	greenyellow	0.03431128	0.858094676	GO:0055515;GO:0042393;GO:0006255	AT5G42790.1	AL3	AL3 domain class transcription factor
Sapur.01G1338900.1	0.014177994	0.091189602	2.904823276	0.031392	0.974956514	NA	greenyellow	0.027050343	0.736650018		AT1T8P2,TRFL9	TRF-like 9	telomere-binding protein
Sapur.01G2951300.1	0.015146102	0.091189602	2.904823276	0.031392	0.974956514	NA	greenyellow	0.017182411	0.83086554				cyclic nucleotide-gated channel protein
Sapur.01G6295200.1	0.015029761	0.091189602	2.904823276	0.031392	0.974956514	NA	greenyellow	0.016615107	0.859377882		AT5G54160.1	O-fucosyltransferase family protein	GDP-fucose protein O-fucosyltransferase, putative
Sapur.01B6124400.1	0.005114485	0.055017653	2.904824386	0.01913	0.984273169	NA	greenyellow	0.078548131	0.32814987	GO:0016491	AT1G49180.2	ATCYS-3A,CYTAC5,CASA1,CASA1	O-acetylserine (thiol) lyase (OAS-TL) isoform A1
Sapur.01G0383300.1	172.38288	0.951889154	0.04931882	38.5785	0	0	greenyellow	0.185208008	6.31E-07	GO:0016021;GO:0016459;GO:0015295	AT1G34470.1		Protein of unknown function (DUF1421)
Sapur.01G0849500.1	263.2529595	2.424509948	0.04916516	49.30424	0	0	greenyellow	0.548004084	1.10E-13		AT5G01480.1		O-fucosyltransferase family protein
Sapur.01W2344200.1	67.04979966	0.786489102	0.109681746	16.5325	3.68E-261	1.62E-258	greenyellow	-0.081608864	0.309309942		AT4G19370.1	EFR,LIP,SOMAGEN	somagen
Sapur.01W5054800.1	16.54380029	0.415179244	0.100738313	-33.9016	6.32E-252	2.62E-250	greenyellow	-0.379638091	9.41E-07		AT5G48550.1	Vacuolar protein sorting-associated protein 26	vacuolar protein sorting-associated protein 26
Sapur.01B0258900.3	53.70781063	0.115485726	0.135408023	30.3859	8.44E-203	2.53E-201	greenyellow	-0.128829332	0.107828177	GO:0009086;GO:0008705;GO:0008871;GO:0008652	AT1G79320.1	ATCIMS,ATMETS,ATMS1	Cobalamin-independent synthase family protein
Sapur.01T0087005.1	96.6318284	0.500691553	0.050238315	-30.0016	9.08E-198	2.24E-196	greenyellow	-0.428237215	0.000000000	GO:0006351;GO:0003700	AT4G40050.1	Protein of unknown function (DUF3532)/HYR0B2	signal transducer, putative
Sapur.01G0051100.1	162.6378648	0.615706802	0.309163364	27.88844	6.44E-171	1.58E-169	greenyellow	0.155295466	4.42E-14	GO:0007165;GO:0005515;GO:0043531	AT5G63930.1	Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.01G0327700.1	114.8100641	0.873089881	0.508015345	27.5363	6.46E-147	1.44E-145	greenyellow	-0.127798422	0.117388001	GO:0006468;GO:0005524;GO:0004672	EMB3013,RLK	Protein kinase family protein with ARM repeat domain	Serine/Threonine kinase domain protein
Sapur.01G1153400.1	340.3100477	-0.033102307	0.039576377	-26.1053	3.17E-150	6.19E-148	greenyellow	-0.222269177	0.005144308	GO:0006872		CCCH-type zinc finger protein with ARM repeat domain	zinc finger CCCH domain protein
Sapur.01G6280600.2	15.77673329	0.466804266	0.121817286	-24.2564	2.19E-130	3.53E-128	greenyellow	-0.38444504	1.61E-07		AT5G27570.1	HIPP26-like cadmium superfamily protein	NA
Sapur.01G0305500.1	1128.775619	0.997783282	0.041938077	23.79296	3.95E-125	6.08E-124	greenyellow	0.359619629	3.71E-06		AT5G47540.1	Me25 family protein	Me25-like plant protein, putative
Sapur.01G6287800.3	17.44613153	2.068149449	0.113878658	-23.6948	4.08E-124	6.21E-123	greenyellow	-0.168962653	0.011883174		AT4G33800.1		hypothetical protein
Sapur.01G1105900.4	6.783587653	0.063727427	0.25667347	23.62467	2.16E-123	3.26E-122	greenyellow	0.151464644	0.058355955		AT5G68870.1	ASL11,BD36	ASYMMETRIC LEAVES 2-like 1
Sapur.01G0856400.4	14.53741329	0.900488812	0.213707131	23.57544	7.56E-113	1.01E-111	greenyellow	-0.413483612	7.35E-08		AT2G39810.1	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region	auxin canalisation protein
Sapur.01G1113700.2	62.4557274	1.357866075	0.06026394	22.52963	2.13E-112	2.82E-111	greenyellow	0.267095005	0.000726661		AT3G09305.1	Cysteine proteinases superfamily protein	cysteine-type peptidase
Sapur.01B6028700.1	32.88037904	0.066381212	0.359127292	22.3929	4.62E-111	6.05E-110	greenyellow	0.49905321	2.89E-11	GO:0010312;GO:0008270;GO:0006508;GO:0004222	AT5G59970.1	Matrixin family protein	NA
Sapur.01B6281800.1	22.29329263	0.033521487	0.193130327	23.32529	1.78E-110	2.31E-109	greenyellow	-0.498663296	3.82E-11	GO:0010312;GO:0008270;GO:0006508;GO:0004222	AT5G59970.1	Matrixin family protein	NA
Sapur.01G6208300.1	39.44750005	0.245180875	0.056115329	-22.1897	4.32E-109	5.51E-108	greenyellow	-0.408579588	1.08E-07	GO:0003677	AT5G11270.1	oxoreisoprene-of-cattleya peroxidase 3	homeobox domain protein
Sapur.01G6224800.1	149.4758862	0.919199159	0.054168916	21.93063	1.10E-106	1.34E-105	greenyellow	0.207936394	0.039370995		AT4G16160.1	ATKCDC4,ATTPK2,KCDC17K2	Ca2+ activated inward rectifying channel 6	outward rectifying potassium channel protein
Sapur.01G0219800.1	270.0215008	1.485852757	0.250377793	21.9103	2.07E-106	2.56E-105	greenyellow	0.429719177	1.95E-08		AT4G30880.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	serpentine inhibitor/seed storage/lipid transfer family protein
Sapur.01G6290600.1	27.32628869	0.775929163	0.356057115	21.84855	8.02E-106	9.93E-105	greenyellow	0.491694225	6.18E-11	GO:0010312;GO:0008270;GO:0006508;GO:0004222	AT5G59970.1	Matrixin family protein	NA
Sapur.01B0618900.1	92.96515784	0.122097651	0.427204666	21.353	3.66E-101	4.23E-100	greenyellow	0.475414666	3.14E-10	GO:0010312;GO:0008270;GO:0006508;GO:0004222	AT5G59970.1	Matrixin family protein	NA
Sapur.01G6293100.1	21.32124303	0.252438526	0.060006687	-20.5711	4.98E-94	5.27E-93	greenyellow	0.080707278	0.334864277		AT5G04340.1	HR-like lesion-inducing protein-related	HR-like lesion-inducing protein
Sapur.01G6274100.4	10.63767571	0.09222627	0.251008999	20.28703	1.67E-91	1.71E-90	greenyellow	0.078548131	0.32814987	GO:0080123;GO:0008664;GO:0006629;GO:0006913	AT4G36730.4	RN219;JAR1	Auxin-responsive GH3 family protein
Sapur.01T0202300.3	23.43097755	0.859386266	0.090902664	-20.2945	1.76E-91	1.80E-90	greenyellow	-0.125882066	0.131812182		AT4G35160.1		PKBP-like peptidyl-prolyl cis-trans isomerase family protein
Sapur.01G0395300.1	85.66264013	-0.48573856	0.074319481	-19.9937	6.26E-88	6.16E-86	greenyellow	-0.039493518	0.623627519		AT5G61160.1	selenium binding protein	selenium binding protein
Sapur.01G0027700.1	51.09086166	1.364483534	0.108333021	-19.9794	8.32E-89	8.17E-88	greenyellow	-0.178804599	0.025051997	GO:0006508;GO:0004185	AT5G23210.1	SCPL34	serine carboxypeptidase-like 34
Sapur.01G5134800.1	7.684128152	0.147867895	0.140018176	-19.7182	1.51E-86	1.46E-85	greenyellow	-0.052109546	0.516193669		AT5G26610.1		Remorin family protein
Sapur.01G1103000.1	318.4484807	0.765035826	0.040208189	-19.5243	6.83E-85	6.37E-84	greenyellow	-0.10425278	0.193813652	GO:0055414;GO:0003777	AT3G64330.1	EMB2750	Tetratricopeptide repeat (TPR)-like superfamily protein	squamosa promoter-binding protein
Sapur.01B0...1	11.88853283	0.342217753	0.122649835	-19.1056	2.26E-81	2.08E-80	greenyellow	-0.08125	4.91E-08	GO:0016604;GO:0005634	AT4G12620.2		Protein phosphatase 2A family protein
Sapur.01B0719900.1	326.1464603	1.538809228	0.080535351	19.09874	2.59E-81	2.30E-80	greenyellow	-0.383258578	6.27E-07		AT5G27655.2		xylose isomerase family
Sapur.01G6130600.1	11.43026003	0.227588794	0.172454658	18.97169	2.86E-80	2.50E-79	greenyellow	-0.414543388	6.30E-08	GO:0006950;GO:0006488;GO:0055114;GO:0046872	AT4G26730.1		Protein kinase superfamily with nucleotide alpha hydrolases-like domain
Sapur.01G6227000.2	196.9015524	1.635372469	0.086976705	18.8914	1.34E-79	1.16E-78	greenyellow	-0.321411204	4.05E-05	GO:0019205;GO:0006139;GO:0055234	AT5G26667.2	PYR6	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.01B2680100.1	15.24657778	0.180697304	0.302413389	18.83378	3.98E-79	3.45E-78	greenyellow	0.166628052	0.037008015	GO:0006468;GO:0004672	AT4G16030.1	LECRK	lectin protein kinase family protein
Sapur.01G5171700.1	17.26715962	1.590865059	0.085153737	-18.6825	6.88E-78	5.80E-77	greenyellow	0.152859565	0.06014543	GO:0003677	AT5G54540.1	HTA11	histone H2A 11
Sapur.01B6287300.4	12.12943622	0.752551535	0.094807182	-18.485	2.72E-76	2.25E-75	greenyellow	0.078548131	0.32814987	GO:0006468;GO:0005524;GO:0004672	AT5G18890.1	Protein kinase superfamily protein	receptor-like kinase
Sapur.01G0311400.1	30.61332121	0.180387591	0.101602637	-18.3647	2.52E-75	2.05E-74	greenyellow	-0.449815466	1.42E-09		AT4G04651.1	Rpp1 motif-containing protein	polyadenylation factor I complex subunit RP1, putative
Sapur.01G1349800.1	13.3351519	2.596931461	0.141472304	-18.3565	2.93E-75	2.38E-74	greenyellow	-0.35413635	5.37E-06				transmembrane protein, putative
Sapur.01G4125300.1	35.88617907	0.424358279	0.087393996	-18.1229	5.52E-75	4.46E-74	greenyellow	-0.248842939	0.00080668		AT3G48180.1		NA
Sapur.01G0610000.4	10.31522693	-0.298281209	0.126718604	-18.1356	1.67E-70	1.32E-72	greenyellow	-0

Sapur.01G0280100.1	146.7358848	1.110295158	0.088104224	12.60207	2.06E-36	8.85E-36	grey	-0.056413637	0.482674094	GO:0045454		ATP03B;ATP01L-2;PDI8;PDI-like 5-2	protein disulfide isomerase-like protein, putative
Sapur.003G135600.1	7.300304974	2.298351615	0.261795533	12.59896	2.14E-36	9.20E-36	grey	-0.446060744	7.67E-09	GO:0016887;GO:0005524;GO:0016020		ATG15520.1	ABC;G40;ATABCG40;ATPDR1 pleiotropic drug resistance 12	NA
Sapur.003G137900.1	5.24058823	2.943101031	0.154323303	12.5693	2.16E-36	1.01E-35	grey	-0.475788861	4.46E-10	GO:0046983		ATG46810.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	hello loop helix DNA-binding domain protein, putative
Sapur.002G000400.1	42.12675657	0.858654009	0.068456823	12.53259	4.95E-36	2.11E-35	grey	-0.345326783	9.43E-06	GO:0005515		ATA597;GE26.5	SET domain protein 25	SET domain protein
Sapur.006G400000.1	33.31443018	0.879207858	0.070050965	12.5105	5.54E-36	2.36E-35	grey	-0.186735655	0.019366408	GO:0016251;GO:0003700		ATG12840.2	AT4G34270;EMB2230;HAP2A nuclear factor Y, subunit A1	nuclear transcription factor Y subunit
Sapur.010G260100.1	89.05120933	0.737491079	0.059107738	-12.4771	9.96E-36	4.22E-35	grey	-0.236832256	0.002812002	GO:0005515		ATG46548.1	ELP2	elongator protein 2
Sapur.006G111200.10	6.505863505	-1.637054145	0.131307258	-12.4674	1.12E-35	4.77E-35	grey	-0.438748226	9.05E-09	GO:0003725		ATG08465.1	YAB2	Plant-specific transcription factor YABBY family protein
Sapur.003G190300.1	3.135887444	4.950604651	0.398420606	12.42565	1.39E-35	8.00E-35	grey	-0.514580512	5.20E-12	GO:0007165;GO:0005515;GO:0043531		ATG36930.2	Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.011G021700.1	9.02609775	5.607254942	0.451488361	12.41949	2.05E-35	8.63E-35	grey	0.462893169	9.38E-10	GO:0048544;GO:0006468;GO:0004672		ATG11340.1	S-locus lectin protein kinase family protein	NA
Sapur.008G198800.1	59.36667992	1.162345383	0.0477182[illegible]	12.4134	2.31E-35	9.36E-35	grey	0.124537564	0.118175368			ATG32020.1	MMS;DMS1 homologue 1	ubiquitin-conjugating enzyme E2
Sapur.007G126200.1	27.18148107	2.315247268	0.186152918	12.41087	2.29E-35	9.63E-35	grey	0.505824629	1.40E-11	GO:0016758;GO:0008152		ATG05675.1	UDP-Glycosyltransferase superfamily protein	NA
Sapur.003G135900.1	35.13315747	0.94976585	0.1167883	12.4065	2.29E-35	9.63E-35	grey	0.519682807	1.07E-12	GO:0016758;GO:0008152		ATG05675.1	UDP-Glycosyltransferase superfamily protein	NA
Sapur.001G173900.1	123.7048849	0.951525551	0.073945732	-12.3756	3.54E-35	1.48E-34	grey	-0.387279923	5.44E-07			ATG64080.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/lipid transfer family protein
Sapur.014G264500.1	7.470104064	1.848863361	0.230361329	12.3665	3.99E-35	1.67E-34	grey	-0.568213661	8.38E-15			ATG62230.1		NA
Sapur.T052300.1	175.1367934	0.578913468	0.046835362	12.36061	4.27E-35	1.79E-34	grey	-0.058199996	0.463555594	GO:0016021;GO:0016020		ATG07080.1	EamA-like transporter family	solute carrier family 35 protein
Sapur.012G039900.2	7.180245551	1.562204197	0.187568533	12.34539	5.16E-35	2.16E-34	grey	-0.177354568	0.030532058	GO:0004648;GO:0006672		ATG27730.1	Serine/Threonine kinase domain protein	Serine/Threonine kinase domain protein
Sapur.003G140800.1	546.324156	0.858279883	0.070333584	12.20269	3.03E-34	1.23E-33	grey	-0.067475564	0.40109418	GO:0016787		ATG76690.1	atnudt3;NUDT3	nudix hydrolase homolog 3	nudix hydrolase
Sapur.002G092300.3	1.668388985	3.691377302	0.302826461	12.19576	3.27E-34	1.35E-33	grey	0.136608879	0.087861115			ATG60810.1			transmembrane protein, putative
Sapur.006G050000.1	6.880473859	1.539378922	0.126278836	12.16249	4.92E-34	1.79E-33	grey	-0.452261778	3.82E-11	GO:0006281;GO:0003676;GO:0003723		ATG28781.1	PIF1 helicase	NA
Sapur.010G030400.1	4.048548898	3.201301854	0.428152923	12.13803	6.64E-34	2.72E-33	grey	0.444105257	5.67E-09	GO:0005524;GO:0003676;GO:0016818;GO:0008270		ATG05130.1	DNA/RNA helicase protein	chromatin remodeling complex subunit, putative
Sapur.006G116200.1	152.5464019	0.917184184	0.076000128	12.1855	8.42E-34	3.46E-33	grey	0.6038371	7.10E-14			ATG20670.1	Protease inhibitor family protein (DUF1273)	DUF1327 family protein
Sapur.004G013600.1	224.4418687	1.191148564	0.09838361	12.10688	9.71E-34	3.96E-33	grey	0.42546869	2.74E-08			ATG05320.2	UBQ10	polyubiquitin 10	ubiquitin
Sapur.004G000300.1	104.5744381	1.152183937	0.096080808	12.0292	1.47E-33	5.96E-33	grey	0.212718558	0.007364646			ATG41950.1	SNARE associated Golgi protein family	SNARE associated protein	
Sapur.005G112200.1	119.5742209	0.581688825	0.048494449	11.99466	3.78E-33	1.52E-32	grey	0.372097394	1.60E-06			ATG49710.3		hypothetical protein	
Sapur.002G092800.1	106.6962891	0.7[illegible]5	0.061[illegible]8	11.9758	4.30E-33	1.73E-32	grey	0.418873774	3.62E-08					hypothetical protein	
Sapur.15W0094200.1	1.330663141	3.551735301	0.296807995	11.96643	5.33E-33	2.14E-32	grey	0.596102778	1.77E-16			ATG88370.1	F-box and associated interaction domains-containing protein	NA	
Sapur.15W0139700.1	36.57315679	0.132068837	0.094759908	-11.9503	6.47E-33	2.60E-32	grey	-0.16930666	0.193435849	GO:0006457		ATG25340.1	ATFKBP53;FKBP53	FKBP6 DNDNG PROTEIN 53	peptidyl-prolyl cis-trans isomerase FKBP53
Sapur.007G126000.4	14.84443261	0.873248782	0.088158569	-11.9384	7.46E-33	2.98E-32	grey	-0.106548877	0.192546188			ATG46870.1			hypothetical protein
Sapur.006G104800.1	2.657224955	1.180544224	0.192420758	11.93007	8.25E-33	3.31E-32	grey	0.483936756	1.35E-10			ATG83925.1			
Sapur.010G020700.1	1.945020255	1.968324412	0.32470047	11.9145	9.94E-33	3.98E-32	grey	0.553692821	5.42E-14	GO:0016846		ATG70560.1	SAV;LTAA1;WEIB	tryptophan aminotransferase of Arabidopsis 1	tryptophan aminotransferase-like protein
Sapur.010G005900.2	7.093755881	2.145632022	0.180455212	11.8901	1.13E-32	5.32E-32	grey	0.484434633	1.26E-10	GO:0005085		ATG61370.1	ATOPT1;OPT1	oligopeptide transporter	oligopeptide transporter OPT family protein
Sapur.010G034400.1	6.503054572	1.447197515	0.122023979	-11.8599	1.91E-32	7.60E-32	grey	0.078438351	-0.01[illegible]9			ATG50502.1			Protein of unknown function (DUF1627)
Sapur.002G060600.1	129.3871497	0.796609912	0.067215252	11.85609	2.00E-32	7.95E-32	grey	0.10614079	0.44E-05			ATG77760.3	ATSAT12;SAT12	interferon-related developmental regulator family protein / IFRD protein family	interferon-related developmental regulator
Sapur.003G135200.1	13.22724537	1.286822116	0.108571545	11.85215	2.09E-32	8.31E-32	grey	0.447080655	4.36E-09			ATG11440.1	CDS1;PIS	CDP-diacylglycerol synthase family protein	hypothetical protein
Sapur.010G026200.1	1.681250763	4.181644297	0.353649551	11.82426	2.92E-32	1.16E-31	grey	0.490005354	7.34E-11	GO:0080408;GO:0006139;GO:003676		ATG36130.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	2'-5' exonuclease	
Sapur.003G163600.1	4.412142688	3.150682556	0.266463194	11.81145	3.46E-32	1.36E-31	grey	0.518313147	1.98E-12	GO:0006355;GO:0005634;GO:0007030;GO:0046983;GO:0003677		ATG63120.1	AGL10;CAL;CAL1	Transcription factor MADS-box protein transcription factor family protein	NA
Sapur.013G014200.1	105.4853445	0.905632236	0.077180295	11.78466	4.68E-32	1.84E-31	grey	0.263835575	0.008737788			ATG05550.1	Hypoxia-responsive family protein	NA	
Sapur.004G047800.1	190.2022461	0.903556223	0.076591021	11.76386	5.99E-32	2.35E-31	grey	0.405880764	1.34E-07	GO:0004866		ATG17860.1	Kunitz trypsin inhibitor and protease inhibitor protein	kunitz-type trypsin inhibitor	
Sapur.007G107500.1	6.196680214	1.988181836	0.169579381	11.75187	6.92E-32	2.72E-31	grey	0.399215537	2.23E-07			ATG22040.1	Receptor-like protein kinase-related family protein	salt stress response/antifungal domain protein	
Sapur.003G152600.1	2.220188906	0.083403442	0.348139819	11.72928	9.02E-32	3.53E-31	grey	0.484890221	1.22E-10	GO:0005515		ATG34930.1	disease resistance family protein / LRR family protein	NA	
Sapur.004G028700.1	20.8674664	0.924862337	0.0237662	11.7277	9.13E-32	3.60E-31	grey	-0.13245726	0.146749862			ATG46550.1		transmembrane protein, putative	
Sapur.009G051000.1	81.64864208	0.815465626	0.069575572	11.7199	1.01E-31	3.96E-31	grey	0.342126858	1.16E-05			ATG60720.1	Protein of unknown function, DUF547	electron transporter, putative	
Sapur.010G136700.1	37.62718282	1.466139704	0.126018474	11.7146	1.07E-31	4.17E-31	grey	-0.240705097	0.016884691	GO:0016020		ATG69410.2	Early-responsive to dehydration stress protein (ERD4)	early-responsive to dehydration stress protein (ERD4), putative	
Sapur.003G188300.1	315.1662579	0.803904019	0.068607735	11.7075	1.22E-31	4.76E-31	grey	0.100154079	0.407293893			ATG36840.1	Sec14p-like phosphatidylinositol transfer family protein	phosphatidylinositol/phosphatidylcholine transfer-like protein	
Sapur.006G224400.1	6.647742756	3.262617021	0.280406664	-11.6883	1.56E-31	5.96E-31	grey	-0.49622216	3.75E-11	GO:0034968;GO:0018024;GO:0008270;GO:0005634;GO:0005515;GO:0042393		ATG73100.1	SUVH9;SUVH3	SUVH9/SUVH3 homologs	histone lysine N-methyltransferase, H3 lysine-9 specific SUVH3 protein, putative
Sapur.013G012200.2	26.37217169	1.472466652	0.126117311	11.67537	1.70E-31	6.63E-31	grey	-0.137559283	1.53E-05			ATG27920.1	F-box family protein	F-box/LRR protein	
Sapur.003G145100.2	4.808861739	2.562119782	0.176707278	11.66573	1.91E-31	7.41E-31	grey	0.307553927	8.92E-05			ATG36100.2	ATMYB33;MYB33	myb domain protein 33	Myb transcription factor
Sapur.005G012800.1	19.13182826	0.921921889	0.0952828	11.65575	2.14E-31	8.32E-31	grey	0.491102045	6.58E-11	GO:0004674;GO:0048544;GO:0006468;GO:0004672		ATG61390.1	B120	S-locus lectin protein kinase family protein	G-type lectin S-receptor-like Serine/Threonine-kinase
Sapur.007G049000.1	51.15079073	2.058854201	0.17765777	11.58736	4.78E-31	1.84E-30	grey	0.457648754	1.68E-09	GO:0003246;GO:0005975;GO:0004553		ATG48930.1	AtGHC1;GHGC1	glycosyl hydrolase 9C1	endo-1X2X4 beta-glucanase
Sapur.008G177700.1	1678.07[illegible]	1.882327	0.162620948	11.5768	5.83E-31	2.24E-30	grey	-0.524717748	9.5E-10			ATG22440.1	Chlorophyll A ethylase family protein	early light-induced protein	
Sapur.001G177200.1	9.900587515	-1.480066418	0.128185325	-11.5465	7.69E-31	2.95E-30	grey	-0.215898485	0.005591629			ATG20020.2		plastid developmental protein, putative	
Sapur.003G135400.1	15.03014949	1.575008021	0.136182024	-11.5346	8.62E-31	3.38E-30	grey	-0.642836966	1.11E-08	GO:0016468;GO:0005777		ATG08640.1	Putative endonuclease or glycosyl hydrolase	limkain b1-like amino terminal LeuA-like domain protein, putative	
Sapur.004G012600.1	288.1467739	0.315102487	0.027506147	-11.4735	1.79E-30	6.81E-30	grey	-0.290906078	0.000218869			ATG68861.1	PCF56	PCF11P-similar protein 4	PCF11P-related protein, putative
Sapur.003G135300.1	6.345452629	1.967181734	0.303868218	11.4617	2.05E-30	7.76E-30	grey	0.477372658	3.68E-10			ATG61870.1	myb domain protein 9	myb transcription factor	
Sapur.15W0071700.1	40.94832228	2.405026051	0.210128777	11.44048	2.62E-30	9.93E-30	grey	0.506219982	1.35E-11	GO:0005515		ATG62600.2	ATIMH1;FIM1	Fimbrin 1	
Sapur.005G025500.1	1.466888838	4.810417152	0.4[illegible]7[illegible]4	11.42766	3.02E-30	1.15E-29	grey	0.515231815	6.57E-14			ATG17860.1	Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor KPI-D1.2	
Sapur.003G134900.1	4.982652813	-0.036518017	0.266213453	-11.4063	3.89E-30	1.47E-29	grey	-0.156363124	4.45E-13			ATG46630.1		NA	
Sapur.010G045300.4	5.336319074	0.878278863	0.164805743	-11.3969	4.33E-30	1.63E-29	grey	-0.388242409	8.77E-07	GO:0005515;GO:0006355;GO:0006352;GO:0003700;GO:0003677		ATG64860.1	RPOD1.SIG1.SIG2.SIGA.SIGB	sigma factor A	RNA polymerase sigma factor
Sapur.013G201700.2	2.365635543	1.064703286	0.209502619	11.3717	5.78E-30	2.17E-29	grey	0.106503932	0.186037545	GO:0005515		ATG17980.1	Calcium-dependent lipid-binding (CaLB domain) family protein	pollen-specific C2 domain protein	
Sapur.003G037900.1	13.61631931	1.977166337	0.175957153	11.36582	6.19E-30	2.32E-29	grey	0.50202472	2.55E-11	GO:0046872		ATG19360.1	Zinc finger (CCCH-type) family protein	zinc finger C-x8-C-x5-C-x3-H type protein	
Sapur.006G042400.1	17.75637884	1.202914	0.152568781	11.2563	1.38E-29	5.16E-29	grey	0.060320061	0.261767054			ATG37630.1	excision family protein	excision family protein	
Sapur.001G186500.1	22.3564275	2.324837715	0.173389529	-11.2845	1.57E-29	5.83E-29	grey	0.087726335	0.274599426	GO:0006355;GO:0005634;GO:0003677;GO:0009725	ARF1	ATG70230.1		auxin response factor	auxin response factor
Sapur.003G012800.1	3.874003266	1.991313304	0.176368633	-11.2564	1.72E-29	6.41E-29	grey	0.348845476	7.55E-06	GO:0008270		ATG21275.2	RING/FYVE/PHD family protein	RING/FYVE/PHD protein	zinc finger protein
Sapur.006G293000.1	16.06874744	-1.291204613	0.116643085	-11.2628	2.00E-29	7.45E-29	grey	0.02574108	0.748960417			ATG11460.1	Protein of unknown function (DUF581)	DUF581 family protein	
Sapur.006G117700.1	14.27587369	1.612027488	0.1[illegible]2[illegible]1	11.2444	2.47E-29	9.15E-29	grey	-0.005624165	0.944262688	GO:0016757		ATG14850.1	Alg8-like mannosyltransferase family protein	dolichyl-phosphate mannose-glycolipid alpha-mannosyltransferase-like protein	
Sapur.015G071500.1	87.64294738	2.48882631	0.221496567	11.23994	2.69E-29	9.63E-29	grey	0.532707364	6.90E-13			ATG15400.1	Actin binding Calponin homology (CH) domain-containing protein	NA	
Sapur.006G067500.1	21.31113323	1.524321885	0.136164649	11.2058	2.74E-29	1.01E-28	grey	-0.047368873	0.609420508	GO:0043565;GO:0006355;GO:0003700	ABI5;GLA1	ATG62763.1	Basic-leucine zipper (bZIP) transcription factor family protein	abscisic acid insensitive protein	
Sapur.011G068600.4	8.66831515	-1.2287523	0.109463135	-11.2209	3.23E-29	1.19E-28	grey	-0.020243539	0.803063489			ATG65400.2	copper ion binding	hypothetical protein	
Sapur.014G070300.1	208.1572812	0.817950734	0.072906857	11.21916	3.28E-29	1.22E-28	grey	0.513774548	5.32E-12	GO:0015940;GO:0003864	KPHMT1;PANB1	ATG46110.1	ketopantoate hydroxymethyltransferase	3-methyl-2-oxobutanoate hydroxymethyltransferase	
Sapur.009G266100.5	15.12109649	1.552883091	0.115499392	11.2018	3.92E-29	1.45E-28	grey	0.069395119	0.265037777	GO:0003682		ATG85852.1	agenet domain containing protein / bromodomain-adjacent homology (BAH) domain-containing protein	agenet domain protein/bromo-adjacent-like (BAH) domain protein	
Sapur.013G008200.1	19.25262526	1.18175165	0.105599221	11.19061	4.52E-29	1.67E-28	grey	0.562952602	1.67E-14			ATG67623.1	F-box family protein	F-box protein	
Sapur.004G266400.4	6.924916639	-1.261374898	0.113175768	-11.1696	4.53E-29	1.67E-28	grey	-0.31446557	6.05E-05			ATG61830.1	TIO;DNT;BEWAKOOR	TIO/DNT/BEWAKOOR	TCP family transcription factor
Sapur.009G127300.1	97.36378009	-2.404502651	0.2102187[illegible]	11.44048	2.62E-30	9.93E-30	grey	-0.328244475	2.71E-05	GO:0007165	TCF2	ATG72610.1	Rho GTPase activating protein with PAK-box/PX-Rho-binding domain	Rho GTPase-activating protein	
Sapur.006G250500.1	1.466888838	4.810417152	0.2387200[illegible]	11.51658	4.56E-29	2.36E-28	grey	0.419625585	1.46E-08	GO:0004866		ATG17860.1	Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor KPI-D2.2	
Sapur.018G219900.1	4.982652813	-0.036518017	0.266213453	-11.4063	3.89E-30	1.47E-29	grey	-0.455332327	2.08E-09	GO:0016020;GO:0006810;GO:0005215		ATG61680.1	Major facilitator superfamily protein	NA	
Sapur.013G201300.4	8.476052625	2.062888884	0.452795713	11.5352	8.24E-29	3.02E-28	grey	-0.329737285	2.47E-05	GO:0016788		ATG35140.1	GDSL-like Lipase/Hydrolase superfamily protein	GDSL esterase/lipase	
Sapur.004G070800.2	35.954066	0.698418025	0.062716506	11.13611	8.37E-29	3.07E-28	grey	0.133193264	0.096314754	GO:0005737;GO:0000045		ATG20480.2	AT3G8C	Ubiquitin-like superfamily protein	gabaA(c) receptor-associated protein, putative
Sapur.010G203700.1	4.373948881	0.703268021	0.153068825	-11.1276	9.21E-29	3.37E-28	grey	0.078548531	0.32814487			ATG18860.1	Ubiquitin-specific protease family C19-related protein	transmembrane protein, putative	
Sapur.003G206800.1	22.88428868	1.507797128	0.125568124	11.1082	9.96E-29	3.63E-28	grey	0.523131394	1.98E-12	GO:0004872;GO:0000166		ATG73140.1	Rhodanese/cyanase family protein / hydroxacid dehalogenase-like hydrolase family protein	calcium-transporting ATPase	
Sapur.010G156200.1	6.296000542	4.956580885	0.447017187	11.08812	1.43E-28	5.20E-28	grey	0.31378526	6.31E-05	GO:0005114;GO:0020037;GO:0016705;GO:0005506		ATG12740.1	CYP87A2	cytochrome P450, family 87, subfamily A, polypeptide 2	
Sapur.006G191000.1	149.9426183	0.465341498	0.042416276	11.05272	2.13E-28	7.74E-28	grey	0.107795456	0.179378722			ATG42480.1			TGN-related, localized SYP41-interacting protein, putative
Sapur.003G119900.1	4.862600955	1.998273102	0.181037568	11.03953	2.46E-28	8.95E-28	grey	0.260518621	0.00098318			ATG01630.1	Sec14p-like phosphatidylinositol transfer family protein	polyphosphoinositide-binding protein Sfh3p	
Sapur.010G154500.1	3.118241151	1.479988634	0.134[illegible]2[illegible]	11.0196	4.53E-28	1.67E-28	grey	0.457419134	1.72E-09	GO:0006508;GO:0004252		ATG26190.1	subtilase family	cucumisin, putative	
Sapur.006G207100.1	32.58868823	0.078350073	0.084656393	10.94842	6.76E-28	2.42E-27	grey	0.447676059	4.14E-09			ATG11420.1	Protein of unknown function, DUF642	plant/F18G18.200 protein	
Sapur.003G045200.1	5.291117867	4.402977582	0.402276906	10.94483	7.03E-28	2.51E-27	grey	0.382872622	2.79E-06	GO:0005515		ATG20400.1	ARM repeat superfamily	NA	
Sapur.003G175300.4	7.16937686	1.198756617	0.109560024	-10.9416	7.29E-28	2.62E-27	grey	-0.484841755	1.24E-10			ATG05120.1	Nucleoporin, Nup133/Nup155-like	nucleoporin	
Sapur.006G094500.1	3.348045837	2.152668444	0.2[illegible]8[illegible]9	10.9258	8.68E-28	3.11E-27	grey	-0.515750507	8.81E-13	GO:0016021;GO:0016020;GO:0022857		ATG16570.1	rodulin MRN1;PIN-like transmembrane family protein	rodulin MRN1;PIN-like protein SNG4	sugar-induced protein SNG4
Sapur.007G082000.1	58.50793424	1.622708218	0.149525077	10.91929	9.32E-28	3.35E-27	grey	0.560621191	2.25E-14	GO:0008168		ATG15125.1	5-adenosyl-L-methionine-dependent methyltransferases superfamily protein	SAM-dependent carboxyl methyltransferase	
Sapur.008G138400.4	5.972186563	1.725715646	0.158128234	-10.9134	9.95E-28	3.57E-27	grey	0.001467606	0.985465706	GO:0008610		ATG25510.1	Cyclophorase family acyl-phosphoglycl synthase	NA	
Sapur.003G068800.1	14.29709322	1.302686779	0.119534641	-10.8867	1.12E-27	4.08E-27	grey	-0.025271148	0.753846656			ATG22120.1	prenylated rab acceptor 1 family protein	phenylcoumaran benzylic ether reductase-like protein	
Sapur.015G143300.1	15.26710828	4.455181876	0.591158222	10.88572	1.35E-27	4.82E-27	grey	0.262132872	0.000912094	GO:0006355;GO:0005634;GO:0003700;GO:0046983;GO:0003677	PI	ATG02040.1	K-box region and MADS-box transcription factor family protein	NA	
Sapur.003G139200.1	3.574323949	1.809306685	0.166066079	-10.8364	1.21E-27	8.24E-27	grey	-0.511032201	7.94E-12			ATG42460.1		kinesin-like protein, putative	
Sapur.003G112800.1	22.06551523	2.506612239	0.231463517	10.82839	2.53E-27	8.97E-27	grey	0.469676033	5.45E-10	GO:0016758;GO:0008152		ATG46130.1	UGT73B3	UDP-glucosyl transferase 73B3	UDP-glucose glucosyltransferase
Sapur.006G148500.1	2.614779994	1.624281485	0.151794288	10.81477	2.84E-27	1.00E-26	grey	0.457419134	1.72E-09			ATG26190.1			cucumisin, putative
Sapur.007G084700.4	22.63014579	0.801877501	0.074248287	-10.7999	3.44E-27	1.22E-26	grey	-0.206515606	0.009446633			ATG10250.1	DOT1	Phosphotic-responsive NPH3 family protein	root phototropism protein
Sapur.015G246800.1	155.8418849	0.854608897	0.1724455[illegible]	-10.7668	4.94E-27	1.74E-26	grey	-0.515050207	8.77E-12	GO:0016758;GO:0008152		ATG61550.1	Protein of unknown function (DUF231)	UDP-glucose flavonoid 7-O-glucosyltransferase	
Sapur.003G141500.1	558.7623883	0.376145837	0.034946763	10.76223	5.19E-27	1.83E-26	grey	-0.251391706	0.001459169	GO:0005515;GO:0003723		ATG62040.2	CUM2;EIF4G	eukaryotic translation initiation factor 4G	eukaryotic translation initiation factor 4G
Sapur.003G188100.1	106.3663201	0.54283849	0.050485347	10.7372	5.25E-27	1.85E-26	grey	0.008519179	0.916846056	GO:0005515		ATG64280.1	NPR1;NIM1;NPR1_SAI1	regulatory protein NPR1	regulatory protein NPR1
Sapur.018G049200.1	2.237515185	-4.005137902	0.372927999	-10.7387	6.63E-27	2.31E-26	grey	-0.437188161	1.03E-08	GO:0003170;GO:0009058		ATG62620.1	ACS7;ATACS7	1-amino-cyclopropane-1-carboxylate synthase 7	1-aminocyclopropane-1-carboxylate synthase
Sapur.016G079900.1	20.32810001	1.100076804	0.105228234	10.75929	6.68E-27	2.36E-26	grey	0.54512176	1.57E-13			ATG10120.1			
Sapur.008G041000.1	8.925178875	1.813881284	0.169072344	10.7371	7.58E-27	2.66E-26	grey	0.575551115	1.38E-15			ATG04740.1	ACT domain-containing protein	NA	
Sapur.15W0071000.1	14.02548845	2.978807553	0.2685305[illegible]	10.72465	7.80E-27	2.74E-26	grey	0.49090602	6.64E-11		FIM2	ATG35700.1	Fimbrin-like protein 2	Fimbrin-like protein 2	NA
Sapur.013G020000.1	50.77164907	2.346631134	0.218848162	10.72264	7.97E-27	2.80E-26	grey	0.544457623	1.61E-13	GO:0004648;GO:0006672		ATG27730.1	Protein kinase family protein	Serine/Threonine-kinase domain protein	
Sapur.15W0067000.1	120.0738156	0.559060743	0.052176881	10.71473	8.68E-27	3.04E-26	grey	0.253383883	0.001365059	GO:0006872		ATG48440.1	Zinc finger C-x8-C-x5-C-x3-H type family protein	zinc finger CCCH domain protein, putative	
Sapur.005G096100.1	1.485747072	1.033305609	0.10017582	10.71383	8.77E-27	3.07E-26	grey	0.428815629	2.08E-08	GO:0046983		ATG47060.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH85, putative	
Sapur.015G071300.1	117.3070058	0.965622491	0.178017631	10.70469	9.68E-27	3.39E-26	grey	0.516862652	4.16E-12			ATG62880.1	ATOPE14-4	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	hypothetical protein
Sapur.003G170600.1	6.752658	0.825408025	0.164077514	-10.6879	1.04E-26	3.64E-26	grey	-0.451798482	1.04E-09			ATG35580.1	Plant protein of unknown function (DUF247)	NA	
Sapur.016G300000.4	6.948726495	1.469809465	0.137559818	-10.6939	1.08E-26	3.80E-26	grey	-0.519860551	3.01E-12			ATG40820.1		transcription factor, putative	
Sapur.011G130300.1	2.755375572	4.356456336	0.407299442	10.69131	1.12E-26	3.91E-26	grey	0.421330772	3.91E-08	GO:0005514;GO:0050660;GO:0016491		ATG44440.1	FAD-binding Berberine family protein	NA	
Sapur.013G060000.1	28.93716169	0.845317552	0.131845517	10.68046	1.26E-26	4.38E-26	grey	0.509297565	9.66E-12			ATG42720.4	Calcineurin-like metallo phosphoesterase superfamily protein	component of high affinity nitrate transporter	
Sapur.15W0132400.1	6.426690723	-1.758136699	0.162828209	-10.6747	1.34E-26	4.67E-26	grey	-0.173204701	0.032245384			ATG45030.1	Trypsin family protein	peptidase, trypsin-like serine and cysteine protease	
Sapur.016G230300.1	15.64370777	0.524538844	0.0[illegible]9[illegible]1	10.6364	1.43E-26	4.96E-26	grey	0.510660846	9.56E-12			ATG46190.1	AtRH9;RH9;AtDEAD27	replication factor-RFC1 interacting protein family	replication factor-RFC1 interacting protein family
Sapur.003G102300.1	147.6227999	1.126068077	0.105597922	10.6373	1.50E-26	5.24E-26	grey	0.368602297	2.03E-06	GO:0005515;GO:0008270	RIN2	ATG52530.2	RPM1 interacting protein 2	RPM1 interacting protein 2	E3 ubiquitin protein ligase RIN3
Sapur.003G145200.1	4.103256759	3.680363462	0.31833847	10.6303	2.16E-26	7.26E-26	grey	0.161880991	0.040168771	GO:0005515;GO:0008270		ATG79790.1			CENP-S-associating nucleoprotein 3
Sapur.009G079300.1	170.7060088	0.117404032	0.190306743	-10.6191	2.43E-26	8.42E-26	grey	-0.436048214	1.14E-08			ATG15530.1			hypothetical protein
Sapur.003G161200.1	10.08863	0.961788814	0.1853456[illegible]	-10.6084	2.78E-26	9.61E-26	grey	-0.448719069	2.19E-09	GO:0004648;GO:0005524;GO:0006472	RLK1	ATG60600.1	receptor-like protein kinase 1	G-type lectin S-receptor-like Serine/Threonine-kinase RLK1, putative	G-type lectin S-receptor-like Serine/Threonine-kinase RLK1, putative
Sapur.007G128400.1	399.5878897	1.875257513	0.176974042	10.596	3.11E-26	1.07E-25	grey	0.512117091	7.11E-12	GO:0015114;GO:0016491;GO:0008270		ATG26320.1	Zinc-binding dehydrogenase family protein	NADP-dependent alkenal double bond reductase	
Sapur.006G087300.1

Sapur.005G123700.1	1.28288355	1.94538945	0.31278783	9.417232	4.63E-21	1.41E-20	grey	0.516424338	4.42E-12				NA
Sapur.016G146800.1	6.56055682	2.39625345	0.148307386	-9.41447	4.75E-21	1.45E-20	grey	-0.08077427	0.314578989				hypothetical protein
Sapur.005G307700.1	6.52884889	4.41891781	0.152908425	9.40255	5.33E-21	1.62E-20	grey	0.123964022	1.89E-12	GO:0016758;GO:0008152	ATSG36138.1	UGT73B3	UDP-glucosyl transferase 73B3
Sapur.010G058000.1	19.88640313	-1.18344811	0.125695461	-9.3995	5.48E-21	1.67E-20	grey	-0.457846858	1.65E-09		ATSG19260.1		Pentatricopeptide repeat (PPR) protein
Sapur.010G082500.1	7.13287078	3.52379703	0.163305472	-9.39231	5.87E-21	1.78E-20	grey	-0.021713632	0.787334236	GO:0006468;GO:0005634;GO:0004672;GO:0005515	ATSG31554.1	SPA3	SPA1-related 3
Sapur.007G013000.1	6.3081701	-4.46274204	0.156050673	-9.38973	6.02E-21	1.83E-20	grey	-0.043762001	0.583608727		ATSG51148.1		Protein of unknown function (DUF3253)
Sapur.002G042900.4	40.77632288	0.018090686	0.065828899	-9.38955	6.04E-21	1.83E-20	grey	-0.432851098	1.92E-08		ATSG06690.1		NADP(H)-linked oxidoreductase superfamily protein
Sapur.001G022200.1	6.90896419	1.45152631	0.152542427	9.384647	6.12E-21	1.92E-20	grey	0.532263448	7.46E-12	GO:0048544;GO:0006488;GO:0004672	ATSG11340.1		5-oxo-ecic protein kinase family protein
Sapur.009G108700.4	53.82718293	0.73451815	0.078352875	9.374689	6.95E-21	2.11E-20	grey	0.410571268	9.13E-08		ATKG35110.3		Arabidopsis phosphoglycan-like protein (PEARL) 4[Tomb]
Sapur.016G044400.2	5.45303765	1.34035997	0.136957963	-9.3083	7.25E-21	2.2E-20	grey	-0.48547607	1.66E-10	GO:0006355;GO:0005739;GO:0003690	ATMG00810.1		Mitochondrial transcription termination factor family protein
Sapur.004G066700.1	159.8697226	6.71797628	0.076670331	-9.36213	7.81E-21	2.37E-20	grey	-0.27706152	0.000463319	GO:0006310;GO:0006281;GO:0003910;GO:0006307;GO:0005524	ATLG62730.1	ATLIG6;LIG6	DNA LIGASE 6
Sapur.009G108900.1	1.47162766	2.98201848	0.31840097	9.36021	7.91E-21	2.36E-20	grey	0.502202227	2.11E-11		ATSG24060.1		Plant self-incompatibility protein S1 family
Sapur.006G136900.1	81.75269522	2.73635492	0.185595381	9.355593	8.31E-21	2.52E-20	grey	0.304866689	3.06E-07	GO:0016788	ATSG45670.1		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.006G258100.1	273.7185486	4.65054219	0.175032098	9.3528	8.58E-21	2.60E-20	grey	0.508838134	1.26E-11	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATMG01360.1	CYP716A1	cytochrome P450 family 716, subfamily A, polypeptide 1
Sapur.016G035400.1	3.65817955	2.11269214	0.226159841	9.33963	9.67E-21	2.92E-20	grey	0.484822272	1.34E-10	GO:0046872;GO:0000166	ATMG00330.1	AHA7;HA7	H(+)-ATPase 7
Sapur.016G034800.2	10.31552762	1.05231888	0.105835043	-9.33031	1.05E-20	3.29E-20	grey	-0.413879744	8.35E-08		ATSG20203.1		C2H2-like zinc finger protein
Sapur.010G103800.1	3.61597661	3.01298087	0.323038279	9.32698	1.08E-20	3.29E-20	grey	0.464328559	9.30E-10		ATSG13510.1		Protein of unknown function (DUF1262)
Sapur.010G295200.1	31.62714674	0.803082102	0.086114921	9.325702	1.10E-20	3.33E-20	grey	0.545399379	1.51E-13	GO:0055085;GO:0016021	ATSG76532.2		Auxin efflux carrier family protein
Sapur.010G137305.1	65.54948615	1.25164572	0.142333345	9.319353	1.17E-20	3.52E-20	grey	0.501369091	2.26E-11	GO:0016758;GO:0008152	ATCG02580.1		UDP-Glycosyltransferase superfamily protein
Sapur.007G051200.1	9.52897476	1.31138479	0.140741062	9.317598	1.19E-20	3.59E-20	grey	0.544238862	1.73E-13	GO:0003677;GO:0006355;GO:0003700	ATCG02850.1	AtbZIP9;bZIP9	basic leucine-zipper 6
Sapur.005G132800.1	27.94670376	1.36210397	0.144526119	9.311088	1.27E-20	3.81E-20	grey	0.4878681	8.91E-10		ATCG75250.1	ATRUL;RL6;RDM3	RAD-like 6
Sapur.002G172400.1	1.18972884	2.36149602	0.302342131	9.309242	1.29E-20	3.88E-20	grey	0.50662095	1.28E-11		ATMG04310.1		Calcium-binding EF-hand family protein
Sapur.002G021400.1	6.37182059	1.66202947	0.178351719	9.3365	1.36E-20	4.08E-20	grey	0.519583652	4.71E-12				NA
Sapur.004G099200.1	2.46356475	0.08831283	0.439617757	9.299696	1.41E-20	4.24E-20	grey	0.315277837	5.77E-05		ATG30900.1	TBL43	TRICHOME BIREFRINGENCE-LIKE 43
Sapur.004G131900.1	35.60262456	0.77032098	0.190408882	9.29742	1.44E-20	4.33E-20	grey	-0.472688042	4.16E-10	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATG45840.1	CYP86A4	cytochrome P450, family 86, subfamily A, polypeptide 4
Sapur.003G125500.1	122.9913463	0.24237193	0.121123346	9.286427	1.45E-20	4.37E-20	grey	0.514857338	5.36E-12		ATG14090.1		hypothetical protein
Sapur.006G170800.2	86.5913333	0.57004588	0.061392089	9.29021	1.54E-20	4.63E-20	grey	0.228424716	0.004655974		ATG11530.1		Vacuolar protein sorting 55 (VPS55) family protein
Sapur.010G200800.1	1243.98812	2.78620129	0.070887906	9.28667	1.56E-20	4.68E-20	grey	0.048523275	0.541179993	GO:0006461;GO:0046933;GO:0015986;GO:0000275	ATG15010.1		ATP synthase subunit epsilon, mitochondrial
Sapur.017G027900.1	59.8448208	-0.97185101	0.076513739	-9.28528	1.63E-20	4.86E-20	grey	-0.5592244	2.69E-14	GO:0048468;GO:0005634;GO:0004672	ATCG82880.1	PRSK	PRS-like receptor kinase
Sapur.016G238000.1	14.22615324	0.07408844	0.11588592	-9.2836	1.65E-20	4.90E-20	grey	-0.003372047	0.966577078	GO:0008017;GO:0000910	ATCG02230.1	ATMAPRS-1;MAPRS-1	microtubule-associated protein MAPRS-1a
Sapur.012G105200.1	2.00217672	2.29809571	0.355466618	-9.28058	1.69E-20	5.06E-20	grey	-0.35228544	6.91E-06	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATCG61550.1	CYP76C4	cytochrome P450, family 76, subfamily C, polypeptide 4
Sapur.002G142800.1	20.76630715	0.76315552	0.085486699	9.276262	1.71E-20	5.17E-20	grey	-0.3481231	7.80E-06	GO:0016024;GO:0006470;GO:0004722	ATCG31481.1		Protein phosphatase 2C
Sapur.T100000.3	1.97423102	2.08604034	0.224838378	9.277955	1.73E-20	5.19E-20	grey	0.182642244	0.022404228		ATCG55915.1		zinc ion binding protein, putative
Sapur.012G110200.5	53.92629133	0.64017283	0.068032588	9.273553	1.80E-20	5.40E-20	grey	-0.081608804	0.339509942	GO:0006468;GO:0005634;GO:0004672	ATCG00720.1	EMB871;MAPK9;K9;YDA	Serine/Threonine kinase family protein
Sapur.004G095300.1	3.63965827	4.92234532	0.530958873	9.270485	1.85E-20	5.56E-20	grey	0.401211967	1.91E-07		ATKG20030.1		F-box family protein with a domain of unknown function (DUF295)
Sapur.014G123700.1	137.0677934	0.88274024	0.107111149	9.268079	1.91E-20	5.68E-20	grey	-0.5610127	0.44842342		ATKG31162.2		EN/TW/Y/H family protein
Sapur.005G040600.1	34.62265174	0.81867429	0.087856568	9.263592	1.98E-20	5.92E-20	grey	0.545674196	1.32E-13				NA
Sapur.002G085900.1	12.88824688	1.16958394	0.126308707	9.259767	2.05E-20	6.14E-20	grey	0.541492994	2.40E-13	GO:0006270;GO:0006276;GO:0005634;GO:0003677	ATMG00320.1	CSDP1	cold shock domain protein 1
Sapur.004G291600.1	266.8283221	0.49134142	0.053285451	9.254765	2.12E-20	6.34E-20	grey	0.560802285	2.2E-14	GO:0016901;GO:0006350;GO:0003677	ATCG00510.1	AGLB;FUL	MADS-box transcription factor FUL-like protein
Sapur.001G088900.1	5.88187744	1.67106889	0.180699951	9.252559	2.19E-20	6.56E-20	grey	0.460377416	1.31E-09				NA
Sapur.004G227700.1	1.60908219	3.57787664	0.430077482	9.246944	2.26E-20	6.75E-20	grey	0.440182107	7.98E-09		ATKG31260.1		Protein of unknown function (DUF761)
Sapur.15WG071100.1	131.5308825	2.43167444	0.261415053	9.241792	2.42E-20	7.25E-20	grey	0.458822969	1.53E-09	GO:0005515	ATMG36700.2	ATFIM1;FIM1	Fimbrin 1
Sapur.010G016400.1	19.98543366	0.78127025	0.091802026	9.240738	2.43E-20	7.28E-20	grey	-0.064221734	0.240452583	GO:0055114;GO:0016491;GO:0008152;GO:0051930;GO:0005887;GO:0016638;GO:000663	ATMG01240.2	GLT1	NADH-dependent glutamate synthase 1
Sapur.001G143300.1	1.00167634	2.58643931	0.280217982	-9.23047	2.68E-20	8.05E-20	grey	-0.563372369	1.61E-14	GO:0055114;GO:0016491	ATCG27780.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.005G280600.1	49.06228369	0.90337724	0.097906512	9.225125	2.83E-20	8.45E-20	grey	-0.492476562	5.70E-11		ATCG38720.1		cyclase/dehydrase
Sapur.014G042700.1	1.3410068	3.56665561	0.386620063	9.224989	2.84E-20	8.46E-20	grey	0.485296637	1.12E-10		ATSG46030.1		transcription elongation factor-like protein
Sapur.006G088900.1	15.43824444	0.86269139	0.093545473	9.22496	2.84E-20	8.46E-20	grey	-0.238285855	0.016026119	GO:0006468;GO:0004672	ATG28780.1		Protein kinase domain protein
Sapur.009G022800.1	3183.314112	0.75541027	0.079720326	9.224896	2.84E-20	8.47E-20	grey	-0.568747556	7.81E-15	GO:0006872	ATMT2-LATMT-4;MT2A	metallothionein 2A	metallothionein-like protein type 2
Sapur.013G085300.2	5.30974242	-1.36636241	0.148136796	-9.22365	2.87E-20	8.57E-20	grey	-0.193503988	0.051170293	GO:0055114;GO:0008677;GO:0005975;GO:0004367;GO:0003311;GO:0006072	ATSG40690.1	GLYL;SFD1	NAD-dependent glycerol 3-phosphate dehydrogenase family protein
Sapur.003G130600.1	11.61594471	0.97431048	0.105281451	9.204358	3.44E-20	1.01E-19	grey	0.648874178	0.153833224	GO:0010991;GO:0006350;GO:0003677	ATSG45190.1		Cyclin family protein
Sapur.006G197700.1	143.8217856	0.66779534	0.072558675	9.20329	3.47E-20	1.03E-19	grey	0.549094548	9.61E-14		ATSG52630.1		Exostosin family protein
Sapur.006G148700.1	4.37572796	0.48807607	0.161746068	9.200415	3.57E-20	1.06E-19	grey	0.538029748	1.26E-13	GO:0006468;GO:0005634;GO:0004672	ATG50640.1		Protein kinase superfamily protein
Sapur.005G095700.1	4.23485258	1.93167384	0.210540344	-9.19623	3.71E-20	1.10E-19	grey	-0.545562861	1.48E-13	GO:0005524	ATG43910.1		F-box containing nucleoside triphosphate hydrolases superfamily protein
Sapur.005G035500.1	13.78164794	1.38527025	0.126705488	9.18369	3.80E-20	1.14E-19	grey	-0.457509761	1.77E-09	GO:0016021;GO:0005515	ATG41460.2	ARLR9;BLR9	receptor like kinase, putative
Sapur.002G053300.1	1.36461229	2.76919846	0.299124916	-9.19054	3.91E-20	1.16E-19	grey	-0.531519546	2.93E-13	GO:0016021;GO:0016020;GO:0022857	ATG45650.2		nodulin MtN21 /EamA-like transporter family protein
Sapur.005G085500.1	11.23816221	0.67536451	0.073573384	9.185555	4.11E-20	1.22E-19	grey	0.132541704	0.09761767	GO:0005515	ATG45403.1	ATXR7;SDG25	SET domain protein 25	histone-lysine N-methyltransferase SETD18, putative
Sapur.003G095300.1	73.96463791	1.04825157	0.114362516	9.166039	4.91E-20	1.45E-19	grey	0.460132632	1.34E-09		ATKG23493.1		hypothetical protein
Sapur.004G089600.1	1.35860015	2.68458228	0.293539349	9.15187	5.63E-20	1.67E-19	grey	0.518730846	4.5E-13				NA
Sapur.005G060600.3	7.10671992	1.05146764	0.110979956	9.150577	5.66E-20	1.67E-19	grey	-0.113511556	0.156772055		ATG10630.1	ARFASF;ATARFASF	ADP-ribosylation factor ASF	ADP-ribosylation factor/Arf/Sar-like (Arf) small GTPase family protein
Sapur.15WG154900.1	6.73665479	1.70533443	0.186404449	-9.14964	5.71E-20	1.69E-19	grey	-0.48197665	1.65E-10		ATG18670.1		Ankyrin repeat family protein
Sapur.006G200400.1	973.5678371	0.34205597	0.037439159	9.139189	6.84E-20	2.02E-19	grey	-0.12858786	0.188494623	GO:0016021	ATG25727.1		Sulfite exporter TauE/SafE family protein	sulfite exporter TauE/SafE
Sapur.013G094100.1	5.10709234	1.45619008	0.157348356	-9.12981	6.86E-20	2.03E-19	grey	-0.516745265	4.27E-12	GO:0016021	ATCG22650.1		SNARE associated Golgi protein family	SNARE associated protein
Sapur.004G127300.1	154.7756113	3.34034795	0.364853118	9.1283	6.96E-20	2.05E-19	grey	0.538856347	1.32E-13	GO:0005085	ATSG15152.1	ATYL3;YSL3	YELLOW STRIPE like 3
Sapur.008G018800.1	62.84009444	0.98150482	0.107557662	9.121679	7.40E-20	2.18E-19	grey	-0.542593732	2.14E-13		ATSG58230.2	ATGAT1;GAT1	Transmembrane amino acid transporter family protein	amino acid transporter, putative
Sapur.007G069500.1	12.4401161	0.57182937	0.126314156	-9.11848	7.73E-20	2.28E-19	grey	-0.547637977	1.52E-13		ATCG32120.1	ATPLIP1	Ipase 1	NA
Sapur.T161400.1	36.09214427	0.77074179	0.084568835	9.113815	7.95E-20	2.34E-19	grey	0.555613001	7.07E-14	GO:0006468;GO:0004672;GO:0005524	ATG40030.1		Protein kinase superfamily protein
Sapur.005G094300.1	1.45008842	2.06358589	0.244430526	9.1014	8.62E-20	2.54E-19	grey	-0.475621796	5.6E-10	GO:0005515	ATG58192.2		receptor like protein 9
Sapur.T085700.1	19.52162615	-1.17826759	0.129423823	-9.10416	8.68E-20	2.56E-19	grey	-0.546684166	1.29E-13		ATG15230.1	ATLIP1;LIP1	Ipase 1	NA
Sapur.016G051100.1	65.0892667	0.97836504	0.077810021	-9.09728	9.26E-20	2.72E-19	grey	-0.144471425	0.075311978	GO:0008270	ATG15080.1		DHHC-type zinc finger family protein	zinc finger protein
Sapur.009G130800.2	2.83630875	2.97794052	0.391182223	9.09163	9.75E-20	2.87E-19	grey	-0.218591766	0.005952305		ATKG38710.2		glycine-rich protein	plant-specific eukaryotic initiation factor 4B
Sapur.T179900.1	0.72873294	7.58631481	0.285055177	9.074762	1.14E-19	3.34E-19	grey	0.578829054	2.02E-15				NA
Sapur.005G149900.1	11.37419876	1.20958136	0.133431361	9.0604	1.24E-19	3.64E-19	grey	0.527775281	1.21E-12	GO:0030170;GO:0019752;GO:0016831	ATG43710.1	emb1075	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	4-oxo decarboxylase
Sapur.012G049400.1	36.20408138	0.26307833	0.03157441	9.05471	1.37E-19	4.01E-19	grey	0.539123836	2.20E-13	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATG50040.2		Leucine-rich receptor-like protein kinase family protein	leucine-rich receptor-like kinase
Sapur.003G227500.1	48.37169944	0.07835903	0.01911887	9.0455	1.37E-19	4.02E-19	grey	0.512064647	8.38E-12		ATG60460.1		GRAM domain family protein	H-GAM; GEM dynamin protein
Sapur.008G085600.1	20.00267823	0.75533656	0.081508152	9.047388	1.46E-19	4.28E-19	grey	0.572926709	4.48E-15	GO:0016988;GO:0006032;GO:0004568	ATG16920.1	ATCTL2;CTL2	chitinase-like protein 2	NA
Sapur.007G039100.5	1.05724265	3.31382794	0.388012022	9.02425	1.61E-19	4.80E-19	grey	-0.331378791	2.21E-05	GO:0006468;GO:0005737;GO:0005524;GO:0004832;GO:0000166;GO:0006418;GO:0004814	ATG62247	EMB2247	ATP binding cassette ligase;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases	valyl-tRNA synthetase
Sapur.012G093000.1	8.35009639	1.78858304	0.192533865	9.031023	1.70E-19	4.97E-19	grey	0.431727224	1.64E-08		ATG11480.1		eukaryotic translation initiation factor-related	translation initiation factor-like protein, putative
Sapur.008G042900.1	16.71179984	0.81544025	0.090386427	9.021711	1.85E-19	5.41E-19	grey	0.524449714	1.79E-12		ATG26055.1			hypothetical protein
Sapur.009G067300.1	64.78174815	-0.57497426	0.081466644	9.010681	1.98E-19	5.54E-19	grey	0.54857273	5.8E-13		ATG19660.1			NA
Sapur.004G166100.1	2.17435092	2.25473846	0.250337758	9.006704	2.12E-19	6.19E-19	grey	0.530485022	8.95E-13		ATG01750.2		Protein of unknown function (DUF567)	
Sapur.014G022300.1	0.80882524	2.07781001	0.230287408	9.003482	2.18E-19	6.37E-19	grey	0.493880932	4.66E-11					NA
Sapur.012G082100.1	4.75814974	1.87875561	0.208712193	9.001658	2.22E-19	6.48E-19	grey	0.474556538	1.41E-10	GO:0006355;GO:0003700	ATG61890.1		Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.005G094500.1	6.27350068	1.1038169	0.122615415	8.9925	2.24E-19	6.54E-19	grey	0.508539541	3.65E-12		ATKG17870.1	PYR1;RCAR11	Polyketide cyclase/dehydrase and lipid transport superfamily protein	abscisic acid receptor
Sapur.010G035000.1	15.4468847	1.65237557	0.183760208	8.991993	2.43E-19	7.07E-19	grey	0.508501191	1.05E-11	GO:0055114;GO:0016616;GO:0060694;GO:0003854	ATC01LCCR;LIR4	ATCCR;LCCR;LIR4	cinnamoyl coa reductase 1	cinnamoyl CoA reductase
Sapur.008G000300.1	261.1008243	0.57887919	0.064377708	8.99192	2.48E-19	7.08E-19	grey	0.414323177	6.87E-08		ATG45180.1	GAMMA-CA1	gamma carbonic anhydrase, putative	gamma carbonic anhydrase, putative
Sapur.009G077400.1	2.07282457	2.74245683	0.304696228	8.991781	2.43E-19	7.09E-19	grey	0.427778819	2.26E-08	GO:0016758;GO:0008152	ATG43131.1	UGT73B3	UDP-glucosyl transferase 73B3	UDP-glucosyltransferase, putative
Sapur.010G056000.3	11.52569709	0.88824346	0.098818429	8.98863	2.52E-19	7.26E-19	grey	0.457171166	5.6E-10		ATG62770.3	AKR2;Ub	Transducin/WD40 repeat-like superfamily protein	Kib repeat phosphoinositide-interacting protein
Sapur.010G033700.1	2.78357466	1.94584001	0.21905699	8.975015	2.83E-19	8.24E-19	grey	0.483498792	1.42E-10					NA
Sapur.008G042900.1	3.63805126	2.16950720	0.239539845	8.972766	2.89E-19	8.40E-19	grey	0.46882158	6.38E-10		ATG16050.1		Cysteine/Histidine-rich C1 domain family protein	DC1; C1-like protein, putative
Sapur.003G210000.2	2.07189727	-1.54782809	0.170152248	-8.96379	3.14E-19	9.11E-19	grey	-0.511389757	2.26406021	GO:0006468;GO:0004672	ATG62610.1	CRN;SOL2	Protein kinase superfamily protein	LRR receptor-like kinase
Sapur.15WG031800.1	87.82104985	-0.07131664	0.105555592	-8.9608	3.23E-19	9.35E-19	grey	-0.510198968	8.76E-12	GO:0006468;GO:0005524;GO:0004672	ATG68920.2		Protein kinase superfamily protein	
Sapur.T141100.1	0.71061924	2.54206358	0.28395514	8.95233	3.48E-19	1.01E-18	grey	0.509405771	5.47E-13		ATG58721.1			hypothetical protein
Sapur.006G277000.1	4.42048568	3.16481491	0.337127208	8.943602	3.86E-19	1.12E-18	grey	0.584601988	8.72E-16					NA
Sapur.003G018800.1	86.71581228	0.87867448	0.098346918	8.936609	4.00E-19	1.16E-18	grey	0.554614992	4.98487711		ATG55150.1	ATMYB123;ATTT2;MYB123	Duplicated homeodomain-like superfamily protein	MYB transcription factor R2R3-like protein
Sapur.009G088300.1	87.48883417	0.44125078	0.049494945	8.91331	4.86E-19	1.40E-18	grey	0.518042409	1.56E-12		ATG5191.1			transmembrane protein, putative
Sapur.015G301000.1	67.85287075	0.97331432	0.109149978	8.913543	4.94E-19	1.43E-18	grey	0.528003881	2.77E-12	GO:0016192;GO:0006904	ATSLY1	Sec1/munc18-like (SM) proteins superfamily	Sec1/munc18-like (SM) proteins	Sec1 family transporter SLY1
Sapur.010G200100.1	2.43931314	0.96182886	0.123431051	8.91304	4.97E-19	1.43E-18	grey	-0.553534778	1.56E-14		ATG14460.1		LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.015G423500.1	218.0501682	0.62596034	0.07202512	8.910964	5.06E-19	1.46E-18	grey	0.017811201	0.824774869		ATG46430.1			ATP synthase 6 kDa subunit
Sapur.014G027300.1	8.15464193	2.06990135	0.230335358	8.902218	5.57E-19	1.61E-18	grey	0.460232877	1.32E-09	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATG19370.1	CYP82C2	cytochrome P450, family 82, subfamily C, polypeptide 2	cytochrome P450 family protein
Sapur.005G073800.1	2.77945619	1.32315763	0.163139688	8.866486	6.79E-19	1.96E-18	grey	0.367513172	2.25E-06	GO:0016787	ATMT07ZLATN1;DX2_NUDT7	nudix hydrolase 7	Nudix hydrolase family	
Sapur.008G038300.1	2.20863744	1.66261006	0.186769134	-8.88938	6.15E-19	1.77E-18	grey	-0.309667621	7.93E-05	GO:0005515	ATG39480.1		F-box family protein	F-box plant protein
Sapur.016G009900.1	157.9014008	1.36435765	0.142368083	8.88512	6.34E-19	1.84E-18	grey	-0.516774683	2.52E-12	GO:0005515;GO:0006468;GO:0004672	ATG44461.1		Leucine-rich receptor transmembrane protein kinase	NA
Sapur.006G182000.1	2.48545836	2.23633859	0.251743332	8.883377	6.49E-19	1.87E-18	grey	0.562569845	1.75E-14					NA
Sapur.016G038000.3	1.85755877	2.16545199	0.247225763	8.88073	6.64E-19	1.91E-18	grey	-0.511918834	7.36E-12	GO:0016020;GO:0009765	ATG45474.2	LHCA5	photosystem I light harvesting complex gene 5	light harvesting complex I chlorophyll-A/B binding protein LhcaS
Sapur.013G046300.1	10.10087924	-0.60337325	0.091717607	-8.88002	6.68E-19	1.92E-18	grey	-0.48014543	1.34E-10	GO:0016788	ATG29670.1		GDSL-like Lipase/Acylhydrolase superfamily protein	NA
Sapur.015G158500.1	1.38661232	2.67509125	0.301323184	8.87674	6.76E-19	1.93E-18	grey	-0.229673707	0.009001311	GO:0006508;GO:0004185	ATG17180.1	scpl10	serine carboxypeptidase-like 10	serine carboxypeptidase
Sapur.015G196100.1	1.12070928	2.95428615	0.330301867	8.874312	7.04E-19	2.02E-18	grey	0.493506077	5.13E-11					NA
Sapur.007G079400.1	3.17601692	-0.02615459	0.054331163	-8.86205	7.84E-19	2.26E-18	grey	-0.278646524	0.000496997		ATG64770.1	RGF9		transmembrane protein, putative
Sapur.015G182000.1	3.80845934	2.32464494	0.262233182	8.860449	7.97E-19	2.29E-18	grey	0.302941243	0.000115395		ATG35451.1			Protein of unknown function (DUF241)
Sapur.013G094200.4	5.59944261	1.38750457	0.134149926	8.848685	8.86E-19	2.54E-18	grey	0.049889007	0.534929464	GO:0048872	ATG31480.1	SGR2	shoot gravitropism 2 (SGR2)	shoot gravitropism 2 (SGR2) protein
Sapur.006G051500.1	17.07353806	0.92142554	0.104205054	8.841399	9.34E-19	2.68E-18	grey	0.459182931	5.56E-11	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATG20950.1	CYP705A32	cytochrome P450, family 705, subfamily A, polypeptide 32	cytochrome P450, family 705 protein
Sapur.016G157500.1	53.91101757	-2.06281914	0.233132407	-8.84145	9.45E-19	2.71E-18	grey	-0.193881616	0.337	GO:0008270;GO:0005515	ATG38140.1		RING/U-box superfamily family protein	RING-H2 zinc finger protein
Sapur.015G123400.1	254.3232168	0.57940571	0.065145294	8.838804	9.56E-19	2.74E-18	grey	0.492076252	4.16E-11	GO:0005515	ATG37920.2	APO2;emb3629	Arabidopsis thaliana protein of unknown function (DUF794)	NA
Sapur.015G054100.1	85.2583302	0.36277326	0.041042222	8.839003	9.66E-19	2.77E-18	grey	0.543022532	2.02E-13	GO:0006810;GO:0005783	ATG13580.2	LAG13	LAG1 longevity assurance homolog 3	
Sapur.15WG071200.1	0.86581854	2.95429618	0.339139688	8.836966	9.68E-19	2.78E-18	grey	-0.470636913	1.97E-11		ATG46600.1			transmembrane protein, putative
Sapur.010G017300.1	4.29794356	1.05809656	0.121622229	8.825699	1.09E-18	3.11E-18	grey	0.523828579	2.05E-12	GO:0006355;GO:0003700;GO:0005515	ATG35040.1	bZIP19	Basic-leucine zipper (bZIP) transcription factor family protein	bZIP transcription factor family protein
Sapur.006G090200.1	4.09817825	2.86950534	0.330006125	8.819319	1.13E-18	3.29E-18	grey	0.350730302	6.07E-08					NA
Sapur.003G146300.1	3.94866182	2.62897026	0.298327649	8.811386	1.23E-18	3.59E-18	grey	0.380836539	8.63E-07	GO:0042546;GO:0016020;GO:0008107	ATG03120.1	ATTT1;ATUT1;FT1;MUR2	fucosyltransferase 1	galactoside 2-alpha-L-fucosyltransferase, putative
Sapur.010G089300.3	2.80263732	1.85227757	0.209315617	8.800808	1.36E-18	3.88E-18	grey	0.463238226	9.93E-10	GO:0055085;GO:0016020;GO:0015297;GO:0015238;GO:0006855	ATG15160.1		MATE efflux family protein	MATE efflux family protein
Sapur.013G088100.10	13.46851294	0.83162023	0.094501168	-8.79604	1.41E-18	4.03E-18	grey	-0.513278636	1.64E-13		ATG02230.1		Uncharacterized protein (DUF2358)	thioredoxin F, putative
Sapur.015G202600.1	7.54081657	0.91830689	0.104236868	8.794042	1.44E-18	4.12E-18	grey	0.543146986	1.99E-13		ATG31950.1			NA
Sapur.15WG042300.2	0.67660454	-2.38188317	0.328192238	-8.78688	1.54E-18	4.38E-18	grey	-0.029783615	0.720456611		ATG37690.1		Protein of unknown function (duplicated DUF1399)	NA
Sapur.006G211900.1	101.4212226	0.05363647	0.074492976	8.78073	1.62E-18	4.63E-18	grey	-0.10595791	0.186581178	GO:0005091	ATKG32160.1		Phox (PX) domain-containing protein	phox (PX) domain protein
Sapur.015G096100.1	1.46091669	1.10318366	0.152107424	-8.7779	1.67E-18	4.75E-18	grey	-0.247588859	0.002374225	GO:0043565;GO:0006355;GO:0003700	ATG16850.1	ABR83;DPBF3	ABA-responsive element binding protein 3	bZIP transcription factor
Sapur.15WG039800.1	1.05345267	2.72628988	0.310684891	8.775558	1.70E-18	4.84E-18	grey	0.

Sapur.001G103100.1	4.030074213	1.77797475	0.212571701	8.362284	6.10E-17	1.66E-16	grey	0.491636847	6.22E-11				NA
Sapur.006G071800.2	67.22526261	6.583575561	0.069813712	-8.15904	6.32E-17	1.72E-16	grey	-0.223072055	0.005186988	GO:0008270	ATSG08320.1	DHHC-type zinc finger family protein	zinc finger protein, putative
Sapur.017G201100.1	12.60294077	1.307251303	0.102743883	8.354541	6.57E-17	1.79E-16	grey	-0.439862386	8.21E-09		ATSG08120.1	transmembrane protein, putative	transmembrane protein, putative
Sapur.016G288400.1	345.5432135	1.160408003	0.138917765	8.353201	6.64E-17	1.81E-16	grey	0.478832841	2.37E-10		ATSG19715.3	Mannose-binding lectin superfamily protein	short chain alcohol dehydrogenase, putative
Sapur.007G208800.1	135.7008021	0.831055883	0.099639685	8.350447	6.83E-17	1.86E-16	grey	0.293010112	0.000195078	GO:0005885;GO:0016020	ATSG04985.1	MSC1 like 2	mechanosensitive channel of small conductance-like protein
Sapur.15WG127600.1	37.60837984	1.487835949	0.178256655	8.346875	7.01E-17	1.90E-16	grey	0.545530313	1.49E-13	GO:0055114;GO:0016491;GO:0050664;GO:0004601	ATSG51060.1	ATB8CHIC_RBCHIC_RHD2	NADPH/respiratory burst oxidase protein D
Sapur.010G125100.1	42.94512569	1.477963543	0.177118524	-8.34449	7.11E-17	1.94E-16	grey	-0.485144231	1.20E-10		ATSG25481.1	HSP20-like chaperones superfamily protein	HSP20-like chaperones superfamily protein
Sapur.016G072600.4	5.215645213	1.565858517	0.187783035	8.340821	7.38E-17	2.00E-16	grey	-0.492867942	1.36E-10	GO:0009611;GO:0004867	ATSG38370.1	Serine protease inhibitor, potato inhibitor I-type family protein	Serine protease inhibitor, potato inhibitor I-type family protein
Sapur.003G200000.1	10.50463739	0.812714402	0.097524834	8.33341	7.85E-17	2.12E-16	grey	0.52988748	9.59E-13	GO:0022900;GO:0005747;GO:0005739	ATSG14450.1	NADH dehydrogenase (ubiquinone)	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 3-B
Sapur.006G057400.4	1.223104962	1.617946752	0.197405229	8.332029	7.95E-17	2.16E-16	grey	-0.108619658	0.119635652	GO:0009058;GO:0008824	ATSG38670.1	phosphoribosylaminoimidazole cyclase/phosphoribosylformylglycinamidine cyclase/phosphoribosylformylglycinamidine synthase family protein	ethanolamine-phosphate cytidylyltransferase
Sapur.010G026100.3	13.55405349	0.711656447	0.085406226	-8.33169	7.97E-17	2.16E-16	grey	-0.231609692	0.003115125	GO:0003677	ATSG31640.1	transcriptional factor B3 family protein	B3 DNA binding domain protein
Sapur.017G147900.1	3.976244491	2.748795816	0.329928416	8.331479	7.98E-17	2.17E-16	grey	-0.423208063	1.32E-08		ATSG35920.1	Protein of unknown function (DUF230)	NA
Sapur.014G038300.1	7.851782845	-3.067265824	0.368426384	-8.3253	8.41E-17	2.28E-16	grey	-0.347329461	8.32E-06		ATSG51160.1	Ankyrin repeat family protein	transmembrane protein, putative
Sapur.005G067900.1	145.6290844	0.712897122	0.086388184	8.319368	8.86E-17	2.40E-16	grey	-0.546077142	5.66E-13	GO:0015186;GO:0008324;GO:0015139;GO:0016892;GO:0009107	ATSG20660.1	Hypoxia responsive family protein	lipid synthase
Sapur.005G084300.1	53.58280911	2.600421305	0.312703361	8.31193	9.10E-17	2.47E-16	grey	-0.357055683	4.42E-06		ATSG52340.1	ABA2,ATABA2,ATSDR1,GINS	NAD(P)-binding Rossmann-fold superfamily protein	short chain alcohol dehydrogenase family protein
Sapur.017I230.1	87.81319456	0.804328843	0.077439346	8.31127	9.17E-17	2.51E-16	grey	-0.548798016	1.65E-13	GO:0009116	ATSG10700.1	PRS3	phosphoribosylpyrophosphate (PRPP) synthase 3
Sapur.016G282000.1	147.8228376	-1.181604723	0.142166156	-8.31143	9.46E-17	2.56E-16	grey	-0.398794722	2.30E-07		ATSG27030.1	FADA,FADA	fatty acid desaturase A
Sapur.006G136400.1	5.693352997	1.094458811	0.131609778	8.310263	9.51E-17	2.58E-16	grey	0.514614045	5.46E-12		ATSG50030.1	TOR	target of rapamycin
Sapur.016G027800.1	47.26358039	-1.761373201	0.211909257	-8.30447	1.01E-16	2.74E-16	grey	-0.620926222	7.01E-14	GO:0006468;GO:0005524;GO:0004672;GO:0003824	ATSG40860.1	protein kinase family protein / protein phosphatase 2C (PP2C) family protein	kinase and PP2C-like domain protein
Sapur.015G112600.1	254.0704524	-0.604574983	0.072832375	-8.30195	1.02E-16	2.77E-16	grey	-0.305614094	9.93E-05	GO:0005975;GO:0004553	ATSG32860.1	Glycosyl hydrolase superfamily protein	glucan endo-1%2C3-beta-D-glucosidase
Sapur.016G000300.1	2.453683914	1.262836754	0.154847063	8.16031	1.24E-16	3.36E-16	grey	0.293509523	0.001091315		ATSG09710.1	dsRNA-binding domain-like superfamily protein	NA
Sapur.007G111600.1	2.72435087	1.976604147	0.228188694	8.298541	1.05E-16	2.85E-16	grey	0.499616068	2.85E-11	GO:0003247;GO:0006468;GO:0005524;GO:0004672	ATSG66920.2	Protein kinase superfamily protein	receptor Serine/Threonine kinase, putative
Sapur.015G132600.1	3.363610287	1.180113388	0.143208416	-8.28881	1.14E-16	3.08E-16	grey	-0.016275177	0.648375627		ATSG14110.2	Tetratricopeptide repeat (TPR)-like superfamily protein	fluorescent in blue light protein
Sapur.010G005500.2	12.12475491	0.763579964	0.092133871	-8.28772	1.15E-16	3.12E-16	grey	-0.296643027	0.000161429	GO:0005515	ATSG33420.1	RING/FYVE/PHD zinc finger superfamily protein	PHD finger protein
Sapur.016G094600.1	3.872726777	2.218991235	0.267618576	8.283636	1.19E-16	3.21E-16	grey	0.52858146	9.94E-13		ATSG48140.1	Hypoxia responsive family protein	lipoic acid synthase
Sapur.016G119100.2	7.001169097	0.869196881	0.104927277	8.282232	1.20E-16	3.24E-16	grey	0.087695861	0.274766933		ATSG27030.3	ACAM-2,CAM5	calmodulin 5
Sapur.003G209300.2	138.2706469	0.527311229	0.064850332	8.28232	1.21E-16	3.26E-16	grey	0.36608846	2.32E-06		ATSG76990.2	structural molecules	coatomer subunit beta'-1 protein
Sapur.T046100.2	5.504621119	2.276716166	0.14008875	8.281863	1.21E-16	3.26E-16	grey	0.398639555	2.20E-07		ATSG47070.1	Eukaryotic translation initiation factor 3 subunit A, putative	eukaryotic translation initiation factor 3 subunit A, putative
Sapur.008G081000.1	2.708671343	3.353047312	0.404999239	8.281064	1.23E-16	3.29E-16	grey	0.396309411	2.78E-07	GO:0043631;GO:0006532;GO:0005634	ATSG06560.1	PAPS3	poly(A) polymerase 3
Sapur.008G037200.1	1.038660027	1.42181456	0.164719885	8.27501	1.28E-16	3.46E-16	grey	-0.462872036	1.04E-09		ATSG39370.1		membrane-associated kinase regulator 4, putative
Sapur.019G060100.1	457.5456191	-1.220812396	0.147540052	-8.27445	1.29E-16	3.48E-16	grey	-0.424425058	3.03E-08	GO:0045893;GO:0008270;GO:0005634;GO:0003677	ATSG56290.1		GATA-type transcription activator, amino-terminal protein
Sapur.015G222500.1	2.288930009	1.48E-14	0.226402379	8.270595	1.30E-16	3.51E-16	grey	0.494338876	4.78E-11	GO:0004564;GO:0006468;GO:0004672	ATSG11940.1	S-locus lectin protein kinase family protein	NA
Sapur.010G078000.1	9.74930008	1.494866767	0.180798154	8.268564	1.38E-16	3.65E-16	grey	0.435447169	1.20E-08	GO:0009611;GO:0004867	ATSG38870.1	Serine protease inhibitor, potato inhibitor I-type family protein	protease inhibitor
Sapur.015G000300.1	491.4578607	0.698052283	0.084487185	8.267766	1.38E-16	3.66E-16	grey	-0.483869201	1.36E-10	GO:0016491	ATSG27230.1	Quinone reductase family protein	quinone oxidoreductase, putative
Sapur.015G116700.2	3.135282571	-1.471192848	0.178004351	-8.26493	1.40E-16	3.77E-16	grey	-0.192385674	0.015782075	GO:0005515	ATSG73720.1	SMU1	transducin family protein / WD-40 repeat family protein	WD40 repeat protein SMU1
Sapur.006G139400.2	7.057543866	0.875354966	0.106000187	8.261458	1.46E-16	3.78E-16	grey	-0.510757784	1.32E-12	GO:0005515;GO:0006468;GO:0004672	ATSG45340.1	Leucine-rich repeat protein kinase family protein	LRR receptor Ser/Thr kinase, putative
Sapur.008G120300.1	63.20228544	-0.537949492	0.065109696	-8.26217	1.43E-16	3.85E-16	grey	-0.413122254	7.57E-08		ATSG19320.1		RNA methyltransferase, putative
Sapur.016G112500.1	16.15221561	-0.388882284	0.131796282	-8.26107	1.44E-16	3.86E-16	grey	-0.484029313	1.34E-10		ATSG63088.1	DVL16,RTL14	ROTUNDIFOLIA like 14
Sapur.008G145100.1	83.18773529	-0.618176277	0.074815576	-8.25976	1.45E-16	3.86E-16	grey	0.534784614	1.41E-12		ATSG48140.1	B120 protein	NADH-ubiquinone reductase complex 1 MLRQ subunit
Sapur.013G132900.1	21.41355747	-0.896494926	0.108688549	-8.24829	1.61E-16	4.32E-16	grey	-0.532805028	6.82E-13	GO:0005515;GO:0045531	ATSG14460.1	LRR and NB-ARC domains-containing disease resistance protein	RING zinc finger protein
Sapur.007G079200.1	4.790564692	-1.231422227	0.180393971	-8.24724	1.62E-16	4.34E-16	grey	-0.539793981	2.98E-13	GO:0016740;GO:0005515	ATSM8L1,RMR1	receptor homology region transmembrane RING H2 motif protein 1	Rad21/Rad50 family protein
Sapur.15WG061700.1	6.334819914	-1.040358285	0.126184617	-8.24476	1.65E-16	4.45E-16	grey	-0.556103964	4.00E-14	GO:0000028	ATSRC8,DIF1,RDC8,SYN1	Rad21/Rec8-like family protein	NA
Sapur.016G073100.1	9.838114974	-0.477690316	0.179819119	-8.24003	1.71E-16	4.61E-16	grey	0.418279657	1.07E-08	GO:0006468;GO:0004672	ATSG38870.1	Serine protease inhibitor, potato inhibitor I-type family protein	protease inhibitor
Sapur.017G055300.1	7.760978262	0.862663819	0.236188519	8.239254	1.73E-16	4.66E-16	grey	0.291314543	0.000214259	GO:0043565;GO:0006355;GO:0003700	ATSWRKY75,WRKY75	WRKY-DNA binding protein 75	WRKY transcription factor
Sapur.016G288700.1	1014.642864	0.904988931	0.109270528	8.23519	1.79E-16	4.81E-16	grey	-0.527634431	1.24E-12	GO:0055114;GO:0016614;GO:0008948;GO:0003854	ATSG47030.1	NAD(P)-binding Rossmann-fold superfamily protein	cinnamoyl-CoA reductase
Sapur.010G061600.3	73.45522864	1.138211812	0.138252946	8.232821	1.83E-16	4.91E-16	grey	0.537707214	1.80E-13		ATSG17860.1	JAI3,JAZ3,TIFY6B	jasmonate-zim-domain protein 3
Sapur.003G047900.1	1.587183253	1.382145627	0.151466549	8.22857	1.86E-16	5.00E-16	grey	0.512343123	2.38E-12	GO:0043565;GO:0006355;GO:0003700;GO:0003677;GO:0005634	ATSB-2,ATHB2,HAT4,HB-2	homeobox protein 2	homeobox leucine zipper protein hat1
Sapur.016G072400.1	9.727933378	1.485172483	0.180461335	8.229865	1.87E-16	5.03E-16	grey	-0.431648834	1.46E-08	GO:0009611;GO:0004867	ATSG38870.1	Serine protease inhibitor, potato inhibitor I-type family protein	NA
Sapur.005G055400.4	8.119697073	-0.960819896	0.116789763	-8.22692	1.92E-16	5.15E-16	grey	-0.161632608	0.038694904	GO:0006412;GO:0005840	ATSG10360.1	EMB3010,RPS6B	Ribosomal protein S6e
Sapur.016G171700.1	1.784018542	2.101818166	0.265122344	8.224806	1.95E-16	5.24E-16	grey	-0.45032678	1.87E-07		ATSG44610.1	ATPRL,PR 1,PR1	pathogenesis-related gene 1
Sapur.013G249700.1	961.2863571	1.598621188	0.194363628	8.223824	1.97E-16	5.29E-16	grey	0.505913567	1.26E-11	GO:0030170;GO:0019752;GO:0016831	ATSG30340.1	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	L-tyrosine decarboxylase
Sapur.007G079200.1	0.96867955	-2.774567564	0.337162925	-8.21992	2.04E-16	5.46E-16	grey	-0.516810001	4.23E-12	GO:0016021	ATSG64570.1	GNS1/SUR4 membrane protein family	3-ketosphinganine synthase
Sapur.T030900.1	55.07086735	0.951174304	0.115751583	8.219915	2.04E-16	5.46E-16	grey	0.529973139	9.49E-13		ATSG26190.1	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	NA
Sapur.013G132600.1	0.023169677	-2.474936316	0.301060768	-8.21858	2.07E-16	5.54E-16	grey	0.439747678	3.30E-09		ATSG57521.1		hypothetical protein
Sapur.016G128000.5	5.427823643	-0.030448112	0.125790122	-8.21565	2.11E-16	5.65E-16	grey	-0.309774266	7.88E-05		ATSG30495.2		FcC2 pre-rRNA processing protein
Sapur.005G050300.1	186.3749844	-0.124814398	0.03856177	-8.21562	2.28E-16	6.11E-16	grey	-0.546578837	1.35E-14	GO:0055085;GO:0046873;GO:0003001;GO:0016020	ZTP29	ZIP metal ion transporter family	zinc transporter
Sapur.016G121900.1	8.26058878	1.971366736	0.24028223	8.20498	2.31E-16	6.17E-16	grey	-0.442711982	6.41E-09		ATSG12735.1		hypothetical protein
Sapur.016G185200.1	1.740705623	2.301912867	0.280670944	-8.20146	2.37E-16	6.36E-16	grey	-0.517512276	9.32E-13		ATSG59760.1	Domain of unknown function (DUF866)	DUF866 domain protein
Sapur.016G219700.1	0.974559984	-2.767014485	0.338207171	8.196294	2.48E-16	6.63E-16	grey	-0.42598806	4.61E-10	ATMYB118,MYB118,PGA37	ATSMYB118	myb domain protein 118	Myb transcription factor, putative
Sapur.005G107200.1	4.342775429	1.000829804	0.145329161	-8.19402	2.53E-16	6.76E-16	grey	-0.547031569	1.24E-13				NA
Sapur.017G297700.1	1.574501198	2.522422497	0.331786097	8.19334	2.54E-16	6.81E-16	grey	0.48387471	4.94E-11		ATSG51550.1	FER	carbohydrate-binding protein of the ER protein
Sapur.007G130200.1	199.7074279	-0.616267429	0.075246663	-8.18996	2.61E-16	6.98E-16	grey	-0.474617796	2.39E-10		ATSG46080.1	ARL	ARG25-like
Sapur.014G054400.1	19.3048819	-0.501766047	0.061842163	-8.18582	2.70E-16	7.22E-16	grey	-0.511319014	1.61E-12		ATSG51160.1	Ankyrin repeat family protein	NA
Sapur.008G106200.1	4.944114665	-7.559882288	0.937259489	-8.18357	2.76E-16	7.36E-16	grey	-0.508443277	1.06E-11				NA
Sapur.008G066200.1	8.918663253	2.882194377	0.341126942	-8.17522	3.05E-16	8.12E-16	grey	-0.515324764	8.83E-12				NA
Sapur.015G057600.1	31.66992013	0.784905961	0.104628287	-8.17328	3.13E-16	8.09E-16	grey	-0.510831114	8.87E-12		ATLIP1,LIP1	lipase 1	L-tyrosine decarboxylase
Sapur.016G020600.13	11.85173669	-0.972351137	0.088405164	-8.17074	3.07E-16	8.18E-16	grey	-0.237595061	0.139705599	GO:0017176;GO:0016021;GO:0006506	ATSG71730.1	N-acetylglucosaminyl transferase component family protein / GpI1 family protein	N-acetylglucosaminyl transferase component
Sapur.016G076800.1	3.941966339	1.481962414	0.181511205	8.164578	3.23E-16	8.60E-16	grey	-0.473803459	3.63E-10				NA
Sapur.001G191700.1	237.3128593	0.474885571	0.058169524	8.163013	3.27E-16	8.71E-16	grey	-0.510963647	1.16E-11	GO:0055114;GO:0016491;GO:0020037	ATSG61510.1	GroES-like zinc-binding alcohol dehydrogenase family protein	zinc-binding dehydrogenase family oxidoreductase
Sapur.016G271500.1	14.42979122	1.824543477	0.29073912	8.161484	3.31E-16	8.81E-16	grey	-0.468274691	1.02E-10	GO:0045944;GO:0006468;GO:0004672	ATSG27290.1	S-locus lectin protein kinase family protein	Serine/Threonine kinase
Sapur.013G095600.1	69.8069534	2.388319398	0.292654527	-8.1652	3.34E-16	8.91E-16	grey	-0.316349709	7.02E-05	GO:0009116;GO:0003824	ATSG24340.1	Phosphorylase superfamily protein	NA
Sapur.T044600.1	1.304460907	1.022021653	0.150060768	8.16008	3.35E-16	8.92E-16	grey	0.49545613	4.38E-11	GO:0005515	ATSG57521.1	Leucine-rich repeat family protein with leucine-rich repeat domain	hypothetical protein
Sapur.006G125600.1	50.15108899	2.143762822	0.262796	8.157517	3.42E-16	9.11E-16	grey	0.306317932	9.55E-05	GO:0055114;GO:0016491	ACO1,LATCO1	ACC oxidase 1	1-aminocyclopropane-1-carboxylate oxidase
Sapur.008G200100.1	195.1068419	-0.580413972	0.071146442	-8.15176	3.47E-16	9.24E-16	grey	-0.212512128	0.005325569		ATSG15451.1	Galactose oxidase/kelch repeat superfamily protein	kelch repeat protein
Sapur.008G141800.1	2.456489955	-1.861606316	0.228230646	-8.15434	3.51E-16	9.35E-16	grey	-0.483736776	1.38E-10	GO:0055114;GO:0050661;GO:0050660;GO:0004499	ATSG04630.1	YLCI1	indole-3-pyruvate monooxygenase YUCCA2, putative
Sapur.016G166300.1	1.167656755	2.450460849	0.292681826	8.152868	3.62E-16	9.62E-16	grey	-0.124431808	0.239462964	GO:0006886	ATSG61361.1	alpha-soluble NSF attachment protein 2	NA
Sapur.012G001500.1	77.84952318	-0.004580879	0.123280063	-8.15009	3.64E-16	9.67E-16	grey	-0.478470988	2.32E-10	GO:0005515	ATSG56480.1	ARLI2,FJL,RLP33	receptor like protein 33
Sapur.016G201800.1	37.79393985	0.832374616	0.102182527	8.145958	3.78E-16	1.00E-15	grey	-0.462985779	1.01E-09	GO:0016758;GO:0008152	ATSG27780.1	UGT73B6	UDP-glucosyl transferase 73B6
Sapur.T189600.1	60.79065772	0.343663069	0.042246988	8.142639	3.87E-16	1.02E-15	grey	0.5028123	1.94E-11	GO:0006355;GO:0005739;GO:0003690	ATSG07600.1	Mitochondrial transcription termination factor family protein	mTERF protein
Sapur.T052400.1	76.82521461	0.490723816	0.060575375	8.100748	5.46E-16	1.45E-15	grey	-0.035207694	0.813680855	GO:0003676	ATSG54680.1	SC1,SI	SC35-like splicing factor 30	serine/arginine-rich splicing factor SRSF10 RNA recognition motif protein
Sapur.015G095200.1	22.05218556	0.642068834	0.079881803	8.09792	5.58E-16	1.48E-15	grey	-0.518328006	1.48E-12	GO:0004674;GO:0048544;GO:0006468;GO:0004672	ATSG27260.1	S-locus lectin protein kinase family protein	Serine/Threonine kinase
Sapur.016G065200.1	1.403044967	2.518472588	0.311088764	-8.09567	5.68E-16	1.51E-15	grey	-0.537807321	1.78E-13		ATSG11860.2	SSP5	SCP5-like small phosphatase 5
Sapur.007G128800.4	0.718799887	2.605886275	0.32612003	8.083871	6.13E-16	1.67E-15	grey	0.515917694	1.16E-12		ATSG69570.1		RNA-binding protein 1
Sapur.001G045300.1	18.27439192	1.120789469	0.138719519	8.079537	6.50E-16	1.72E-15	grey	0.457787892	6.84E-09	GO:0000160	ERD3	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase, putative
Sapur.016G088400.1	252.8950684	0.463033266	0.058458326	8.07573	6.75E-16	1.77E-15	grey	-0.454904907	1.31E-08		ATSG26450.1	RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.005G011000.1	35.1672929	1.602284846	0.198526308	8.070894	6.98E-16	1.84E-15	grey	-0.473178895	4.62E-10	GO:0005515;GO:0006468;GO:0004672;GO:0003824	ATSG47530.1	Leucine-rich repeat protein kinase family protein	Serine/Threonine kinase domain protein
Sapur.006G136500.1	2.785442288	1.573285456	0.195495113	8.065633	7.23E-16	1.91E-15	grey	-0.524085813	1.38E-12	GO:0008660	ATSG44580.1	selenium-binding protein	SE-Mo selenium-binding protein (SBP56)
Sapur.006G140400.1	3.85792372	2.403412114	0.174106694	-8.06051	7.68E-16	2.01E-15	grey	-0.247587978	0.001770206	GO:0006468;GO:0004672;GO:0005524	ATSG36350.1	Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.15WG123300.1	141.0189404	-1.536801126	0.190663383	-8.05933	7.67E-16	2.02E-15	grey	-0.522489862	2.26E-12		ATSG70660.1	Regulator of chromosome condensation (RCC1) family protein	NA
Sapur.005G058000.1	0.983684952	-2.545511591	0.316629274	8.048882	8.36E-16	2.20E-15	grey	0.493972554	5.09E-11				NA
Sapur.013G111000.1	302.2562514	0.843239912	0.104796113	8.046376	8.53E-16	2.25E-15	grey	0.446102259	4.76E-09	GO:0016740	ATSG39940.1	DCR,EMB3009,FE13	HXXXD-type acyl-transferase family protein	alcohol acyltransferase, putative
Sapur.015G117900.1	423.5547753	0.518183885	0.064406428	8.042362	8.56E-16	2.26E-15	grey	0.505241492	1.50E-11	GO:0005515	ATSG57320.1	YELLOW STRIPE like 7	oligopeptide transporter OPT family protein
Sapur.016G261000.9	2.93858655	-1.564793399	0.194478812	-8.04625	8.54E-16	2.25E-15	grey	-0.459003784	1.48E-09		ATSG21500.1		stress responsive alpha-beta barrel domain protein
Sapur.015G058200.1	23.20743476	0.768391933	0.095912156	8.045669	8.62E-16	2.27E-15	grey	0.446013444	7.9E-11	GO:0046883	ATSG45460.1	basic helix-loop-helix(bHLH) DNA-binding superfamily protein	BHLH transcription factor, putative
Sapur.004G075300.1	1.602426952	2.384662259	0.358500138	8.044466	8.66E-16	2.28E-15	grey	0.388725239	4.88E-07	GO:0016788	GLIP7	GDSL-motif lipase 7	zinc finger protein, putative
Sapur.016G033800.1	275.8670906	-0.724854388	0.090107051	-8.04419	8.67E-16	2.28E-15	grey	-0.500731132	4.20E-11	GO:0016020;GO:0006810;GO:0005215	ATSG68670.1	nitrate transporter 2.7	nitrate transporter, putative
Sapur.016G281500.1	180.4245572	0.279853134	0.034680839	8.043437	8.74E-16	2.30E-15	grey	0.537813956	3.78E-13	GO:0008080	ATSG38130.1	ATMAK3	Acyl-CoA N-acyltransferases (NAT) superfamily protein	N-acetyltransferase MAK3-like protein
Sapur.001G108100.1	8.408298859	1.628322431	0.202503777	8.040998	8.91E-16	2.35E-15	grey	0.512861017	6.25E-12				NA
Sapur.004G201405.1	24.11667202	1.005659721	0.126183833	8.037508	9.17E-16	2.41E-15	grey	0.518945164	1.34E-12				NA
Sapur.009G048800.1	29.00080848	1.223802088	0.152502353	8.029497	1.02E-15	2.67E-15	grey	0.42207712	4.05E-08	GO:0055114;GO:0016491;GO:0008270	ATSG27990.1	ATCAD6,CAD-B2,ELI3,ELI3-1	eliicitor-activated gene 3-2	NA
Sapur.010G175200.1	78.76051177	0.725395365	0.091456868	8.014868	1.02E-15	2.67E-15	grey	-0.528745096	1.08E-12	GO:0006367;GO:0006366;GO:0005674	ATSG22730.1	Transcription initiation factor IIF, beta subunit	transcription initiation factor IIF, beta subunit
Sapur.010G080000.1	1.522164275	2.569635576	0.317965881	8.024134	1.02E-15	2.69E-15	grey	0.462853277	1.04E-09		ATSG23250.1	CRK17,DUF26-CC,EMB1290	kinases;protein kinases	PPR containing-like protein, putative
Sapur.016G000100.1	16.76058463	0.758842927	0.09067997	8.0147	1.04E-15	2.74E-15	grey	-0.447887352	5.76E-09		ATSG40620.1	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing-like protein, putative
Sapur.006G047000.2	17.12948109	0.969623168	0.11850341	-8.01042	1.14E-15	3.00E-15	grey	-0.382814983	7.49E-07	GO:0008324;GO:0006470;GO:0004722	ATSG35630.1	AtDBP1,DBP1	DNA-binding protein phosphatase 1C	DNA-binding protein phosphatase 2C
Sapur.008G118700.1	288.6581104	0.267918153	0.033429168	8.008368	1.16E-15	3.04E-15	grey	-0.538812009	2.28E-12	GO:0008270;GO:0005634;GO:0005515;GO:0005739;GO:0005524;GO:0015923;GO:0006013	ATSG19860.2	glycosyl hydrolase family 28 protein / polygalacturonase (pectinase) family protein	glycosyl hydrolase family 28 protein
Sapur.007G020900.1	2199.191776	0.221021103	0.040000209	8.007379	1.17E-15	3.07E-15	grey	0.523451152	2.01E-12	GO:0016853	ATSG18040.1	PIN7,T2	peptidyl-prolyl cis-trans isomerase, NIMA-interacting 1	peptidyl-prolyl cis-trans isomerase
Sapur.T035100.1	6.86983676	1.505943515	0.188601675	8.002166	1.21E-15	3.16E-15	grey	0.437278819	4.91E-10		ATSG50140.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.T171100.1	21.12402663	-0.891029203	0.111408853	-7.9962	1.28E-15	3.36E-15	grey	-0.559847282	2.48E-14				NA
Sapur.008G082000.1	5.508863124	-0.307898711	0.136113368	-7.99201	1.33E-15	3.48E-15	grey	-0.506649701	1.29E-11	GO:0005355;GO:0006486;GO:0004672	ATSG06620.1	PAS domain-containing protein tyrosine kinase family protein	tyrosine kinase domain protein
Sapur.014G114100.5	6.707809823	-0.953161156	0.119076092	-7.99142	1.36E-15	3.49E-15	grey	-0.422820564	3.46E-08	GO:0006355;GO:0005739;GO:0003690	ATSG29060.1	Mitochondrial transcription termination factor family protein	transcription terminator factor family protein
Sapur.004G038200.1	1.324396058	-2.026505281	0.253782821	7.991145	1.38E-15	3.50E-15	grey	-0.534573089	5.55E-13		ATSG31130.1		hypothetical protein
Sapur.003G092700.1	3.338676117	-0.627369108	0.08476637	-7.98966	1.39E-15	3.53E-15	grey	-0.509832194	1.36E-11				NA
Sapur.017G115500.1	43.08754439	1.340264847	0.167915583	7.981896	1.44E-15	3.77E-15	grey	0.38692507	5.56E-07		ATSG61820.1		microsomal glutathione S-transferase, putative
Sapur.015G081000.1	19.85819949	0.755604375	0.094796107	7.98477	1.45E-15	3.78E-15	grey	0.510864165	8.56E-12		ATSG39940.1	CDI1	RNI-like superfamily protein	corronate-inserting protein
Sapur.005G007300.1	0.770680604	1.780700076	0.345573623	7.977454	1.48E-15	3.91E-15	grey	0.489048836	8.10E-11	GO:0006351	ATSG15020.2	SNL2	SIN3-like 2	paired amphipathic helix protein
Sapur.016G110600.1	8344.717666	1.614938872	0.205280216	7.970642	1.50E-15	3.95E-15	grey	0.515377794	1.03E-12	GO:0004378;GO:0005524	MAT4,ATD3,SAM53	S-adenosylmethionine synthetase family protein	S-adenosylmethionine synthetase
Sapur.013G194600.1	3.732765481	1.264943318	0.158658988	7.972673	1.51E-15	4.06E-15	grey	0.516398968	4.26E-12		ATSG73730.1	AtEIL3,ATSUM1,EIL3,SUM1	ETHYLENE-INSENSITIVE3-like 3	ethylene insensitive (EIN3/EIL)-like transcription regulator
Sapur.018G095100.1	3.963224014	1.683374476	0.211192027	7.968851	1.63E-15	4.38E-15	grey	-0.48805167	8.08E-11	GO:0055114;GO:0016491	ATSG49390.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2OG-Fe(II) oxygenase family oxidoreductase
Sapur.008G128500.2	29.06026005	-0.575173604	0.069552129	-7.96631	1.65E-15	4.43E-15	grey	-0.532210851	7.28E-13	GO:0006282	ATSG31226.1	regulatory protein RecX	regulatory protein RecX
Sapur.003G122800.1	19.50391435	1.784801614	0.224082351	7.962526	1.66E-15	4.31E-15	grey	0.371487134	1.67E-06	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATSG45550.1	CYP76C4

Sapur.T178700.1	24.0861134	-1.82158399	0.107193768	-7.6661	1.77E-14	4.49E-14	grey	-0.553643209	6.18E-14					NA
Sapur.013G053700.1	240.3709867	0.319279304	0.041656032	7.66466	1.79E-14	4.54E-14	grey	-0.501365429	2.26E-11		ATSG31890.1		FMN binding	root border cell-specific protein, putative
Sapur.016G198300.1	0.5670958	2.532902977	0.330620345	7.66315	1.81E-14	4.60E-14	grey	-0.564884134	1.38E-14		ATSG40460.1		PAR1 protein	PAR1 protein
Sapur.013G035300.2	36.44812145	0.678471079	0.088540737	7.662853	1.82E-14	4.61E-14	grey	-0.017681821	0.816027562		ATSG31590.1	SDE5	silencing defective 5	NRK13.5 protein, putative
Sapur.012G087000.1	21.64313278	1.145234498	0.149526435	7.662464	1.82E-14	4.61E-14	grey	0.443986602	6.82E-09					hypothetical protein
Sapur.014G276400.1	2.038158934	1.436519766	0.215636398	7.660304	1.85E-14	4.70E-14	grey	0.495979808	1.97E-11	GO:0005085,GO:0016020,GO:0008081,GO:0005216	ATSG53130.1	ATCNGC1,CNGC1	cyclic nucleotide gated channel 1	cyclic nucleotide-gated ion channel protein, putative
Sapur.012G033400.1	970.0892003	0.356209893	0.046495518	7.65751	1.90E-14	4.80E-14	grey	0.503412342	1.82E-11		ATMCP2-1,MTACP1		mitochondrial acyl carrier protein 1	acyl carrier protein
Sapur.014G068900.1	514.4001018	-0.228885205	0.029898318	-7.65677	1.91E-14	4.83E-14	grey	-0.528032094	1.35E-12	GO:0008270,GO:0005515	ATG08070.1		Zinc finger, C3HC4 type (RING finger)	RING zinc finger protein, putative
Sapur.015G090700.1	1.580754889	2.052042884	0.268067259	7.654959	1.93E-14	4.88E-14	grey	0.450439905	3.23E-09	GO:0005515,GO:0043531	ATG27190.1		NB-ARC domain-containing disease resistance protein	BED finger NB5-LRR resistance protein
Sapur.012G000100.1	50.80867201	0.780132215	0.102000425	7.65329	1.95E-14	4.94E-14	grey	0.322841439	7.8E-05		ATSG50940.1	ETHLPHA	electron transfer flavoprotein alpha	electron transfer flavoprotein subunit alpha
Sapur.012G068000.1	6.0724732	1.091009943	0.142630522	7.649835	2.01E-14	5.09E-14	grey	0.488647229	8.41E-11	GO:0005524,GO:0007165,GO:0005515	ATG27170.1		transmembrane receptor, ATP binding	NA
Sapur.015G112000.1	837.7738866	0.311502742	0.04	7.576758	2.02E-14	5.11E-14	grey	-0.512802663	4.55E-12	GO:0005975,GO:0004553	ATG32620.1		Glycosyl hydrolase superfamily protein	glucan endo-1,3(2,3)-beta-glucosidase, basic protein
Sapur.018G030100.2	1.79647521	-1.760950681	0.230237068	7.648447	2.03E-14	5.14E-14	grey	-0.506841464	1.26E-11	GO:0005524,GO:0003678,GO:0006260,GO:0003887,GO:0003677	ATG32700.2	TEB	helicase; ATP-dependent helicase;nucleic acid binding;ATP binding;DNA-directed DNA polymerase;DNA binding	DNA polymerase I
Sapur.003G214400.1	1965.672385	0.779272008	0.101809439	7.64763	2.04E-14	5.16E-14	grey	-0.512372816	5.1E-12	GO:0016161,GO:0000270	ATG37080.1	BAM3,BMY8,CT-BAM	Glycosyl hydrolase family 1 protein	beta-amylase
Sapur.003G159700.1	1.417941369	-1.962156838	0.256567183	-7.64773	2.05E-14	5.17E-14	grey	-0.4762619	2.89E-10					NA
Sapur.T165300.1	2.427377565	1.161384525	0.152086525	7.636756	2.14E-14	5.39E-14	grey	0.51347436	5.16E-12	GO:0005085,GO:0016020,GO:0016020,GO:0008810,GO:0005215	ATG52190.1		Major facilitator superfamily protein	Major facilitator superfamily protein
Sapur.013G138400.1	164.5894475	-0.564597042	0.073857621	-7.6444	2.10E-14	5.30E-14	grey	-0.504378682	1.64E-11	GO:0043531	ATG14440.1		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.159G012000.3	26.67795369	-0.53323337	0.069760439	-7.64378	2.11E-14	5.33E-14	grey	0.078548531	0.328149497	GO:0016192,GO:0016023,GO:0008810	ATG24170.1		Golt1/SFG2-like vesicle transport protein family	vesicle transporter SFT2A, putative
Sapur.004G208500.1	57.86218569	-0.4167103397	0.10282786	-7.63724	2.12E-14	5.35E-14	grey	-0.52522396	5E-12		ATA5T4G26120.1		ARM repeat superfamily protein	ubiquitin-protein ligase, putative
Sapur.008G047000.3	9.0648126	0.782663136	0.102466229	7.636454	2.23E-14	5.64E-14	grey	0.408193979	1.12E-07	GO:0005515	ATG39760.1	ATBPM1/BPM3	BTB/POZ/MATH domains containing protein	speckle-type POZ protein, putative
Sapur.005G197500.1	2.564419129	2.758125316	0.348	7.626455168	2.24E-14	5.66E-14	grey	0.434017629	3.46E-08	GO:0005515	ATG29426.1	ATGSTU7,GST25,GSTU7	glutathione S-transferase tau 7	tau class glutathione transferase GSTU14
Sapur.001G141700.2	10.89322678	-0.018442396	0.08180846	-7.63053	2.34E-14	5.90E-14	grey	-0.51038125	5.8E-12		ATSG45890.1	RUS1	Protein of unknown function, DUF647	DUF647 domain protein
Sapur.008G134300.2	4.71147321	1.037795164	0.130203319	7.628848	2.37E-14	5.98E-14	grey	0.493973819	4.86E-11	GO:0046983	ATG44410.1	bHLH104	basic helix-loop-helix transcription factor family protein	basic helix-loop-helix transcription factor
Sapur.T178600.1	14.65726175	-0.866758897	0.11640007	-7.62722	2.40E-14	6.05E-14	grey	-0.538845877	8.58E-12					NA
Sapur.016G140700.1	26.45278085	-0.955022625	0.120819439	-7.62503	2.44E-14	6.15E-14	grey	-0.481888866	6E-12	GO:0016765	ATG58730.1		Undecaprenyl pyrophosphate synthetase family protein	undecaprenyl pyrophosphate synthase
Sapur.010G114500.2	347.9634517	0.412189039	0.054059351	7.62475	2.45E-14	6.17E-14	grey	0.162579134	0.041915258	GO:0072546,GO:0016021,GO:0005783	ATG49540.1		Rab5c-interacting family protein (RabSip)	Rab5c-interacting protein (RabSip)
Sapur.012G030300.1	25.34657822	3.300061231	0.170519996	-7.6241	2.46E-14	6.20E-14	grey	-0.472151784	4.64E-10		ATG75240.1	AHB33,HB33	homeobox protein 33	zinc finger homeodomain protein, putative
Sapur.005G051900.1	0.727276196	2.144266372	0.320519369	7.621638	2.50E-14	6.30E-14	grey	0.50179682	2.56E-11					NA
Sapur.012G162700.1	8.483615782	1.352962317	0.164145582	7.620687	2.51E-14	6.36E-14	grey	0.34976404	7.12E-06					transmembrane protein, putative
Sapur.004G209400.1	0.658653183	2.294267468	0.169866055	7.614804	2.54E-14	6.40E-14	grey	0.443783333	1.84E-09		ATG30340.1			hypothetical protein
Sapur.005G030600.1	9.533251662	-1.129053941	0.14817827	-7.61956	2.55E-14	6.41E-14	grey	-0.494494975	4.65E-11	GO:0003677,GO:0005634	ATKLXNAT2	KNOTTED-like from Arabidopsis thaliana 2	Putative endosomal K+/H+ antiporter	NA
Sapur.013G093300.1	10.08747546	-0.461874881	0.196624545	-7.61947	2.55E-14	6.42E-14	grey	-0.526672229	1.96E-12	GO:0016468,GO:0005777	ATG22920.1		Peroxisomal membrane protein 22 kd family protein	NA
Sapur.015G077000.1	81.34067164	-0.384610992	0.050404047	-7.61512	2.63E-14	6.63E-14	grey	-0.51422429	5.64E-12	GO:0008080	ATG42040.1		Acyl-CoA N-acyltransferases (NAT) superfamily protein	GNAT family acetyltransferase
Sapur.012G118300.1	6.451376578	1.407926781	0.188810446	7.61492	2.66E-14	6.69E-14	grey	-0.474269777	3.51E-10	GO:0016021,GO:0008365,GO:0005337	ATG02630.1		Nucleoside transporter family protein	equilibrative nucleoside transporter
Sapur.001G191400.4	49.91947855	0.613171804	0.080531182	7.6139	2.66E-14	6.70E-14	grey	-0.068234562	1.39580635	GO:0016301	ATG51290.1		Diacylglycerol kinase family protein	ceramide kinase
Sapur.013G070800.1	23.00745059	-0.855122197	0.112600102	-7.6076	2.75E-14	7.03E-14	grey	-0.464030430	9.36E-10	GO:0016568,GO:0004403,GO:0016573,GO:0006248,GO:0005634	ATG63190.1	HAD57,HAC7,HAG22,HAG2	histone acetyltransferase type B catalytic subunit, putative	histone acetyltransferase type B catalytic subunit, putative
Sapur.019G108900.1	307.6174621	0.880529805	0.115758099	7.606571	2.81E-14	7.08E-14	grey	-0.454593547	2.22E-09	GO:0004866	ATG73325.1		Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor KPI-A1
Sapur.017G058500.1	45.12214541	-0.070849997	0.088213381	-7.60484	2.85E-14	7.18E-14	grey	-0.486817972	1.03E-10		ATG88260.1		binding;RNA binding	NA
Sapur.007G081100.1	5.942663669	-1.748857026	0.229898435	-7.60241	2.87E-14	7.21E-14	grey	-0.362704169	2.32E-07	GO:0005507,GO:0055114,GO:0016491	ATG98830.1		Cupredoxin superfamily protein	L-ascorbate oxidase
Sapur.010G119900.1	111.6869009	0.353889338	0.046802884	7.604005	2.87E-14	7.22E-14	grey	0.483301757	1.94E-10		ATG88680.1			NA
Sapur.009G094000.1	0.996056519	-2.344187989	0.309662026	-7.6004	2.94E-14	7.46E-14	grey	-0.464014532	8.94E-10	GO:0046983,GO:0003677	AGL62	AGAMOUS-like 62	MADS box transcription factor, putative	MADS box transcription factor, putative
Sapur.007G057600.1	2.0452739	-1.455316479	0.191636023	-7.59417	3.10E-14	7.79E-14	grey	-0.524536209	1.77E-12	GO:0016998,GO:0006032,GO:0004568	ATG12500.1	ATHCHIB.B-CHI.CHI-B.BHCHI	basic chitinase	NA
Sapur.001G051600.1	11.38245014	0.611759093	0.081196679	7.591288	3.12E-14	7.84E-14	grey	0.51173768	5.96E-12		ATG13070.1		MSF1-like family protein	dowmo family protein
Sapur.013G140000.1	151.0709388	-0.862580304	0.110696174	-7.59292	3.13E-14	7.86E-14	grey	-0.418284232	5.20E-08	GO:0007165	ATG58180.1	CIPK10,PKS2,SPK1,SNRK3.8	SOS3-interacting protein 1	CBL-interacting Serine/Threonine-kinase
Sapur.016G241400.1	321.1327034	0.434547791	0.044078116	7.589456	3.21E-14	8.06E-14	grey	0.49413307	1.41E-09	GO:0003674	ATG34450.1	CID9	CTC-interacting domain 9 plant thaliana CTC-interacting domain protein CID8	RNA recognition motif 2 plant thaliana CTC-interacting domain protein CID8
Sapur.003G079700.1	340.3423262	0.545136294	0.071832856	7.588955	3.22E-14	8.10E-14	grey	0.464221681	9.13E-10	GO:0005509	ATG12310.1		Calcium-binding EF-hand family protein	calcium-binding protein CML7, putative
Sapur.005G070400.1	19.23794821	1.181781863	0.147232137	7.587583	3.26E-14	8.18E-14	grey	0.423725676	4.31E-10					NA
Sapur.013G135200.1	47.5633989	1.190031016	0.157020125	7.580175	3.45E-14	8.66E-14	grey	-0.162575459	0.041917233		ATG60030.1			hypothetical protein
Sapur.002G012600.1	270.6126597	0.22401883	0.029561891	7.578637	3.49E-14	8.76E-14	grey	0.503271749	2.54E-11		ATG75980.1		Single hybrid motif superfamily protein	glycine cleavage H-protein
Sapur.016G113200.2	8.023072714	-0.918369877	0.120514155	-7.5758	3.51E-14	8.80E-14	grey	-0.379272048	9.68E-07	GO:0000228,GO:0005515	ATRAD21.2,ATSYN3,SYN3	Rad21/Rec8 like family protein	histone acetyltransferase type B catalytic subunit, putative	sister chromatid cohesion 2-protein, putative
Sapur.004G203400.1	1341.916384	0.495758279	0.065479491	7.571199	3.70E-14	9.27E-14	grey	0.48670105	1.03E-10	GO:0005759	ATG50050.1		Mitochondrial glycoprotein family protein	succinate dehydrogenase subunit 4
Sapur.004G229600.1	21.97004888	1.381168889	0.182439842	7.570464	3.72E-14	9.32E-14	grey	0.453050675	3.06E-09	GO:0005515,GO:0006355,GO:0003700	ATG75390.1	AtbZIP44,bZIP44	basic leucine zipper 44	bZIP transcription factor
Sapur.013G107300.2	49.38747212	0.458812923	0.060608834	7.570129	3.73E-14	9.35E-14	grey	0.523091495	2.62E-12	GO:0003926	ATG09510.2	CIN V2	cytosolic invertase 2	neutral/alkaline invertase
Sapur.003G055600.2	16.86765157	0.511759093	0.05866765	7.56675	3.76E-14	9.42E-14	grey	-0.505131419	1.51E-11		ATG45690.1		ubiquitin interaction motif-containing protein	FAN1EBA protein
Sapur.002G200200.6	9.86932767	-0.73448747	0.097048132	-7.56828	3.78E-14	9.48E-14	grey	0.073411098	1.36286319	GO:0006810,GO:0005622	ATG93660.1		Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain	Ras GTPase-activating protein-binding protein
Sapur.016G186700.3	13.20789841	-0.651867053	0.113550475	-7.56537	3.84E-14	9.62E-14	grey	-0.54302003	1.87E-13		ATG68630.1		Bcl6-like family protein	transcription regulator, putative
Sapur.012G092500.1	10.06011148	-0.943588671	0.124732868	-7.56488	3.88E-14	9.73E-14	grey	0.535181865	5.16E-13	GO:0051603,GO:0005839,GO:0004298	ATG79233.2		N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	NA
Sapur.017G008700.1	354.109138	0.384510828	0.050843713	7.562603	3.95E-14	9.90E-14	grey	0.479390395	2.13E-10		ATG20560.1		DNA heat shock family protein	Dnaj heat shock family protein
Sapur.006G194500.2	1.429671585	-0.765207247	0.232312846	-7.56096	4.08E-14	1.00E-13	grey	-0.514229969	1.41E-09		ATG72710.1		lysine decarbonylase family protein	cyclotron-dioxide 5'-monophosphate phosphorbiohydrolase LOG3
Sapur.T101400.1	0.6919812	2.423881389	0.320620116	7.55975	4.04E-14	1.01E-13	grey	0.496130867	3.91E-11					NA
Sapur.015G117500.1	79.78946605	0.61875686	0.11455193	7.55787	4.13E-14	1.03E-13	grey	0.41697852	1.05E-08		ATG17230.1	ATHSL1/S1	heat stable protein 1	stress responsive A/B barrel domain protein
Sapur.016G184800.1	69.03607593	0.882375927	0.116757292	7.557366	4.11E-14	1.03E-13	grey	0.362887432	3.41E-06	GO:0055114,GO:0016491	ATG05120.1		FAD/NAD(P)-binding oxidoreductase family protein	monooxygenase, putative
Sapur.015G000300.1	5.863715664	0.775397852	0.103268629	-7.55688	4.13E-14	1.03E-13	grey	-0.536191798	1.58E-13	GO:0016020,GO:0004970	ATG14810.1	ATGLR3.6,GLR3.6	glutamate receptor 3.6	glutamate receptor
Sapur.004G089800.1	1.13135556	1.529564349	0.134763901	7.556264	4.15E-14	1.04E-13	grey	-0.430948586	1.85E-08					NA
Sapur.007G126300.1	69.98261317	0.638267127	0.091262409	7.55287	4.18E-14	1.05E-13	grey	-0.505038384	1.52E-11	GO:0016758,GO:0008152	ATG43840.2	UGT74F1	UDP-glycosyltransferase 74 F1	NA
Sapur.002G052100.1	61.52917424	-0.494783947	0.065571269	-7.54574	4.56E-14	1.13E-13	grey	-0.29917119	0.000138062					hypothetical protein
Sapur.003G060600.1	21.75623688	-0.681681856	0.090609942	-7.54466	4.62E-14	1.15E-13	grey	-0.5047537	1.58E-11	GO:0016020,GO:0008375	ATG25970.1		Cox6c-1/-2/-3 branching beta-1,6-N-acetylglucosaminyltransferase family protein	cox6c-1/-2/-3 branching enzyme
Sapur.016G039100.3	2.50927956	-1.433717626	0.190114927	-7.54132	4.65E-14	1.16E-13	grey	-0.13790038	0.030352527	GO:0007264,GO:0005525	ARAC1.ATROPG,RAC3.RHO1	RAC-like 3		Ras small GTPase family Rho protein
Sapur.012G094400.1	1421.063827	0.520207748	0.068349064	7.540389	4.68E-14	1.17E-13	grey	0.476414165	3.42E-10		ATG74510.1		Aluminium induced protein with YGL and LRDR motifs	stem-specific protein tsj1 protein, putative
Sapur.015G146700.1	5.842794855	-1.161202237	0.175552288	-7.53987	4.76E-14	1.18E-13	grey	0.467037863	7.01E-10		ATG51690.1	ESK1,TBL29	Plant protein of unknown function (DUF828)	NA
Sapur.010G152200.1	15.68369717	0.594271523	0.078845515	7.537093	4.81E-14	1.20E-13	grey	0.489737414	7.55E-11		ATG37975.1		Yos1-like protein	Yos1-like protein
Sapur.005G028200.1	5.828718122	-2.066038884	0.27168726	-7.53489	4.88E-14	1.21E-13	grey	-0.505131419	1.51E-11					kinesin-12 family protein, putative
Sapur.006G074500.1	6.215140861	-1.858188229	0.246625549	-7.53445	4.90E-14	1.22E-13	grey	-0.48355362	1.41E-10	GO:0055114,GO:0016491,GO:0005507	ATG29130.1	ATLAC1,LAC2	laccase 2	laccase
Sapur.003G139300.1	39.47261162	0.777060647	0.101410322	7.53227	4.95E-14	1.24E-13	grey	-0.498962969	2.91E-11	GO:0006412,GO:0003824	ATHRR1,PRR1	pinoresinol reductase 1	pinoresinol-lariciresinol reductase-like protein	pinoresinol-lariciresinol reductase-like protein
Sapur.013G140400.1	48.22787743	-0.390820904	0.051890496	-7.53162	5.00E-14	1.25E-13	grey	-0.529642032	9.98E-13		ATG20730.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.016G184300.1	17.67373122	-0.461874881	0.062146128	-7.53148	5.01E-14	1.25E-13	grey	-0.488309046	4.98E-11	GO:0005515,GO:0030117,GO:0016192,GO:0006886,GO:0005198	ATG22360.1		Vesicle transport protein SFT2 family protein	coatomer beta subunit, putative
Sapur.002G084000.1	72.5837664	0.61384264	0.081519643	7.529997	5.07E-14	1.27E-13	grey	0.500578861	2.45E-11	GO:0016758,GO:0008152	ATG22400.1	ATUGT84A1,UGT84A1	UDP-Glycosyltransferase family protein	UDP-glucosyltransferase family protein
Sapur.013G135200.1	1427.943861	0.305684432	0.021998842	7.52867	5.08E-14	1.27E-13	grey	0.482898611	8.22E-11		ATG49750.1	ACS1,ATLS-8,CPACS1,OASB	D-serine/serine (thiol) lyase B	cysteine synthase
Sapur.015G197005.1	21.53863753	0.581401197	0.082304387	7.52775	5.12E-14	1.28E-13	grey	-0.52589175	2.76E-12	GO:0008270,GO:0005515	ATG58935.3		RING/U-box superfamily protein	ariadne and alpha-actinin-binding protein
Sapur.018G053500.4	2.347836615	-1.421600988	0.188836134	-7.52627	5.14E-14	1.28E-13	grey	-0.388962423	4.79E-07		ATG00602.2		alpha/beta-Hydrolases superfamily protein	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.016G093200.1	46.26119465	1.011380168	0.134368083	7.528061	5.15E-14	1.28E-13	grey	0.467288297	9E-10		ATG47540.1		Mo25 family protein	NA
Sapur.006G118100.1	1297.533804	0.304964409	0.040520202	7.52787	5.24E-14	1.31E-13	grey	0.511802594	3.68E-12	GO:0055114,GO:0016491,GO:0010181	ATG60550.2	DDE1,ORR3	oxophytodienoate-reductase 3	12-oxophytodienoate reductase
Sapur.016G034500.2	218.0667839	0.941868895	0.125113471	-7.52139	5.42E-14	1.36E-13	grey	-0.506692621	1.28E-11	GO:0005515	ATG10260.1	AtRAB41or,AtRAB1e	RAB GTPase homologs 1E	NA
Sapur.15WG119800.3	3.06218869	-1.499092629	0.199371225	-7.5191	5.52E-14	1.38E-13	grey	-0.195683369	0.01404562		ATG29550.1	ACP4	acyl carrier protein 4	acyl carrier protein
Sapur.010G200200.2	1.673501151	1.248318853	0.166954209	7.519454	5.56E-14	1.39E-13	grey	-0.508487298	1.1E-11		ATG40410.1		D11/CYCD-12 family protein	D11/CYCD-12 family protein
Sapur.013G101900.1	66.69642553	0.644864659	0.085833229	-7.51307	5.78E-14	1.44E-13	grey	-0.257576265	0.001126752	GO:0015126,GO:0003824,GO:0055139,GO:0009451	ATG72090.1		Methylthiotransferase	radical SAM methylthiotransferase, MiaB/RimO family protein
Sapur.014G014400.1	4.366252869	-2.050271594	0.273574074	-7.51194	5.83E-14	1.45E-13	grey	-0.506170136	1.3E-11		ATG52461.1			cytochrome P450 family
Sapur.018G028500.3	5.4873113	0.974461555	0.129727416	7.511254	5.88E-14	1.46E-13	grey	-0.011505209	0.886280242		ATG11440.1	CID1,DPD1	CTC-interacting domain 5	hypothetical protein
Sapur.006G023100.2	1.687406891	2.230080977	0.296992562	7.508965	5.96E-14	1.49E-13	grey	0.202195554	0.010103134	GO:0005515	ATG79590.1	ATSYP52,SYP52	syntaxin of plants 52	syntaxin-52 protein
Sapur.018G068200.2	3.4427862	-1.061984856	0.141438979	-7.50818	6.06E-14	1.49E-13	grey	-0.537848176	3.72E-13		ATG74810.1		Arfadin/phosphoinositide binding protein	arfadin and alpha actinin-binding protein
Sapur.010G124000.2	2.344898363	-1.726605295	0.230205409	-7.50614	6.09E-14	1.52E-13	grey	-0.465503453	8.10E-10	GO:0005515,GO:0006468,GO:0004672	ATG14390.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.002G060400.1	1.421164203	1.547786385	0.19043137	7.506048	6.09E-14	1.52E-13	grey	-0.428604229	2.24E-08					NA
Sapur.014G095800.1	96.90140415	-0.654803352	0.087296528	-7.50091	6.34E-14	1.58E-13	grey	-0.517605684	3.84E-12		ATG47360.1			transmembrane protein, putative
Sapur.006G134400.1	5.116824126	1.350207825	0.180156859	7.495053	6.41E-14	1.60E-13	grey	-0.506692621	1.28E-11	GO:0055114	AHL20	AHL20	AT-hook motif nuclear-localized protein 20	AT-hook DNA-binding protein, putative
Sapur.014G088800.3	12.51378204	-0.808853364	0.107909547	-7.49369	6.51E-14	1.63E-13	grey	0.015924985	0.843078011	GO:0005525	ATTOC32,PP11,TOC33	translocon at the outer envelope membrane of chloroplasts 33	translocon at the outer envelope membrane of chloroplasts 33	SDS-ribosome-binding GTPase
Sapur.018G000300.1	23.20682854	1.020885826	0.133017963	7.49523	6.62E-14	1.65E-13	grey	0.485131032	1.20E-10		ATG42570.1	DIC2	dicarboxylate carrier 2	NA
Sapur.015G148600.3	3.260867129	-1.144377608	0.15269616	-7.49448	6.66E-14	1.66E-13	grey	-0.49351016	5.13E-11	GO:0016788	ATG11230.1		SGNH hydrolase-type esterase superfamily protein	GDSL esterase/lipase
Sapur.018G018000.1	2.825687372	1.182096804	0.158377557	7.493172	6.72E-14	1.67E-13	grey	0.494096657	4.81E-11	GO:0005515,GO:0016020,GO:0008810,GO:0005215	ATG21980.1		Major facilitator superfamily protein	NA
Sapur.016G038200.1	18.30622172	-2.629012927	0.351150881	-7.48941	6.92E-14	1.72E-13	grey	-0.35821626	4.10E-06		ATG11000.1		Ankyrin repeat family protein	NA
Sapur.001G080800.1	4.273875457	1.023760869	0.136708862	7.488803	6.95E-14	1.73E-13	grey	-0.477101638	2.68E-10		ATG21260.1		Protein of unknown function (DUF761)	DUF761 domain protein
Sapur.005G038800.1	2.105089938	-0.754562446	0.104259322	-7.48767	7.01E-14	1.74E-13	grey	-0.464841452	1.05E-10					NA
Sapur.013G019500.1	71.48276828	-0.812000026	0.108583045	-7.48671	7.06E-14	1.76E-13	grey	-0.163539662	0.040700493	GO:0005515,GO:0043531	ATG27190.1		NB-ARC domain-containing disease resistance protein	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.006G057000.1	35.91953025	-0.563462861	0.075185643	-7.48623	7.08E-14	1.76E-13	grey	-0.517284119	4.04E-12	GO:0004843,GO:0006470,GO:0004722	ATG40180.1	ATHPP2C5,PP2C5	phosphatases 2C 5	protein phosphatase 2C
Sapur.015G053700.1	2.529710738	2.513422319	0.33592297	7.482189	7.31E-14	1.82E-13	grey	-0.400823834	1.97E-07	GO:0004064,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0006553	ATG23730.1	ATH16	xyloglucan endotransglucosylase/hydrolase 16	xyloglucan endotransglucosylase/hydrolase
Sapur.015G060200.1	9.817060201	1.036884293	0.138611391	7.481091	7.37E-14	1.83E-13	grey	0.506169483	1.35E-11		ATG60460.1	ATCPSF30,CPSF30	cleavage and polyadenylation specificity factor 30	NA
Sapur.004G172800.1	0.847646284	2.621258463	0.350682241	7.476476	7.74E-14	1.92E-13	grey	0.439425272	8.53E-09					NA
Sapur.016G150000.5	181.9684947	0.554870164	0.074106063	7.469922	8.02E-14	1.99E-13	grey	-0.142058276	0.035604669	GO:0006396,GO:0003723,GO:0003676	ATG52120.1		SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein	splicing factor-like protein
Sapur.006G155700.14	6.06621561	-0.881665101	0.118030825	-7.46079	8.03E-14	1.99E-13	grey	-0.078548531	0.328149497		ATG13020.1	Emsy N Terminus (ENT)/ plant Tudor-like domains-containing protein		plant/MPWIS-14 protein, putative
Sapur.006G231300.1	2.709369413	1.483853985	0.198650376	7.469686	8.04E-14	2.00E-13	grey	-0.48948851	7.74E-11					NA
Sapur.014G080400.1	211.9650708	0.614404703	0.081610016	7.468488	8.11E-14	2.01E-13	grey	-0.4707595	4.32E-10	GO:0005525	ATG01200.1	ATRAB-A2,ATRABA3,RABA3	RAB GTPase homolog A3	Rab/-related GTPase family A
Sapur.018G017700.1	711.4488188	-0.408791114	0.054739293	-7.468	8.14E-14	2.02E-13	grey	-0.467214313	6.89E-10	GO:0055114,GO:0051537,GO:0016491,GO:0010277	ATG26820.1	TIC55-II	translocon at the inner envelope membrane of chloroplasts 55-II	dioxygenase Rieske iron-sulfur component, putative
Sapur.011G042000.1	153.6748888	0.232437109	0.031166009	7.46602	8.17E-14	2.02E-13	grey	-0.378877229	1.6E-13		ATG48810.1	ATLEA-6,ATEDS-D,ED6	LEA protein family	cytochrome protein b6
Sapur.009G084000.1	1163.760144	0.297901702	0.039800734	7.462624	8.48E-14	2.10E-13	grey	0.495165593	4.32E-11	GO:0006468,GO:0005524,GO:0004672	ATG33950.1	ATOST1/OST1,PAK5,NRK2-6.	Protein kinase superfamily protein	Serine/Threonine-kinase SAPK10
Sapur.016G122700.1	43.08865664	-0.79892968	0.107136939	-7.4557	8.94E-14	2.21E-13	grey	-0.444466611	5.1E-10		ATG45450.1	NF-YB3	nuclear factor Y subunit B3	nuclear transcription factor Y subunit B-3
Sapur.013G139200.1	3.209253173	1.763287882	0.236785954	7.453265	8.97E-14	2.22E-13	grey	-0.452432232	2.51E-09	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATG26730.1	BASL,CYP73B1,CYP73A1	Cytochrome P450 superfamily protein	cytochrome P450 family protein
Sapur.006G000300.1	216.1165033	0.232878405	0.031206752	7.453175	8.97E-14	2.22E-13	grey	-0.445020338	1.28E-09	GO:0016021	ATG02780.1		Nodulin MtN21/EamA-like transporter family protein	sugar efflux transporter for intercellular exchange protein
Sapur.009G096800.1	71.42293933	-0.600252603	0.080543858	-7.45259	9.15E-14	2.27E-13	grey	-0.459845631	1.36E-09	GO:0051205,GO:0016021	ATG44370.1		Membrane insertion protein, OxaA/YidC with tetratricopeptide repeat domain	inner membrane protein
Sapur.003G040600.1	5.130000444	-0.934561378	0.125658153	-7.44383	9.96E-14	2.46E-13	grey	-0.4934726	1.2E-11		ATG60530.1		Tropomyosin-related	transmembrane protein, putative
Sapur.008G029600.1	4.3517834	0.958575986	0.128802754	-7.4422	9.98E-14	2.45E-13	grey	-0.537041716

Sapur.005G036600.1	42.06705627	6.46284462	0.06290782	7.235825	4.63E-13	1.12E-12	grey	0.47726771	2.62E-10	AT3G72580.1	ATEC91	Seed maturation protein	NA
Sapur.013G047800.1	0.69342849	2.85232882	0.39432573	7.233528	4.71E-13	1.14E-12	grey	0.44362549	5.92E-09	AT5G39110.1		RmlC-like cupins superfamily protein	NA
Sapur.013G207100.1	3.30581791	1.55320997	0.21008479	7.232	4.79E-13	1.16E-12	grey	0.47609804	2.96E-10	AT1G01580.1	ATPS1,PS1	Fenthiaval-associated (FHA) domain-containing protein	NA
Sapur.016G203900.3	9.99343015	0.73461928	0.10162612	7.23859	4.88E-13	1.18E-12	grey	0.00517045	0.94875671	AT3G70550.1			plant/MD/10-14 protein
Sapur.006G027300.1	11.53053353	1.80743614	0.19200569	7.22774	4.93E-13	1.19E-12	grey	0.36272027	3.05E-06				transmembrane protein, putative
Sapur.008G005400.1	1.36448863	2.08983731	0.28928916	7.224534	5.03E-13	1.21E-12	grey	0.44141878	7.18E-09	AT2G28690.1		Protein of unknown function (DUF1635)	UPA23, putative
Sapur.007G003500.1	0.82356289	2.39265806	0.31744205	7.22231	5.11E-13	1.23E-12	grey	-0.48940013	8.64E-05	AT3G23755.1			transmembrane family 220 helix protein
Sapur.016G190900.1	0.93562359	2.38269086	0.32698923	7.205521	5.18E-13	1.25E-12	grey	0.45181036	2.85E-09	AT5G62240.1		F-box family protein	F-box protein interaction domain protein
Sapur.006G167700.1	939.2189685	0.34967489	0.04843129	7.21997	5.20E-13	1.26E-12	grey	0.48141246	1.76E-10	GO0065008,GO0004190		Eukaryotic aspartyl protease family protein	aspartyl protease
Sapur.014G041300.1	0.86323539	2.58188189	0.35811839	7.2184	5.26E-13	1.27E-12	grey	-0.49506139	4.37E-11				NA
Sapur.003G133100.1	14.46565236	-0.02730245	0.14233734	-7.21755	5.29E-13	1.28E-12	grey	-0.47436182	4.07E-10	AT3G24220.1	ATNCED6,NCED6	nine-cis-epoxycarotenoid dioxygenase 6	9-cis-epoxycarotenoid dioxygenase
Sapur.002G208700.1	7.00041413	1.36132016	0.18811741	7.21703	5.31E-13	1.28E-12	grey	-0.48166779	1.70E-10	AT1G01251.1	ATPS1,PS1	Fenthiaval-associated (FHA) domain-containing protein	NA
Sapur.014G092600.1	10.85833945	0.84606855	0.11736327	7.216833	5.32E-13	1.28E-12	grey	0.43820899	9.48E-09				hypothetical protein
Sapur.004G004300.4	1.49526815	2.71581309	0.37617761	7.22015	5.37E-13	1.30E-12	grey	0.50243183	1.81E-11	AT3G01083.1	PFC1	Ribosomal RNA adenine dimethylase family protein	ribosomal RNA small subunit methyltransferase A
Sapur.012G051300.3	0.81591184	2.15339288	0.29842084	7.21541	5.38E-13	1.30E-12	grey	0.47962816	2.08E-10	AT3G18040.1	MPK9	MAP kinase 9	MAP kinase
Sapur.016G071300.1	122.7338284	0.60497647	0.08831524	7.21525	5.38E-13	1.30E-12	grey	0.45938959	5.68E-09	AT3G26363.1			transposon mutator subclass protein, putative
Sapur.004G036300.1	821.168837	0.20921841	0.02900122	7.213966	5.43E-13	1.31E-12	grey	0.50067581	2.43E-11	GO0016787			nudix hydrolase
Sapur.017G082200.1	2.97064209	-2.17226526	0.27000849	-7.21196	5.52E-13	1.33E-12	grey	-0.49423086	4.77E-11				ADP%2C ATP carrier protein
Sapur.005G139300.1	157.9164213	0.53024388	0.07218659	7.21095	5.58E-13	1.35E-12	grey	0.45511602	2.07E-09				hypothetical protein
Sapur.001G120300.1	453.4613223	0.24779547	0.03438186	-7.20863	5.65E-13	1.36E-12	grey	-0.50903669	9.94E-12				hypothetical protein
Sapur.004G004900.1	13.85509477	0.82223853	0.11402037	7.20875	5.66E-13	1.36E-12	grey	0.46277885	1.60E-09				hypothetical protein
Sapur.015G209500.1	49.23188039	-0.82319863	0.11540831	-7.20577	5.77E-13	1.39E-12	grey	-0.49720258	1.49E-11	GO0140853,GO0050975		DRT102	DNA-damage-repair/toleration protein (DRT102)
Sapur.014G080800.4	1.30590881	2.60327824	0.12684878	7.20574	5.77E-13	1.39E-12	grey	-0.48116254	1.76E-10	GO0004488,GO0005524,GO0004672		ATMAPK4,MPK4	MAP kinase 4
Sapur.010G071400.1	113.27056	0.59166936	0.08124649	-7.20489	5.81E-13	1.40E-12	grey	-0.49982534	2.66E-11	GO0016021			Cytochrome b561/ferric reductase transmembrane protein family
Sapur.002G084800.2	15.04176658	0.75108409	0.10425163	7.09495551	5.82E-13	1.40E-12	grey	0.45469703	9.93E-10				transducin family protein / WD-40 repeat family protein
Sapur.001G136400.2	3.98009368	-1.12476546	0.15618528	-7.20135	5.96E-13	1.43E-12	grey	-0.13066005	0.08396772	GO0006355,GO0005634,GO0003700		AGL6,SEP3	K-box region and MADS-box transcription factor family protein
Sapur.006G146300.1	15.20045705	-0.27202899	0.17698537	-7.19861	6.08E-13	1.46E-12	grey	-0.52832845	2.76E-12			ATNAS4,NAS4	nicotianamine synthase 4
Sapur.017G023600.1	19.15768204	0.48673648	0.06756896	7.19762	6.12E-13	1.47E-12	grey	-0.50904042	9.93E-12	GO0005515,GO0043531			LRR and NB-ARC domains-containing disease resistance protein
Sapur.015W0204600.1	52.48082044	0.75438421	0.10483325	7.196515	6.18E-13	1.48E-12	grey	0.39580991	2.88E-07	GO0005886,GO0016020,GO0008811,GO0005216		ATCNGC20,CNBT,CNGC20	cyclic nucleotide-gated ion channel protein, putative
Sapur.005G135400.2	4.76411347	1.09682705	0.15869374	7.195469	6.22E-13	1.50E-12	grey	0.50017191	2.47E-11				O-fucosyltransferase family protein
Sapur.006G181700.5	3.72017302	-1.15260608	0.16015743	-7.19456	6.27E-13	1.51E-12	grey	-0.50488454	1.62E-11				hypothetical protein
Sapur.009G000300.1	1.08578922	-1.36779872	0.25960539	-7.19445	6.27E-13	1.51E-12	grey	-0.52874244	1.86E-12	GO0043139,GO0003697			toprim domain-containing protein
Sapur.009G105100.4	4.13350192	-0.15266854	0.15363524	-7.1941	6.29E-13	1.51E-12	grey	-0.48224125	1.08E-10				crossover junction endodeoxyribonuclease, putative
Sapur.004G103300.1	8477.848861	0.40600152	0.05855612	7.19384	6.30E-13	1.52E-12	grey	-0.52302294	2.64E-12	GO0016758,GO0005886,GO0006694,GO0003854		ATUGT82A1,UUG2	NADP(+)-binding Rossmann-fold superfamily protein
Sapur.004G146600.1	31.87602736	-2.17165408	0.17679605	-7.19206	6.38E-13	1.54E-12	grey	-0.52692758	1.39E-12	GO0004180,GO0030410		ATNAS4,NAS4	nicotianamine synthase 4
Sapur.015G201900.1	5.84608387	-0.97966195	0.13267813	-7.19169	6.39E-13	1.54E-12	grey	-0.48809135	1.32E-11	GO0005515,GO0043531			LRR and NB-ARC domains-containing disease resistance protein
Sapur.002G015300.1	5.72104059	1.14796783	0.15960994	7.191581	6.40E-13	1.54E-12	grey	0.46288545	1.03E-09	GO0046872,GO0030001		AT4G16380.1	Heavy metal transport/detoxification superfamily protein
Sapur.016G247500.1	0.60729618	3.73264808	0.38103693	7.188698	6.54E-13	1.57E-12	grey	0.45251605	2.68E-09				NA
Sapur.009G080600.1	0.86291512	2.34806015	0.32671169	7.188687	6.54E-13	1.58E-12	grey	-0.49516844	4.12E-11				NA
Sapur.007G009800.1	1.23082283	2.58326512	0.35972662	7.18142	6.90E-13	1.66E-12	grey	-0.4225239	3.54E-08	GO0003677		PGAL,WUS,WUS1	Homeodomain-like superfamily protein	wuschel protein
Sapur.008G005200.1	18.86805102	0.61182748	0.08514884	7.18124	6.91E-13	1.66E-12	grey	-0.12708026	0.11209969	GO0004419,GO0005524,GO0048812,GO0000166			Tyrosyl-tRNA synthetase, class Ib, bacterial/mitochondrial
Sapur.006G101200.1	894.7829797	0.31253527	0.04352415	7.180747	6.93E-13	1.67E-12	grey	0.50719111	1.22E-11	GO0008152,GO0003824			phosphoadenosine phosphosulfate (PAPS) reductase family protein
Sapur.014G078200.1	29.29608884	0.72111275	0.10076574	7.179721	6.99E-13	1.68E-12	grey	0.03934221	0.65108756	GO0005515			Galactose cyclonase-like family protein
Sapur.013G087300.1	54.7924176	0.81947509	0.11414347	7.179161	7.03E-13	1.69E-12	grey	0.46356153	9.72E-10				Tyrosine phosphatase family protein
Sapur.004G164100.2	24.64863420	0.92700181	0.07063197	7.179065	7.07E-13	1.70E-12	grey	0.45429566	2.28E-09	GO0050307,GO0005886			Sucrose-6F-phosphate phosphohydrolase family protein
Sapur.006G076600.1	25.41529691	0.80240517	0.11180402	-7.17705	7.12E-13	1.71E-12	grey	-0.48482133	1.24E-10	GO0015434,GO0016021,GO0005375		AT5G59030.1	COPT1	copper transporter 1	copper transporter
Sapur.008G089100.1	4.70268838	1.12326528	0.15609129	7.17025	7.12E-13	1.71E-12	grey	0.41429566	5.26E-08	GO0046983,GO0003677		AT5G56180.1	MADS box transcription factor (DNA-binding and dimerization domain) protein	34-type transcription factor (DNA-binding and dimerization domain) protein
Sapur.003G052300.1	4.88574137	-0.21862853	0.14109529	-7.17658	7.15E-13	1.72E-12	grey	-0.48584895	1.12E-10				NA
Sapur.005G189100.2	1.86159487	-1.71037639	0.23859172	-7.17081	7.46E-13	1.79E-12	grey	-0.50530842	1.48E-11	GO0016747			HXXXD-type acyl-transferase family protein
Sapur.007G107700.1	0.86010193	2.62329095	0.3714042	7.168242	7.50E-13	1.80E-12	grey	0.47388543	4.61E-10		AGL22,SVP	AGL22,SVP	K-box region and MADS-box transcription factor family protein
Sapur.001G057700.1	191.6847823	0.52181122	0.07280185	7.16811	7.60E-13	1.82E-12	grey	0.43995878	8.15E-09				NA
Sapur.005G127100.1	0.95348557	2.17788614	0.30274827	7.167779	7.62E-13	1.83E-12	grey	0.47461755	1.36E-10	GO0009055			Cupredoxin superfamily protein
Sapur.010G138200.5	9.62001562	0.77184776	0.10769557	-7.16686	7.67E-13	1.84E-12	grey	0.20679976	0.00936003	GO0055114,GO0016491,GO0008270		AT5G03080.1	Zinc-binding dehydrogenase family protein	alcohol dehydrogenase
Sapur.T085400.1	13.34319922	0.55379359	0.07718654	7.16643	7.70E-13	1.85E-12	grey	-0.46092256	5.76E-10	GO0080167,GO0070718,GO0015124,GO0003777,GO0005871	ATPS1,PS1	AT1G01580.1	Fenthiaval-associated (FHA) domain-containing protein	NA
Sapur.013G050000.1	241.7979572	0.46593114	0.06598124	7.164871	7.73E-13	1.87E-12	grey	0.46960524	1.49E-10	GO0016758,GO0005886,GO0016614		AT3G03040.1	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	NA
Sapur.006G027400.1	592.5519803	0.42648436	0.05950445	7.16296	7.98E-13	1.92E-12	grey	-0.50834762	1.07E-11	GO0042561,GO0006355,GO0005634,GO0003700	AT-HSFB3,HSFB3	AT4G18880.1	heat shock transcription factor B3	heat shock transcription factor
Sapur.015W0204500.1	0.76392043	2.19191922	0.30607189	7.16133	7.99E-13	1.92E-12	grey	-0.40726839	1.20E-07				NA	NA
Sapur.006G047000.1	11.60311245	-1.12532589	0.15882985	-7.15885	8.14E-13	1.95E-12	grey	-0.45339125	2.08E-09	GO0003824,GO0006370,GO0004731	AIDBP1,DBP	AT2G26320.1	DNA-binding protein phosphatase 2C	DNA-binding protein phosphatase 2C
Sapur.009G139500.1	3.11847739	-0.60857889	0.17469707	-7.15441	8.46E-13	2.03E-12	grey	-0.4528984	2.16E-09	GO0004040,GO0016762,GO0006027,GO0005618,GO0005975,GO0004553		AT2G22120.2	xyloglucan endotransglucosylase/hydrolase 9	xyloglucan endotransglucosylase/hydrolase, putative
Sapur.001G075200.1	4.80424271	-1.79634709	0.25135325	-7.15383	8.44E-13	2.02E-12	grey	-0.49172006	6.17E-11				hypothetical protein
Sapur.003G028800.1	6.42992552	2.03047154	0.29572561	7.1488	8.48E-13	2.03E-12	grey	-0.49184201	2.16E-11	GO0006355,GO0003700		AT5G11590.1	TINY2	Integrase-type DNA-binding superfamily protein	AP2 domain transcription factor 2
Sapur.005G049600.1	257.7879574	0.90477762	0.12613281	7.1509	8.62E-13	2.07E-12	grey	0.47581535	3.02E-10	GO0055114,GO0016491		AT2G31.3,ATGA2OXO2,GA2OX2	gibberellin 20 oxidase 2	gibberellin 20-oxidase
Sapur.006G096600.1	54.54734384	0.92388276	0.1298933	7.1498943	8.66E-13	2.08E-12	grey	0.35726538	3.82E-06				sequence-specific DNA binding transcription factors	Myb/SANT-like DNA-binding domain protein
Sapur.005G189100.1	20.37995696	-0.78208517	0.10930233	-7.14936	8.72E-13	2.09E-12	grey	-0.01679547	0.83471414	GO0055085,GO0016021		AT3G16980.2	Major facilitator superfamily protein	Hypocampus abundant transcript protein
Sapur.T016400.1	0.76085457	2.16401143	0.29452783	7.1449	8.74E-13	2.10E-12	grey	0.50965426	9.26E-12				NA	NA
Sapur.010G070300.1	14.17934803	0.73164198	0.10245391	-7.14152	9.22E-13	2.21E-12	grey	-0.50472051	1.58E-11	GO0063151,GO0003677		AT3G61850.1	DAG1	Dof type zinc finger DNA-binding family protein	NA
Sapur.009G037300.1	68.4236534	0.76369032	0.10684476	7.140419	9.32E-13	2.23E-12	grey	0.45268064	2.81E-09	GO0046872,GO0030001		AT4G27580.2	Heavy metal transport/detoxification superfamily protein	heavy metal associated domain protein
Sapur.010G120700.1	3.27817163	-1.25562066	0.17585239	-7.14004	9.33E-13	2.23E-12	grey	-0.01626109	0.84077483	GO0005975		AT1G13700.1	PGL1	6-phosphogluconolactonase 1	gluconamine-6-phosphate isomerase
Sapur.013G074400.1	24.98369012	0.72024182	0.10087774	7.139983	9.38E-13	2.25E-12	grey	0.46181765	1.44E-09	GO0016020,GO0006886,GO0006605			sec1/sec61-gamma protein transport protein	protein transport Sec61 subunit gamma
Sapur.007G082500.1	1119.894994	0.27462568	0.03924702	7.13945	9.37E-13	2.24E-12	grey	0.47939346	2.34E-10	GO0016301,GO0003700		AT3G26030.1	related to AP2 6	dehydration-responsive element-binding protein	dehydration-responsive element-binding protein
Sapur.015W0207400.1	40.67252247	0.55680975	0.07998935	7.136953	9.54E-13	2.28E-12	grey	0.04840281	0.54719276	GO0112251,GO0016490,GO0010215		AT5G60920.1	COB	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family	phytochelatin synthetase-like protein
Sapur.007G043900.1	24.39212884	0.58842409	0.08245762	7.13664	9.60E-13	2.30E-12	grey	-0.02820742	0.75362045	GO0003824,GO0030770,GO0015124,GO0003777,GO0005871		AT5G47620.2	FRA1	F-box containing-ubiquitin-dependent proteasome subunit family protein	chromosome-associated kinesin KIF5, putative
Sapur.006G171900.1	17.68871828	-0.47887785	0.20657033	-7.13504	9.68E-13	2.31E-12	grey	-0.45654708	1.86E-09	GO0055114,GO0050660,GO0016614			NA	NA
Sapur.006G181300.1	460.0807572	0.23620389	0.03300261	7.13427	9.73E-13	2.33E-12	grey	-0.50915605	1.82E-12	GO0006950		AT1G13360.3	Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.018G086500.1	35.71025275	-0.46865659	0.06291825	-7.13093	9.97E-13	2.38E-12	grey	-0.47975032	2.05E-10	GO0046408,GO0004672,GO0005975,GO0004553	CRK10,RLK4	AT4G21380.1	cysteine-rich RLK (RECEPTOR-like protein kinase) 10	NA
Sapur.014G083800.2	0.80542799	-2.57656357	0.36179461	-7.1309	9.97E-13	2.38E-12	grey	-0.52414606	1.85E-12	GO0046983		AT5G60150.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.010G253800.1	3.80324957	-1.00549781	0.14100482	-7.13039	1.00E-12	2.39E-12	grey	0.50710194	1.22E-11	GO0008270,GO0005515		AT5G38895.3	RING/U-box superfamily family protein	RING zinc finger protein, putative
Sapur.015W0201400.1	0.58791989	-2.61959496	0.36738784	-7.13034	1.00E-12	2.39E-12	grey	-0.52393763	1.97E-12	GO0055114,GO0020037,GO0016705,GO0005506	CYP718T	AT1G13110.1	cytochrome P450, family 71 subfamily B, polypeptide 7	cytochrome P450 family protein
Sapur.014G086300.2	468.757456	0.41870123	0.05873246	7.128861	1.01E-12	2.40E-12	grey	0.51496085	0.15163946			AT1G61310.4	Cytochrome c oxidase subunit Va family protein	NA
Sapur.006G149800.1	236.7679608	0.27570922	0.03867829	-7.12854	1.01E-12	2.41E-12	grey	-0.52796495	1.28E-12			AT2G42630.1	zinc ion binding nucleic acid binding	C2H2 type of rmt: zinc -finger protein
Sapur.005G175000.1	40.28622843	0.30700442	0.18342925	7.12804	1.02E-12	2.42E-12	grey	0.36005036	2.42E-06	GO0055114,GO0016491	ACOL,EAT1,EFE	AT5G05010.1	ethylene-responsive	NA
Sapur.002G043400.1	60.92656317	0.50031705	0.07019162	7.125085	1.04E-12	2.49E-12	grey	0.49327111	5.25E-11	GO0016020,GO0008236,GO0006508	PLSP1	AT2G45590.1	plastidic type I signal peptidase 1	signal peptidase I
Sapur.005G137200.1	223.7793834	0.32382615	0.04546213	7.12149	1.04E-12	2.49E-12	grey	-0.42832711	2.08E-08			AT1G21520.1	Histone H3-K4-specific methyltransferase SET7/9 family protein	phosphatidylinositol-4-phosphate 5-kinase, putative
Sapur.007G009600.1	100.4546183	0.19874301	0.02790176	7.122321	1.06E-12	2.54E-12	grey	-0.48670295	1.03E-10			AT5G60590.3	oxidoreductase, 2OG-Fe(II) oxygenase family protein	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein
Sapur.012G082600.1	49.78718562	0.87806584	0.11762025	7.121725	1.07E-12	2.56E-12	grey	0.47230246	5.43E-08			AT2G25140.1	Protein of unknown function (DUF227)	DUF227 family protein
Sapur.001G127000.1	16.54650887	0.70609947	0.11001624	-7.11884	1.08E-12	2.58E-12	grey	-0.50243238	2.02E-11	GO0071949		AT3G56680.1	CTF2A	FAD/NAD(P)-binding oxidoreductase family protein	CTF2A-like oxidoreductase
Sapur.006G194300.1	2.16234887	-1.33052138	0.18689420	-7.11821	1.09E-12	2.61E-12	grey	-0.48337344	1.64E-10	GO0016020,GO0006810,GO0005215		AT2G31861.1	AtZIN2,CIRS,ZIN2,ZRA3,OR	NRAMP metal ion transporter family protein	ER/Golgi zinc protein, vacuolar transporter
Sapur.008G020400.3	1.06215735	-1.95726649	0.27406611	-7.11811	1.09E-12	2.61E-12	grey	-0.29725291	0.00015649			AT3G21735.2	DNA binding	plastid DNA-binding protein, putative
Sapur.018G112300.1	3.12663827	2.34981164	0.33127344	7.117895	1.10E-12	2.62E-12	grey	0.44627196	7.92E-09			AT3G44600.1	Pentatricopeptide repeat (PPR-like) superfamily protein	NA
Sapur.014G100600.1	1.76142233	-0.34276499	0.04815721	-7.11579	1.10E-12	2.63E-12	grey	0.64879041	5.94E-10			AT4G09670.1	NADH-ubiquinone oxidoreductase-related	NA
Sapur.010G072200.1	806.5118916	0.17863878	0.02510714	7.116314	1.11E-12	2.65E-12	grey	0.49342875	5.17E-11	GO0005208,GO0005838	RPN12a	AT5G65320.1	regulatory particle non-ATPase 12A	26S proteasome non-ATPase regulatory subunit, putative
Sapur.005G181000.1	47.87845864	0.48532033	0.06824053	7.1164	1.12E-12	2.68E-12	grey	-0.49006239	1.54E-11			AT4G03570.1	trx18 protein	Trx18
Sapur.009G123000.1	19.85995514	0.65582593	0.09216247	7.114423	1.12E-12	2.68E-12	grey	0.39214743	1.80E-07	GO0016491,GO0008152		AT3G24190.2	NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase
Sapur.006G184700.2	1.56454885	-1.69372628	0.2281243	-7.11187	1.14E-12	2.71E-12	grey	-0.51475447	1.87E-12			AT3G10100.1	NA	prolyl oligopeptidase family protein
Sapur.012G058800.1	42.23375292	-0.61466497	0.08430882	-7.11246	1.14E-12	2.72E-12	grey	-0.15493755	0.05485714	GO0005515	IQD31	AT4G26690.1	IQ-domain 31	IQ calmodulin-binding motif protein, putative
Sapur.T018300.1	2.08792435	-1.56457213	0.22000456	-7.11168	1.15E-12	2.74E-12	grey	-0.46221539	5.82E-09	GO0005515	ATPS1,PS1	AT1G01580.1	Fenthiaval-associated (FHA) domain-containing protein	NA
Sapur.003G079300.1	1.20158192	2.32825367	0.32709767	7.111402	1.15E-12	2.74E-12	grey	0.45731884	1.75E-09			AT5G19180.1	NA	NA
Sapur.009G037600.1	8.90877214	-0.71561786	0.10052387	-7.10979	1.16E-12	2.77E-12	grey	-0.51439642	5.53E-12			AT3G46420.1	NRAMP metal ion transporter family	NRAMP metal ion transporter family
Sapur.003G231100.2	47.66755559	0.54321536	0.07640658	7.109691	1.16E-12	2.77E-12	grey	-0.25387946	0.00137209			AT5G11190.1	LITAF-like zinc ribbon domain protein	LITAF-like zinc ribbon domain protein
Sapur.015W0104400.1	128.4921519	0.56288044	0.07917833	7.100041	1.17E-12	2.79E-12	grey	0.48012219	1.98E-10	GO0005515,GO0006468,GO0005524,GO0004672	AT3G21880.1	EVR,SOBIR1	Leucine-rich repeat protein kinase family protein	NA
Sapur.016G202100.1	14.98042818	-0.70083014	0.10372692	-7.10746	1.18E-12	2.81E-12	grey	-0.47851409	2.24E-10	GO0043531	AT4G27220.1	NB-ARC domains-containing disease resistance protein	NA
Sapur.001G076500.1	20.59150522	-0.67981221	0.09655391	-7.10688	1.19E-12	2.83E-12	grey	-0.47848715	1.78E-10			AT4G18930.1	NA	AwPCF-9 rapidly elicited protein, putative
Sapur.009G051300.1	18.56193121	0.60806136	0.09414857	7.106413	1.19E-12	2.84E-12	grey	0.47463381	3.70E-10	GO0004333,GO0005737,GO0005524,GO0004827	CHAL,PROR51	AT5G25120.1	Class II aarB and biotin synthetases superfamily protein	NA
Sapur.013G098800.1	27.41188995	0.93833982	0.13201416	7.105479	1.20E-12	2.86E-12	grey	0.43605939	8.76E-09	GO0055114,GO0016491,GO0010181	ATOPR2,OPR2	AT2G06050.2	12-oxophytodienoate reductase 2	NA
Sapur.005G096800.2	120.9656327	2.13141465	0.30146623	7.101839	1.21E-12	2.88E-12	grey	0.13736753	0.08623247			AT5G19150.1	NA	hypothetical protein
Sapur.007G018200.1	15.40269992	1.27265188	0.23639924	7.099208	1.22E-12	2.90E-12	grey	0.37889508	9.17E-07	GO0008168		AT3G48080.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase
Sapur.015G244400.1	3.08409869	1.73576372	0.24512734	7.088159	1.26E-12	3.01E-12	grey	0.42427804	2.04E-08			AT5G44640.1	methyl esterase 18	polyneuridine-aldehyde esterase, putative
Sapur.011G105400.1	105.8889822	0.64830076	0.09139148	7.093663	1.31E-12	3.11E-12	grey	0.47880149	2.24E-10	GO0046261,GO0015979,GO0009654,GO0009523	AT5G60461.1	PSB8	photosystem II subunit R	photosystem II 10 kDa polypeptide PsbR
Sapur.002G098000.1	2.06553624	1.47432245	0.20792563	7.093077	1.31E-12	3.12E-12	grey	0.46858095	7.66E-10	GO0055085,GO0016021		AT5G75230.1	Major facilitator superfamily protein	sugar transporter ERD6-like protein
Sapur.017G052900.1	3.16451614	-1.30368521	0.17050329	-7.09088	1.33E-12	3.17E-12	grey	-0.49987325	2.64E-11			AT3G16930.2	ATSBL1,SBL1	shikimate kinase 1	shikimate kinase
Sapur.005G088400.4	1.29176328	2.37836265	0.31545979	7.089959	1.34E-12	3.19E-12	grey	-0.03877572	0.42968958	GO0004298,GO0005525	AT1G78600.2	ARACI1,ATGP2,ATRACI1,ATR	Arabidopsis RAC-like 1	Rac-like small GTPase
Sapur.019G021200.1	0.77362996	2.40132605	0.41819869	7.088619	1.35E-12	3.20E-12	grey	0.39263618	3.65E-07		AT2G46561.1		Domain of unknown function (DUF213)	DUF213 domain protein
Sapur.006G103800.2	7.24235613	0.91885479	0.12972766	-7.08348	1.41E-12	3.35E-12	grey	-0.42123801	1.94E-08	GO0043565		AT3G70100.1	Translin family protein	translin
Sapur.009G000500.1	6.12446647	2.27963888	0.32174184	7.081605	1.42E-12	3.36E-12	grey	-0.47863182	2.56E-10	GO0005515	AtRLP5,RLP5	AT1G74170.1	receptor like protein 5	NA
Sapur.009G134900.1	4.54895034	-1.13180187	0.16005195	-7.08133	1.43E-12	3.40E-12	grey	-0.48353203	1.41E-10			AT3G27630.1	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.011G096500.1	1.65867105	-1.94268392	0.27488224	-7.08094	1.44E-12	3.41E-12	grey	-0.68267608	1.02E-10			AT5G45461.1	Tetratricopeptide repeat (TPR)-like superfamily protein	hypothetical protein
Sapur.016G181300.1	734.6537514	0.30628776	0.04362262	7.079106	1.45E-12	3.45E-12	grey	0.46637868	7.46E-10	GO0005515		AT4G34150.1	Calcium-dependent lipid-binding (CaLB domain) family protein	C2 domain protein
Sapur.008G105300.1	1.86406475	-1.38464829	0.19538885	-7.07593	1.47E-12	3.49E-12	grey	-0.49644881	1.47E-10		ATSNAP30,SNAP30	AT5G08390.1	soluble N-ethylmaleimide-sensitive factor adaptor protein 30	synaptosomal-associated protein
Sapur.006G070900.1	11.3091682	0.62455162	0.08823928	-7.07753	1.47E-12	3.49E-12	grey	-0.45965138	1.40E-09			AT2G37650.1	GRAS family transcription factor	GRAS family transcription factor
Sapur.006G200800.1	151.1309004	0.42575754	0.06017337	-7.07734	1.47E-12	3.50E-12	grey	-0.49234605	5.78E-11			AT1G12700.1	ATP binding;nucleic acid binding;helicases	NA
Sapur.T192900.1	2.22603842	-2.64161114	0.28892172	-7.07588	1.48E-12	3.51E-12	grey	0.44452611	1.71E-09	GO0007165,GO0005515,GO0043531		AT5G66930.2	Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.015G051900.1	1.66206083	2.31531827	0.27350421	7.074555	1.50E-12	3.57E-12	grey	0.42842884	3.26E-08	GO0005515		AT5G07040.1	Leucine-rich repeat transmembrane protein kinase	NA
Sapur.008G207100.1	1.98854572	2.34843294	0.27294382	7.07405	1.50E-12	3.57E-12	grey	-0.45531185	2.07E-09			AT5G55520.1	pollen protein-pile E I-like protein	pollen protein-pile E I-like protein
Sapur.007G012900.1	2.82665054	-1.47245626	0.20814629	-7.074	1.51E-12	3.58E-12	grey	-0.48269165	1.54E-10				NA	NA
Sapur.T020300.1	122.4403474	0.50580197	0.07151003	7.07343	1.51E-12	3.58E-12	grey	-0.03817545	0.63514603		AT3G07730.2	CYT1,EMB3101,GMP1,SD21	Glucose-1-phosphate adenylyltransferase family protein	mannose-1-phosphate guanyltransferase

Sapur.004G079900.1	49.73885189	-1.0140073	0.14676585	-6.90901	4.88E-12	1.14E-11	grey	-0.491427855	6.35E-11	ATSG15980.1	TBL19	TRICHOME BIREFRINGENCE-LIKE 19	Pm5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.003G125400.1	18.59692255	-0.51466487*	0.07451741	-6.90661	4.98E-12	1.16E-11	grey	-0.459429674	1.41E-09	GO:0003676	ATG27330.1	RNA-binding (RNA/RBD/RNP motifs) family protein	RNA recognition motif, a.k.a. RRM/ribo2 RBD protein
Sapur.010G201800.1	75.91608844	-0.41679388	0.06034975	-6.90564	4.98E-12	1.16E-11	grey	-0.472360607	0.0E+00		AT-TCP20,ATTCP20,PCF13,TC	TEOSINTE BRANCHED 1, cycloidea, PCF (TCP)-domain family protein 20	TCP transcription factor
Sapur.007G081000.1	8.917821732	-0.84802454	0.12282036	-6.90461	5.03E-12	1.18E-11	grey	-0.465858116	1.28E-09	GO:0046983	ATSG38070.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	helix loop helix DNA-binding domain protein
Sapur.004G300600.1	15.91608604	-0.37538364	0.05438357	-6.90266	5.06E-12	1.18E-11	grey	-0.48890132	7.42E-11	GO:0008270	ATSG42900.1	CW-type Zinc Finger protein, putative	CW-type zinc finger protein, putative
Sapur.013G160800.1	891.7701524	-0.61195398	0.08865874	-6.90233	5.13E-12	1.19E-11	grey	-0.496935631	6.89E-11		ATSG22710.1	sucrose-proton symporter 2	sucrose transporter
Sapur.013G105900.6	4.12405029	-0.38038449	0.15360885	-6.90185	5.13E-12	1.20E-11	grey	-0.472509131	4.16E-10	GO:0003676	ATSG16633.1	RNPS1,SR45	arginine/serine-rich 45
Sapur.003G112300.2	18.08581818	-0.50364709	0.07297941*	-6.89848	5.28E-12	1.23E-11	grey	-0.478606926	2.30E-10		ATSG12120.1	ubiquinol-cytochrome C chaperone family protein	ubiquinol-cytochrome C chaperone protein
Sapur.012G011600.3	21.71110888	-0.72922165	0.10578856	-6.89649	5.33E-12	1.24E-11	grey	-0.432265158	1.57E-08		ATSG30502.3	alpha/beta-Hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.004G304000.1	236.4322517	0.34747592	0.05034052	6.89684	5.25E-12	1.24E-11	grey	-0.492045652	1.66E-08	GO:0008152,GO:0003824	ATSG34590.1	Transketolase family protein	pyruvate dehydrogenase E1 component subunit beta
Sapur.009G022500.1	89.66892956	0.36387476	0.05270722	6.89529	5.37E-12	1.25E-11	grey	0.501457772	2.23E-11	GO:0003824,GO:0006470,GO:0004722	ATSG07630.1	PLL5	pectin phosphatase 2C, putative
Sapur.002G050600.1	6.391644448	-0.81682425	0.11873325	-6.88608	5.38E-12	1.36E-11	grey	-0.45693892	1.79E-09				transmembrane protein, putative
Sapur.010G147400.7	7.531549727	-0.75266521	0.10916132	-6.8945	5.41E-12	1.36E-11	grey	-0.483957447	1.35E-10	GO:0008138,GO:0006470	ATSG52730.1	MTMKP1,MKP1	MAP kinase phosphatase
Sapur.006G163700.1	34.31554832	-0.46388733	0.12124133	-6.88369	5.42E-12	1.37E-11	grey	-0.512461239	1.51E-09	GO:0016247,GO:0006842	ATG18A.1	plant U-box 54	E3 ubiquitin-protein ligase PUB22
Sapur.001G143800.1	2311.27303	0.19111746	0.07724969	6.89343	5.45E-12	1.27E-11	grey	-0.455217751	1.32E-09	GO:0005515	ATG52730.2	Transducin/WD40 repeat-like superfamily protein	Serine/Threonine kinase receptor-associated protein, putative
Sapur.010G065600.1	1011.479207	-0.38187288	0.10037988	-6.88257	5.48E-12	1.28E-11	grey	-0.48851154	1.54E-10	GO:0016788	ATSG45670.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-esterase/lipase
Sapur.003G163700.1	23.11616349	-0.74452234	0.10802692	-6.89228	5.48E-12	1.28E-11	grey	-0.293319209	0.000214187		ATSG02580.1	CLPP5,NCLVP1,NCLPP5	nuclear encoded CLP protease 5
Sapur.003G062400.1	1656.149974	0.27018592	0.03910164	6.89223	5.49E-12	1.28E-11	grey	-0.482319112	1.61E-10	GO:0016021,GO:0008250,GO:0004679	ATSG35320.1	DAD2	Defender against death (DAD family) protein
Sapur.019G082100.1	28.34517837	-0.28844981	0.07017909	-6.89095	5.52E-12	1.28E-11	grey	-0.47854211	2.31E-10	GO:0016887,GO:0005524,GO:0006810,GO:0005215	ABC2 family protein	ATATHILATH6	NA
Sapur.010G093000.1	14.30494664	-0.63960343	0.09280731	-6.89172	5.51E-12	1.28E-11	grey	-0.42657243	2.54E-08				NA
Sapur.007G075500.1	13.62173888	-0.52811396	0.16600475	-6.88945	5.56E-12	1.29E-11	grey	-0.438856578	1.36E-08	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATKG38490.1	CYP86A10	cytochrome P450 family 86 protein
Sapur.15W0077600.1	1.267585676	-0.65186334	0.24028578	-6.88841	5.64E-12	1.31E-11	grey	-0.443603665	5.93E-10		ATKG36190.1	Holocaid dehalogenase-like hydrolase (HAD) superfamily protein	HAD superfamily protein
Sapur.15W0072400.1	0.818012467	-0.71828724	0.26853448	-6.88603	5.74E-12	1.34E-11	grey	-0.542078394	2.78E-11		ATG09702.1	dsRNA-binding domain-like superfamily protein	dsRNA-binding domain-like superfamily protein
Sapur.019G072000.1	48.21652647	0.58325468	0.08479667	6.88148	5.92E-12	1.38E-11	grey	0.428647	2.14E-08		ATKG32480.1	Protein of unknown function (DUF506)	DUF506 family protein
Sapur.004G300900.1	2.267026457	-0.98938088	0.34913671	-6.88052	5.96E-12	1.39E-11	grey	-0.4752367	1.8E-10	GO:0005634,GO:0003677	ATKG34760.2	KNOTTIN KNOTTIN-like protein	hevein-like protein
Sapur.002G096000.1	11.50621299	-1.43827795	0.20840053	-6.88058	5.97E-12	1.39E-11	grey	-0.484616104	1.32E-10	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATKG10340.1	CYP76C7	cytochrome P450, family 76, subfamily C, polypeptide 7
Sapur.016G380500.1	11.8972542	0.75025145	0.10905492	6.87961	6.03E-12	1.40E-11	grey	-0.483729103	1.38E-10	GO:0005509	ATKG36470.2	Calcium-binding EF-hand family protein	calcium ion-binding protein
Sapur.018G280800.1	731.013024	-0.22324356	0.03215761	-6.87684	6.05E-12	1.41E-11	grey	-0.44676192	4.49E-09	GO:0055114,GO:0005839,GO:0004298	ATGE45410.1	20S proteasome beta subunit G1	proteasome subunit beta type protein
Sapur.013G160100.1	4.804780431	-0.92792394	0.134887	-6.87926	6.03E-12	1.42E-11	grey	-0.466283511	7.52E-10		ATSG19850.1	alpha/beta-Hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.007G028700.1	6.070274918	-2.23889841	0.33998328	-6.87925	6.04E-12	1.41E-11	grey	-0.508208241	1.08E-11		ATSG66030.1	Protein of unknown function, DUF247	electron transporter, putative
Sapur.007G072000.1	57.35413871	-0.34488254	0.05013571	-6.87724	6.16E-12	1.42E-11	grey	-0.456796006	1.82E-09	GO:0005515	ATSG67082.2	RPN5B	regulatory particle non-ATPase subunit 5B
Sapur.004G300500.1	2.389489974	-0.37008219	0.15573687	-6.8769	6.17E-12	1.42E-11	grey	-0.56228141	4.07E-09	GO:0007275,GO:0006355,GO:0003700	ATSG10640.1	Integrase-type DNA-binding superfamily protein	AP2 domain transcription factor
Sapur.010G034900.1	4.23943807	3.47172477	0.77750684	6.87584	6.18E-12	1.43E-11	grey	0.227063842	0.00241521		ATSG19380.1		NA
Sapur.004G085400.1	3.90607923	1.75028984	0.25460705	6.87393	6.26E-12	1.45E-11	grey	0.42269263	1.03E-09	GO:0048544,GO:0006488,GO:0004672	ATKG27260.1	S-locus lectin protein kinase family protein	Serine/Threonine kinase
Sapur.016G235700.2	36.71562035	0.41800593	0.06372716	6.87347	6.27E-12	1.46E-11	grey	0.521958316	2.38E-12	GO:0003676	ATSG11224.2	RNA-binding (RNA/RBD/RNP motifs) family protein	RNA recognition motif 2 in RNA-binding protein musashi-like musashi protein
Sapur.005G197200.1	43.46146656	0.56126165	0.08330309	6.87267	6.28E-12	1.46E-11	grey	-0.119518007	0.172173163	GO:0008270,GO:0003677	ATSG27180.1	Zim17-type zinc finger protein	DNL zinc finger protein
Sapur.008G165800.1	3.589907569	1.55250083	0.22589569	6.87258	6.30E-12	1.47E-11	grey	-0.449420788	5.28E-09	GO:0045454,GO:0015035,GO:0009055	ATSG11600.1	Glutaredoxin family protein	monothiol glutaredoxin-S2 protein
Sapur.T07G000.1	20.28569882	0.76780882	0.11732224	-6.87186	6.34E-12	1.47E-11	grey	-0.445143992	5.18E-09		ATSG12000.1	Phosphofructokinase family protein	NA
Sapur.017G021100.1	1.231062949	-2.38810088	0.34913671	-6.86852	6.54E-12	1.51E-11	grey	-0.450022563	1.43E-07	GO:0006488,GO:0005524,GO:0004672	ATGE46980.1	SNC4	suppressor of npr1-1 constitutive 4
Sapur.003G103300.1	21.03167607	1.76965288	0.25769933	6.86827	6.55E-12	1.51E-11	grey	0.426606334	2.53E-08				hypothetical protein
Sapur.010G090500.1	361.4168007	0.52148816	0.07624126	6.86787	6.56E-12	1.52E-11	grey	0.479268547	1.5E-09	GO:0016042,GO:0006629	ATKG16070.1	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	NA
Sapur.005G079000.1	191.1901919	1.83066827	0.26749769	6.86724	6.55E-12	1.52E-11	grey	0.437315503	1.02E-08	GO:0008152,GO:0003824	ATG17650.1	AMP-dependent synthetase and ligase family protein	acyl-CoA synthetase
Sapur.T10G200.1	6.436064888	0.86161884	0.12908549	6.66361	6.57E-12	1.52E-11	grey	-0.51497927	1.41E-13		ATG44880.1	Helicase/SNF2, DNA/chromatin binding superfamily protein	NA
Sapur.001G086700.1	1.208505956	2.60644705	0.37664412	6.86534	6.62E-12	1.54E-11	grey	0.385546667	6.15E-07		ATG43410.1	Protein of unknown function (DUF567)	tubby C 2 protein
Sapur.004G300400.1	28.19715562	0.90837655	0.13237038	6.86214	6.77E-12	1.57E-11	grey	-0.429498465	1.36E-08	GO:0004674,GO:0048544,GO:0006488,GO:0004672	ARK1,RK3	receptor kinase 3	Serine/Threonine kinase
Sapur.012G107400.1	37.8562986	-0.66393782	0.09688793	-6.85823	6.97E-12	1.62E-11	grey	-0.190108852	0.017089005	GO:0005515	ATG07240.1	IQD24	IQ-domain 24
Sapur.15W0086700.3	4.487616267	1.20162531	0.18009779	6.85755	7.00E-12	1.62E-11	grey	0.079825993	0.325132741	GO:0055114,GO:0016491	ATGE08370.2	PDE189,SPC1_ZDS	zeta-carotene desaturase
Sapur.004G087200.2	10.88403723	-0.67546067*	0.11087682	-6.85313	7.23E-12	1.67E-11	grey	-0.396730375	2.70E-07	GO:0046872	AL1G12,EBI54	Zinc finger C-x8-C-x5-C-x3-H type family protein	zinc finger protein, putative
Sapur.016G014400.1	0.92122883	2.27528989	0.32090737	6.85141	7.31E-12	1.69E-11	grey	-0.412222667	7.51E-08	GO:0016758,GO:0008152	ATG21760.1	UDP-Glycosyltransferase superfamily protein	UDP-glucose flavonoid 3-O-glucosyltransferase
Sapur.010G068000.1	10.34466172	0.72391124	0.1684422	6.84921	7.41E-12	1.71E-11	grey	-0.437963174	9.61E-09	GO:0016758,GO:0008152	ATLU0TEAS,LUGT8LAS	UDP-glucosyltransferase family protein	UDP-glucosyltransferase family protein
Sapur.003G065000.3	22.64136682	-0.96751507	0.14135862	-6.84645	7.57E-12	1.75E-11	grey	-0.429325965	2.02E-08	GO:0055114,GO:0051537,GO:0016491	ATCAO,CAO,CHS	Phosphorbide a oxygenase family protein with Rieske [2Fe-2S] domain	chlorophyllide A oxygenase
Sapur.T13B100.1	280.1664087	0.52148816	0.07624126	6.84487	7.64E-12	1.76E-11	grey	-0.437412725	2.01E-09	GO:0004527,GO:0003676	AHWH1,XRN3	5'-3' exoribonuclease 3	5'-3' exoribonuclease
Sapur.016G079300.1	475.9185661	-0.29408778	0.04266589	-6.84186	7.82E-12	1.81E-11	grey	-0.477595859	2.54E-10		ATG02730.1		hypothetical protein
Sapur.015G050800.4	3.153778611	-0.32102372	0.04686018	-6.84064	7.88E-12	1.81E-11	grey	-0.232991006	0.007405731		ATG29752.2	RKF3	receptor-like kinase in flowers 1	receptor-like kinase, putative
Sapur.013G158800.1	27.20512343	0.61509452	0.09285259	6.83889	7.98E-12	1.85E-11	grey	-0.455384407	2.07E-09		ATG52565.1		transmembrane protein, putative
Sapur.015G088300.1	16.45413859	-0.85161194	0.13003349	-6.83862	8.00E-12	1.85E-11	grey	-0.473070904	1.34E-10	GO:0016747	AT4G30040.1	HXXXD-type acyl-transferase family protein	NA
Sapur.006G203800.1	259.4971658	0.86355781	0.12629018	6.83754	8.04E-12	1.86E-11	grey	-0.382414353	7.71E-07	GO:0016020,GO:0006810,GO:0005215	ATG68570.1	Major facilitator superfamily protein	peptide transporter PTR
Sapur.012G240500.2	20.9203904	0.59006792	0.08645628	-6.83545	8.17E-12	1.88E-11	grey	-0.423105384	1.38E-08	GO:0005515	GTE4	global transcription factor group E4	global transcription factor group protein, putative
Sapur.003G113200.1	33.08718834	0.50347428	0.08494169	6.83845	8.28E-12	1.92E-11	grey	-0.68873021	8.36E-11	GO:0016757	AL1G12,EBI54	homolog of Lectins-linked glycosylation 12	NA
Sapur.006G172500.1	0.614678567	2.44330075	0.35752501	6.83643	8.28E-12	1.92E-11	grey	0.462496291	1.07E-09	GO:0009733	ATG38210.1	SAUR-like auxin-responsive protein family	auxin responsive SAUR protein
Sapur.012G087700.1	708.7319452	0.29108219	0.04214168	6.83324	8.30E-12	1.92E-11	grey	0.476315425	1.87E-10	GO:0008480	ATG27601.2	ATIRP2BETA,IPK2B,IPK2BET	inositol polyphosphate multikinase
Sapur.15W0127300.1	11.71368899	0.71371294	0.10632872	6.83141	8.41E-12	1.95E-11	grey	0.467494748	6.71E-10		ATG07380.2		hypothetical protein
Sapur.016G353800.1	3.664865585	1.19882258	0.17549929	6.83093	8.44E-12	1.96E-11	grey	-0.474368255	4.17E-10		ATG48820.1	Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.012G094800.1	11.5712245	0.08769167	0.19299698	6.829841	8.58E-12	1.97E-11	grey	-0.475202335	3.78E-10	GO:0005085	ATG43880.1	ATYSL2,YSL2	YELLOW STRIPE like 2	NA
Sapur.015G079600.1	5.365178272	-0.93613284	0.13619545	-6.82697	8.51E-12	1.97E-11	grey	-0.472868216	1.97E-10				NA
Sapur.016G115400.1	0.585286431	2.27498011	0.33324041	6.82607	8.57E-12	2.0E-11	grey	0.461190453	1.21E-09				hypothetical protein
Sapur.016G025100.1	0.420139847	2.78208185	0.41430437	6.82404	8.69E-12	2.04E-11	grey	0.424027151	1.11E-08	GO:0006468,GO:0005524,GO:0004672	ATG54820.1	Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.T103500.1	28.02400917	0.88856178	0.1302048	6.82344	8.83E-12	2.06E-11	grey	-0.457576745	1.76E-09		ATG63681.1	LCR78,PDF2.5	Scorpion toxin-like knottin superfamily protein	NA
Sapur.008G077500.1	194.03876	-0.47064448	0.08956746	-6.82165	8.84E-12	2.06E-11	grey	-0.488436896	8.61E-11		ATG69160.1		plant/FAN2-9 protein, putative	plant/FAN2-9 protein, putative
Sapur.T13B100.1	5.317993174	-0.70409886	0.10750745	-6.82408	8.85E-12	2.06E-11	grey	-0.516488089	1.5E-12	GO:0005524	ATG25181.1	TCP-1/cpn60 chaperonin family protein	NA
Sapur.006G064200.1	438.9484008	0.26156018	0.03168523	6.82308	8.91E-12	2.06E-11	grey	0.469449415	5.57E-10	GO:0016787	ATMUTD2.ATMUD2.NUDT2	nudix hydrolase homolog 2	nudix hydrolase
Sapur.002G055200.2	2.647383866	-0.51388374	0.16620456	-6.82285	8.93E-12	2.06E-11	grey	-0.48983032	1.8E-10	GO:0005524,GO:0004003,GO:0003677,GO:0016818,GO:0008026,GO:0006139,GO:0003677	ATGD0720.1	RADD Rad3-like helicase protein	DNA helicase
Sapur.006G170200.2	2.071846775	-2.26105022	0.78258426	-6.82209	8.97E-12	2.07E-11	grey	-0.42674279	2.50E-08		ATG15583.3	LETM1-like protein	LETM1-like protein
Sapur.003G108100.4	1.486208276	2.77224627	0.50514494	6.82188	8.98E-12	2.08E-11	grey	0.226874703	0.002272273	GO:0007010,GO:0003779	ATLVN1,VLN2	villin 2	villin-1 protein
Sapur.010G201400.1	41.76503739	0.65816081	0.09647268	6.821802	8.99E-12	2.08E-11	grey	-0.46417669	9.17E-10				hypothetical protein
Sapur.15W0154400.4	24.62481871	-0.51025251	0.07485141	-6.81853	9.20E-12	2.12E-11	grey	0.074374224	0.354576287		ATG61830.1		mras up-regulated Nxd 18 protein
Sapur.007G004300.2	2.308702408	-3.78871556	0.202391177	-6.81627	9.34E-12	2.16E-11	grey	-0.085908005	0.28470651		ATG67640.1		hypothetical protein
Sapur.006G064600.2	23.27134364	0.50378236	0.08779284	6.81182	9.35E-12	2.16E-11	grey	-0.473146615	2.68E-10		ATG57890.1	Tubulin binding cofactor C domain-containing protein	tubulin-binding cofactor C
Sapur.011G161700.1	282.3275056	-0.5997857	0.14606542	-6.81157	9.38E-12	2.16E-11	grey	-0.378809149	9.02E-07		ATG70320.1	fatty acid desaturase A	Rua-ubiquitin-conjugating enzyme hybrid localization domain protein
Sapur.016G280800.1	5.508591857	1.66400573	0.24188581	6.81497	9.47E-12	2.19E-11	grey	0.354912618	5.09E-06	GO:0055114,GO:0020037,GO:0006979,GO:0004601	ATG14540.1	Peroxidase superfamily protein	lignin-forming anionic peroxidase, putative
Sapur.007G067700.1	2.406645325	-5.48364448	0.21790753	-6.81323	9.54E-12	2.20E-11	grey	-0.411587059	3.54E-08				NA
Sapur.001G117300.1	230.4927672	-1.38047549	0.20261037	-6.81307	9.55E-12	2.21E-11	grey	-0.341667203	1.19E-05				transmembrane protein, putative
Sapur.T086300.1	2.473328833	-0.41128184	0.07595944	-6.81184	9.57E-12	2.21E-11	grey	-0.460810147	2.91E-09	GO:0005515	ATF5G1,FS1	forkhead-associated (FHA) domain-containing protein	NA
Sapur.15W0045500.1	2.174594616	-1.48288388	0.27604602	-6.81172	9.64E-12	2.22E-11	grey	-0.069539987	0.386808919		ATG62610.1	CKL1,CKL1	casein kinase I-like protein	casein kinase I-like protein
Sapur.004G047000.1	62.10125752	0.57344931	0.10296922	6.81012	9.75E-12	2.25E-11	grey	-0.488545832	9.51E-11				transmembrane protein, putative
Sapur.018G094300.1	155.9618939	-0.57934729	0.08510006	-6.80777	9.91E-12	2.29E-11	grey	-0.477802009	2.49E-10	GO:0043531	ATG14470.1	NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.006G030800.1	2108.368162	0.46426887	0.06820887	6.80693	9.97E-12	2.30E-11	grey	0.425232018	2.86E-08				NA
Sapur.013G135000.1	1916.599458	0.18475300	0.02714139	6.80619	9.99E-12	2.30E-11	grey	0.460944695	1.26E-09	GO:0019773,GO:0006511,GO:0004175,GO:0051603,GO:0005839,GO:0004298	PAE2	20S proteasome alpha subunit E2	proteasome subunit alpha type-5 protein
Sapur.006G173500.1	4.477448854	-1.30700111	0.16278353	-6.8062	1.00E-11	2.31E-11	grey	-0.29682036	0.000161818	GO:0005515	ATG68570.1	Phototropic-responsive NPH3 family protein	BTB/POZ domain plant protein
Sapur.15W0188900.1	2.38855777	-0.58374974	0.23275231	-6.80501	1.01E-11	2.33E-11	grey	-0.442121726	6.75E-09	GO:0034755,GO:0005886,GO:0006821,GO:0005886,GO:0005829,GO:0000938	ATG22190.2	nucleotide-sensitive chloride channel family protein	CLC chloride channel protein
Sapur.016G084700.1	1519.908679	-0.96381681	0.14160708	-6.80417	1.02E-11	2.34E-11	grey	-0.410722234	9.15E-08	GO:0006020,GO:0008183,GO:0005215	ATG57170.1	PIP2;2,PIP2B	plasma membrane intrinsic protein PIP2;2
Sapur.005G000400.1	261.3451336	-0.52811486	0.07761682	-6.80343	1.03E-11	2.35E-11	grey	-0.257708676	0.001189	GO:0003723,GO:0004521,GO:0004601,GO:0005622,GO:0003735	ATG07090.1	Ribosomal protein S4 (RPS4A) family protein	40S ribosomal protein S4
Sapur.009G077100.1	40.7275855	-0.89686909	0.13185032	-6.80218	1.03E-11	2.38E-11	grey	-0.452552871	2.67E-09				NA
Sapur.015G139200.1	470.8834206	-0.56372203	0.08210742	-6.80173	1.04E-11	2.38E-11	grey	-0.48265323	1.41E-10				transmembrane protein, putative
Sapur.15W0085600.1	122.6138398	1.15179341	0.16450557	6.80174	1.03E-11	2.38E-11	grey	0.363927152	2.80E-06	GO:0009607,GO:0006952	ATG14960.1	Polyketide cyclase/dehydrase and lipid transport superfamily protein	pathogenesis-related protein Bet V I family protein
Sapur.003G138700.1	8.837278873	-0.88696365	0.13080611	-6.8009	1.04E-11	2.40E-11	grey	-0.482281663	1.36E-10				NA
Sapur.003G138700.1	2.004725605	-1.87751979	0.2761341	-6.79928	1.05E-11	2.41E-11	grey	-0.475297287	3.02E-10		ATG44430.1		NA
Sapur.015G344000.2	1.509231195	-1.32328398	0.18042569	-6.79852	1.06E-11	2.44E-11	grey	-0.453525018	2.86E-09		ATG27570.1	RBJG	gigantea protein (GI)	gigantea protein, putative
Sapur.010G051400.1	383.6165612	-0.22982893	0.03481635	-6.79773	1.08E-11	2.45E-11	grey	-0.47543534	4.62E-10	GO:0015969	ATCR5H,CRSH	Ca2+-activated RelA/SpoT homolog	guanosine-3'5'2'C-bis(diphosphate) 3'-pyrophosphohydrolase, putative
Sapur.002G182300.3	3.629161615	-1.00000942	0.15019632	-6.79734	1.07E-11	2.45E-11	grey	-0.05605246	0.48561128		ATG44200.1	Pentatricopeptide repeat (PPR) superfamily protein	salt-inducible protein, putative
Sapur.005G187200.1	2.280662849	-1.42892935	0.21029939	-6.79718	1.05E-11	2.46E-11	grey	-0.46896229	1.92E-10	GO:0005515	ATG66330.1	Leucine-rich repeat (LRR) family protein	receptor-like kinase
Sapur.013G134400.1	19.27777684	-1.03378193	0.15230146	-6.79682	1.07E-11	2.46E-11	grey	-0.463645653	9.64E-10	GO:0048544	ATG61630.1	S-locus lectin protein kinase family protein	NA
Sapur.005G192700.1	51.7482706	0.61858621	0.09608805	6.79572	1.08E-11	2.50E-11	grey	0.449941747	1.37E-09	GO:0005437,GO:0003755,GO:0006013	ROC3	rotamase CYP 3	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.005G148800.1	4.981645227	-1.61420488	0.23760123	-6.79373	1.09E-11	2.52E-11	grey	-0.375991235	1.22E-06		ATG76780.2	pathogenesis-related family protein	pathogen-like protein
Sapur.005G143000.1	3.303661587	-1.32870111	0.19516155	-6.79182	1.10E-11	2.52E-11	grey	0.444478526	7.14E-09		ATG46510.2		transmembrane protein, putative
Sapur.014G139000.1	2.948870446	-1.03603103	0.15253126	-6.79255	1.10E-11	2.54E-11	grey	-0.48070799	1.87E-10		ATG07600.1	Heavy metal transport/detoxification superfamily protein	NA
Sapur.006G110500.1	0.831639485	2.41206359	0.35525561	6.79234	1.10E-11	2.54E-11	grey	0.418605548	9.41E-08				NA
Sapur.016G164400.1	17.18526516	-0.61207831	0.09018509	-6.78891	1.13E-11	2.60E-11	grey	-0.498207953	3.13E-11		ATG58570.1		transmembrane protein, putative
Sapur.014G183000.3	5.582437641	-0.78283819	0.11529878	-6.78778	1.14E-11	2.61E-11	grey	-0.295136291	0.000175126	GO:0034968,GO:0018024,GO:0008270,GO:0005634,GO:0005515,GO:0042393	ATG73100.1	SDG19,SUVH3	SUVH/KRYPTONITE homologs 3	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3 protein
Sapur.010G085400.1	10.65801054	-0.32385858	0.05080026	-6.78623	1.16E-11	2.66E-11	grey	-0.423883179	1.17E-08	GO:0009733	ATG38870.1	SAUR-like auxin-responsive protein family	auxin-responsive family protein
Sapur.018G067500.1	537.2037991	0.59183187	0.08190076	6.780062	1.15E-11	2.65E-11	grey	-0.42670622	2.51E-08		ATG67060.1	RBCS1A	ribulose bisphosphate carboxylase small chain 1A	ribulose bisphosphate carboxylase small chain
Sapur.016G094700.1	1.631282372	-1.38238398	0.21761652	-6.78388	1.17E-11	2.68E-11	grey	-0.485762188	1.18E-10	GO:0005515	ATG47732.1	Calcium-dependent lipid-binding (CaLB domain) family protein	Arf GTPase activator, putative
Sapur.016G019900.1	6.285102993	-1.73607103	0.24751752	-6.78254	1.18E-11	2.72E-11	grey	0.381352968	8.32E-07				NA
Sapur.015G000300.1	6.05932709	-0.76481833	0.1117615	-6.78172	1.18E-11	2.73E-11	grey	-0.44068555	7.7E-10	GO:0005515,GO:0016787,GO:0003998	ATG23120.2	nucleotide binding/nucleic acid binding protein	RNA binding protein with multiple splicing protein
Sapur.009G138800.1	3.300315122	2.21264941	0.17879832	6.781671	1.19E-11	2.73E-11	grey	-0.475542227	3.10E-10				NA
Sapur.006G028200.1	92.2861849	-0.51618306	0.08029459	-6.7795	1.21E-11	2.77E-11	grey	-0.464054279	2.28E-10		ATG54860.1	Glycoprotein membrane precursor GPI-anchored	GPI-anchored protein, putative
Sapur.004G062200.1	2.637063644	-2.90696093	0.39045666	-6.77725	1.22E-11	2.81E-11	grey	-0.479511544	2.16E-10	GO:0003677,GO:0006334,GO:0005634,GO:0000786	ATG44900.1	HMGA	high mobility group A	linker histone H1 and H5 family protein
Sapur.004G300300.1	6.792455627	-0.79508132	0.11732163	-6.77639	1.23E-11	2.82E-11	grey	-0.473850022	4.02E-10		ATG45460.1	MUB2	membrane-anchored ubiquitin-fold protein 2	membrane-anchored ubiquitin-fold protein
Sapur.003G105800.1	4.4753976	-1.11011845	0.16284735	-6.77625	1.23E-11	2.83E-11	grey	-0.491383681	6.38E-11		ATG10850.1		Nodulin MtN3 family protein	bidirectional sugar transporter SWEET4
Sapur.016G132000.3	11.92558899	-0.70932248	0.10662891	-6.77504	1.24E-11	2.86E-11	grey	-0.22091289	0.005430008	GO:0005515	ATG03020.1	transducin family protein / WD-40 repeat family protein	LEC14B protein
Sapur.017G024900.1	4.343616146	-0.66223922	0.10343426	-6.77486	1.24E-11	2.86E-11	grey	-0.451610971	2.48E-09	GO:0005515,GO:0043531	ATG07870.1	LRR and NB-ARC domain-containing disease resistance protein	NA - FTMB
Sapur.001G121200.12	7.332171047	-1.04093624	0.16842399	-6.77412	1.25E-11	2.88E-11	grey	-0.44629688	4.62E-09	GO:0000160	ATG18020.2	APRR2,PRR2	Cheb-like two-component responsive regulator family protein	PRR response regulator, putative
Sapur.008G122200.2	6.716147966	0.56214451	0.08607373	6.77409	1.25E-11	2.88E-11	grey	-0.460579226	1.19E-10	GO:0005515,GO:0032857,GO:0016021	ATG36240.1	MSBP7,MSL1,LTP13	Major facilitator superfamily protein	hexose transporter
Sapur.017G

Sapur.001G160700.3	2.372108527	-1.402953364	0.210939902	-6.65096	2.91E-11	6.60E-11	grey	-0.439303823	8.62E-09		AT5G50340.1		ATP-dependent peptidases;nucleotide binding;serine-type endopeptidases;DNA helicases;ATP binding;damaged D	DNA repair protein RadA
Sapur.016G253400.1	5.839130411	-0.93283437	0.140288638	-6.64939	2.94E-11	6.67E-11	grey	-0.392830946	3.60E-07		AT1G31660.1			NA
Sapur.007G124100.1	20.7457634	-1.036685474	0.155911003	-6.64921	2.95E-11	6.68E-11	grey	-0.4342758	1.33E-08	GO:0006468,GO:0005524,GO:0004672,GO:0007094	AT2G20635.1		ATP binding;protein kinases;protein serine/threonine kinases	NA
Sapur.005G005600.1	7.432568257	-1.055895569	0.158803711	-6.64906	2.95E-11	6.69E-11	grey	-0.440799753	7.57E-09	GO:0006265,GO:0003916,GO:0003677,GO:0003917	AT5G63920.1	TOP3A	topoisomerase 3alpha	NA
Sapur.016G057400.1	151.5358448	-0.570719333	0.085855549	-6.64744	2.98E-11	6.76E-11	grey	-0.458589335	1.54E-09		AT1G58170.1		Disease resistance-responsive (dirigent-like protein) family protein	disease resistance response protein, putative
Sapur.006G042900.1	6.539956979	1.443587877	0.217305204	6.643135	3.07E-11	6.96E-11	grey	0.437792679	9.82E-09		AT3G55515.1	DVL8,RTFL7	ROTUNDIFOLIA like 7	DVL family protein
Sapur.010G128800.1	4362.216159	0.392315858	0.059056253	6.643088	3.07E-11	6.96E-11	grey	0.437545675	1.00E-08		AT1G69530.1	AT-EXP1.ATEXP1.ATEXPA1.A	expansin A1	alpha-expansin
Sapur.004G150700.1	145.2397045	0.254089276	0.038250642	6.642745	3.08E-11	6.97E-11	grey	0.47021606	5.18E-10		AT5G22280.1			NAC domain protein
Sapur.011G078900.1	76.06755574	0.69313256	0.104357247	6.641921	3.10E-11	7.01E-11	grey	0.45884232	1.51E-09	GO:0008152,GO:0003824	AT5G57850.1		D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein	NA
Sapur.009G088200.1	50.17984527	-1.900031556	0.286116851	-6.64075	3.12E-11	7.07E-11	grey	-0.400324991	2.05E-07					transmembrane protein, putative
Sapur.011G063300.1	18.83735475	0.917462957	0.138158901	6.640636	3.12E-11	7.07E-11	grey	0.452491941	2.69E-09	GO:0005515	AT3G11010.1	AtRLP34,RLP34	receptor like protein 34	receptor-like kinase, putative
Sapur.001G190500.1	0.634814471	2.112063381	0.318134543	6.6389	3.16E-11	7.15E-11	grey	0.479230328	2.16E-10	GO:0006468,GO:0004672	AT5G49760.1		Leucine-rich repeat protein kinase family protein	somatic embryogenesis receptor-like kinase
Sapur.013G096600.1	340.3394632	-0.779933819	0.117497487	-6.63788	3.18E-11	7.20E-11	grey	-0.505245299	1.49E-11		AT1G33800.1		Protein of unknown function (DUF579)	NA
Sapur.001G147900.1	5.347361912	1.266635125	0.190822626	6.637762	3.18E-11	7.21E-11	grey	0.40938629	1.02E-07		AT5G14750.1	ATMYB66.MYB66.WER.WEF	myb domain protein 66	Myb-like transcription factor 2, putative
Sapur.013G095900.1	10.93063932	-2.160657097	0.325546615	-6.63701	3.20E-11	7.24E-11	grey	-0.406363551	1.29E-07	GO:0016747,GO:0008610,GO:0016020,GO:0006633	AT2G26640.1	KCS11	3-ketoacyl-CoA synthase 11	3-ketoacyl-CoA synthase
Sapur.011G029900.1	150.198893	0.600274918	0.090444148	6.636968	3.20E-11	7.25E-11	grey	0.414140196	6.98E-08	GO:0055114,GO:0016491	AT1G07180.1	ATNDI1,NDA1	alternative NAD(P)H dehydrogenase 1	internal alternative NAD(P)H-ubiquinone oxidoreductase
Sapur.018G096500.1	209.4418385	0.26834695	0.040434426	6.636596	3.21E-11	7.26E-11	grey	0.455636172	2.02E-09	GO:0034314,GO:0030833,GO:0005885,GO:0005856	AT1G60430.1	ARPC3	actin-related protein C3	actin-related protein 2/3 complex subunit 3
Sapur.013G095700.1	11.86247461	-3.024499727	0.455737174	-6.6365	3.21E-11	7.27E-11	grey	-0.236775977	0.00282966	GO:0009116,GO:0003824	AT4G24340.1		Phosphorylase superfamily protein	bark storage protein, putative
Sapur.005G133200.1	9.373114519	-0.76562082	0.115415356	-6.63361	3.28E-11	7.41E-11	grey	-0.451607792	2.91E-09	GO:0043565,GO:0006355,GO:0003700,GO:0006351	AT1G77920.1		bZIP transcription factor family protein	transcription factor TGA7, putative
Sapur.014G092700.1	132.4720144	0.426735376	0.064365358	6.629892	3.36E-11	7.60E-11	grey	0.449034616	3.67E-09					hypothetical protein
Sapur.T066400.1	3.79383566	2.323148661	0.350466613	6.62873	3.39E-11	7.66E-11	grey	0.470529365	5.03E-10					NA
Sapur.15WG138300.1	514.6419545	-0.549545385	0.08290501	-6.62861	3.39E-11	7.66E-11	grey	-0.503676843	1.77E-11		AT5G03170.1	ATFLA11,FLA11	FASCICLIN-like arabinogalactan-protein 11	fasciclin and-related adhesion glycoprotein
Sapur.006G014900.1	1.349934506	-1.817289033	0.274219769	-6.62713	3.42E-11	7.74E-11	grey	-0.418642537	4.86E-08					transmembrane protein, putative
Sapur.010G174500.1	55.90578092	-0.684090325	0.10322981	-6.62687	3.43E-11	7.75E-11	grey	-0.461573628	1.17E-09		AT2G35790.1			NA
Sapur.007G069100.1	211.5815198	-0.157778406	0.023811823	-6.62605	3.45E-11	7.79E-11	grey	-0.486692935	1.03E-10	GO:0005515	AT5G49610.1		F-box family protein	F-box protein interaction domain protein
Sapur.019G094700.1	1.36495009	-1.592767957	0.240532208	-6.62185	3.55E-11	8.02E-11	grey	-0.465746676	7.91E-10	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G08850.1		Leucine-rich repeat receptor-like protein kinase family protein	NA
Sapur.014G027400.1	919.2108624	0.877583074	0.132532091	6.621665	3.55E-11	8.03E-11	grey	0.398059565	2.43E-07	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G31940.1	CYP82C4	cytochrome P450, family 82, subfamily C, polypeptide 4	NA
Sapur.008G068800.1	3.531865473	1.435966656	0.216959354	6.618598	3.63E-11	8.19E-11	grey	0.409212835	1.03E-07	GO:0055114,GO:0050660,GO:0016614	AT1G14190.1		Glucose-methanol-choline (GMC) oxidoreductase family protein	NA
Sapur.15ZG056000.1	5.538388069	1.020444646	0.154180098	6.618524	3.63E-11	8.20E-11	grey	0.446924104	4.42E-09		AT1G49000.1			transmembrane protein, putative
Sapur.017G114900.1	288.3822308	0.552265476	0.083455428	6.61749	3.65E-11	8.25E-11	grey	0.46658337	7.31E-10		AT1G65920.1		Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain	Ran GTPase-binding protein, putative
Sapur.009G112500.4	1.966906596	-1.794490462	0.27121383	-6.61652	3.68E-11	8.31E-11	grey	-0.460570482	1.28E-09	GO:0006419,GO:0005524,GO:0004813,GO:0000166	AT5G22800.1	EMB1030,EMB263,EMB86	Alanyl-tRNA synthetase, class IIc	NA
Sapur.007G119800.1	7.374703952	0.684190829	0.103407703	6.61644	3.68E-11	8.31E-11	grey	0.484712133	1.25E-10					NA
Sapur.009G113000.1	6.656676785	0.813419172	0.122953887	6.615644	3.70E-11	8.35E-11	grey	0.45247575	2.69E-09		AT2G17080.1		Arabidopsis protein of unknown function (DUF241)	NA
Sapur.012G084000.1	67.58692896	-0.380446692	0.057524166	-6.61368	3.75E-11	8.46E-11	grey	-0.474578384	3.40E-10	GO:0005515.GO:0016818.GO:0008270.GO:0003676.GO:0008081.GO:0006281.GO:000563	AT5G07400.1		forkhead-associated domain-containing protein / FHA domain-containing protein	tyrosyl-DNA phosphodiesterase
Sapur.004G055700.1	474.7549065	0.3157612	0.047749338	6.612892	3.77E-11	8.51E-11	grey	0.452724292	2.63E-09		AT5G52540.1		Protein of unknown function (DUF819)	integral membrane protein, putative
Sapur.001G057800.1	1.003437064	2.552825855	0.386117323	6.611529	3.80E-11	8.58E-11	grey	0.414664788	6.69E-08		AT1G43760.1		DNAse I-like superfamily protein	NA
Sapur.016G233100.1	154.8172082	-0.263198265	0.039809344	-6.61147	3.81E-11	8.59E-11	grey	-0.46899941	5.82E-10	GO:0070403	AT5G55760.1	SRT1	sirtuin 1	NAD-dependent protein deacetylase family, SIR2 family protein
Sapur.017G055400.1	58.55909686	0.619916165	0.093784941	6.609976	3.84E-11	8.67E-11	grey	0.415026732	6.50E-08		AT5G14090.1			NA
Sapur.016G203700.1	2048.413568	0.358924846	0.054328318	6.606589	3.93E-11	8.87E-11	grey	0.430558266	1.82E-08	GO:0016020,GO:0006886,GO:0006605	AT5G50460.1		secE/sec61-gamma protein transport protein	protein transporter Sec61 subunit gamma
Sapur.001G101300.1	15.37855213	0.611305457	0.092575108	6.603346	4.02E-11	9.07E-11	grey	0.47351604	3.77E-10		AT4G17250.1			plant/MNJ7-17 protein, putative
Sapur.006G129100.1	210.1149199	-0.608874397	0.092217661	-6.60258	4.04E-11	9.11E-11	grey	-0.502126865	2.08E-11		AT1G43580.1		Sphingomyelin synthetase family protein	NA
Sapur.016G230200.1	273.0816061	0.22324519	0.03381535	6.601889	4.06E-11	9.15E-11	grey	0.449916555	3.39E-09	GO:0008289	AT1G04970.1		lipid-binding serum glycoprotein family protein	LBP/BPI/CETP family, carboxy-terminal domain protein
Sapur.019G041100.1	57.28046465	0.82268932	0.124629934	6.601057	4.08E-11	9.21E-11	grey	0.461666094	1.16E-09	GO:0006468,GO:0005524,GO:0004672	AT1G16130.1	WAKL2	wall associated kinase-like 2	LysM type receptor kinase
Sapur.010G103300.1	74.51049948	-0.691396994	0.104742967	-6.60089	4.09E-11	9.21E-11	grey	-0.476997745	2.69E-10	GO:0046872.GO:0000166.GO:0016021.GO:0015914.GO:0005524.GO:0004012.GO:000028	AT1G68710.1		ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	phospholipid-transporting ATPase, putative
Sapur.001G150800.1	24.24282461	-0.518662055	0.078576173	-6.60075	4.09E-11	9.22E-11	grey	-0.465825588	7.86E-10		AT1G45688.1			late embryogenesis abundant protein
Sapur.002G058600.1	1433.337083	-0.236060557	0.035763378	-6.60062	4.09E-11	9.23E-11	grey	-0.477550279	2.55E-10	GO:0016597,GO:0008152	AT1G76990.1	ACR3	ACT domain repeat 3	ACR3
Sapur.018G023700.4	3.120986293	1.054403919	0.159814636	6.597668	4.18E-11	9.41E-11	grey	0.130805114	0.102487976		AT4G32342.1			DUF4050 family protein
Sapur.007G118600.1	4.323662737	-1.740015314	0.263742012	-6.59741	4.18E-11	9.43E-11	grey	-0.443483598	5.99E-09		AT2G28580.1		Plant protein of unknown function (DUF247)	DUF247 domain protein
Sapur.016G018400.1	277.757804	-0.658580223	0.099836584	-6.59658	4.21E-11	9.48E-11	grey	-0.461551537	1.17E-09		AT1G33800.1		Protein of unknown function (DUF579)	glucuronoxylan 4-O-methyltransferase, putative
Sapur.003G094100.1	1.213235088	2.177951869	0.330204049	6.595776	4.23E-11	9.53E-11	grey	0.35597387	4.75E-06					hypothetical protein
Sapur.15WG122200.1	5.173175079	-1.372260532	0.20806236	-6.59543	4.24E-11	9.55E-11	grey	-0.424759453	2.95E-08	GO:0006355,GO:0003677	AT5G61850.1	LFY,LFY3	floral meristem identity control protein LEAFY (LFY)	floricaula/LEAFY-like protein
Sapur.011G121800.1	20.09427168	-0.953021082	0.144528363	-6.59401	4.28E-11	9.64E-11	grey	-0.373902516	1.41E-06	GO:0006096,GO:0004332	AT4G26530.1		Aldolase superfamily protein	fructose-bisphosphate aldolase
Sapur.008G040500.2	4.000152608	0.967301599	0.146735844	6.592129	4.34E-11	9.76E-11	grey	0.448974417	3.69E-09		AT3G12590.1			hypothetical protein
Sapur.005G004400.1	150.8143153	-0.917893077	0.139265805	-6.59094	4.37E-11	9.84E-11	grey	-0.476927916	2.71E-10	GO:0007264,GO:0005525	AT5G10260.1	AtRABH1e,RABH1e	RAB GTPase homolog H1E	NA
Sapur.014G025500.1	62.31930676	-0.429781195	0.065249298	-6.58676	4.50E-11	1.01E-10	grey	-0.457417466	1.72E-09	GO:0003697,GO:0006260	AT1G47720.1	OSB1	Primosome PriB/single-strand DNA-binding	NA
Sapur.013G112500.1	0.615631338	2.620553844	0.39798632	6.584532	4.56E-11	1.03E-10	grey	0.487695671	9.28E-11		AT1G06280.1	LBD2	LOB domain-containing protein 2	NA
Sapur.006G133700.1	5.854944545	-0.830819688	0.126198341	-6.58344	4.60E-11	1.03E-10	grey	-0.408509193	1.09E-07	GO:0003968	AT2G19920.1		RNA-dependent RNA polymerase family protein	NA
Sapur.016G155000.1	246.1725549	0.695135938	0.105605039	6.582413	4.63E-11	1.04E-10	grey	0.422263687	3.62E-08					transmembrane protein, putative
Sapur.016G073000.1	17.03952571	1.151264152	0.174958302	6.58022	4.70E-11	1.06E-10	grey	0.422960981	3.42E-08	GO:0009611,GO:0004867	AT2G38870.1		Serine protease inhibitor, potato inhibitor I-type family protein	NA
Sapur.005G103000.1	10.34172095	-1.483523694	0.225532	-6.57789	4.77E-11	1.07E-10	grey	-0.383379649	7.19E-07					transmembrane protein, putative
Sapur.011G027300.1	0.914774287	3.125610212	0.475260883	6.57662	4.81E-11	1.08E-10	grey	0.377668341	1.08E-06					DUF3774 domain protein
Sapur.013G048100.1	0.544398362	2.410647475	0.366554352	6.576508	4.82E-11	1.08E-10	grey	0.440967646	7.46E-09		AT5G39110.1		RmlC-like cupins superfamily protein	NA
Sapur.006G160900.1	419.0100461	-0.309320125	0.04703516	-6.57636	4.82E-11	1.08E-10	grey	-0.495508096	4.17E-11		AT5G06610.1		Protein of unknown function (DUF620)	NA
Sapur.016G183100.2	5.297332682	-0.90136877	0.137077991	-6.57559	4.85E-11	1.09E-10	grey	-0.452587131	2.66E-09	GO:0007264,GO:0005525	AT5G08650.1		Small GTP-binding protein	translation factor GUF1-like protein
Sapur.016G158800.1	0.677037116	2.480141473	0.377206228	6.575028	4.86E-11	1.09E-10	grey	0.211610887	0.007802775	GO:0016787	AT5G12200.1	PYD2	pyrimidine 2	dihydropyrimidinase
Sapur.003G163300.4	1.638775562	-1.522546156	0.231573931	-6.57477	4.87E-11	1.10E-10	grey	-0.269130364	0.000653559	GO:0055085,GO:0016021,GO:0008324,GO:0006812	AT3G58060.1		Cation efflux family protein	cation efflux protein/zinc transporter, putative
Sapur.006G029600.1	191.0806265	0.335685076	0.051059976	6.574329	4.89E-11	1.10E-10	grey	0.436532327	1.09E-08		AT3G56750.1			plant/T8M16-80 protein
Sapur.003G066600.1	119.3960978	0.740872577	0.1127434	6.571317	4.99E-11	1.12E-10	grey	0.43831239	9.39E-09		AT5G45580.1		Homeodomain-like superfamily protein	myb family transcription factor
Sapur.014G094600.1	146.4461465	-0.951952263	0.14487376	-6.57091	5.00E-11	1.12E-10	grey	-0.43534113	1.21E-08		AT2G47270.1		sequence-specific DNA binding transcription factors;transcription regulators	transcription factor, putative
Sapur.016G120100.1	18.82148562	-1.079544872	0.164296098	-6.57073	5.01E-11	1.13E-10	grey	-0.413017845	7.63E-08	GO:0005975,GO:0004553	AT2G44480.1	BGLU17	beta glucosidase 17	beta-glucosidase
Sapur.016G206400.1	109.5467334	0.42432321	0.064578121	6.570696	5.01E-11	1.13E-10	grey	0.461421914	1.19E-09	GO:0006468,GO:0004672	AT3G01840.1		Protein kinase superfamily protein	receptor-like kinase
Sapur.013G040700.1	2.919728821	-1.347326864	0.205083987	-6.56963	5.04E-11	1.13E-10	grey	-0.458016033	1.63E-09		AT3G56710.1	SIB1	sigma factor binding protein 1	VQ motif protein
Sapur.005G082900.1	1.652660104	-1.753181703	0.266883284	-6.5691	5.06E-11	1.14E-10	grey	-0.414728996	6.66E-08		AT4G35690.1		Arabidopsis protein of unknown function (DUF241)	DUF241 domain protein
Sapur.012G066800.1	1029.88725	1.496638335	0.227833658	6.568996	5.07E-11	1.14E-10	grey	0.426393934	2.57E-08	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G45570.1	CYP76C2	cytochrome P450, family 76, subfamily C, polypeptide 2	NA
Sapur.T170700.1	0.529384989	2.540571028	0.386788721	6.568369	5.09E-11	1.14E-10	grey	0.469078341	5.77E-10					NA
Sapur.011G058900.1	226.0686073	0.183883788	0.027995911	6.568237	5.09E-11	1.14E-10	grey	0.452741719	2.63E-09		AT3G21610.1		Acid phosphatase/vanadium-dependent haloperoxidase-related protein	acid phosphatase/vanadium-dependent haloperoxidase-like protein
Sapur.018G018900.4	9.667803925	-0.605995487	0.09228648	-6.56646	5.15E-11	1.16E-10	grey	-0.256319285	0.001193978		AT5G11040.1	AtTRS120,TRS120	TRS120	transporter Trs120
Sapur.003G140700.2	15.48922859	-0.565702707	0.08617796	-6.56435	5.23E-11	1.17E-10	grey	-0.434895367	1.26E-08		AT1G16080.1			hypothetical protein
Sapur.005G180300.2	4.996631194	1.313935775	0.20017584	6.563908	5.24E-11	1.18E-10	grey	0.154208099	0.053813837	GO:0008168	AT1G04430.2		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.15WG015300.1	13.13501573	-0.640528911	0.097595069	-6.56313	5.27E-11	1.18E-10	grey	-0.439880879	8.20E-09	GO:0055085,GO:0016020,GO:0006811,GO:0005216	AT5G53130.1	ATCNGC1,CNGC1	cyclic nucleotide gated channel 1	cyclic nucleotide-gated ion channel protein
Sapur.010G115200.2	5.30021446	-0.901023427	0.137299326	-6.56248	5.29E-11	1.19E-10	grey	-0.440099245	8.05E-09		AT1G47970.1			hypothetical protein
Sapur.008G170200.1	2.660142619	-1.358043611	0.207062483	-6.55862	5.43E-11	1.22E-10	grey	-0.465669802	7.97E-10	GO:0006807,GO:0006542,GO:0004356	AT5G35630.1	ATGSL1,GLN2,GS2	glutamine synthetase 2	glutamine synthetase
Sapur.011G059700.1	8.199058494	-0.76412442	0.116521982	-6.55777	5.46E-11	1.23E-10	grey	-0.448859738	3.71E-09		AT1G29380.1		Carbohydrate-binding X8 domain superfamily protein	carbohydrate-binding module family 43 protein
Sapur.018G104100.1	1.620022814	-1.351610926	0.206131283	-6.55704	5.49E-11	1.23E-10	grey	-0.432406482	1.56E-08					NA
Sapur.016G078100.1	2.378308067	2.199149878	0.335430812	6.556195	5.52E-11	1.24E-10	grey	0.362478026	3.08E-06	GO:0009611,GO:0004867	AT2G38870.1		Serine protease inhibitor, potato inhibitor I-type family protein	NA
Sapur.006G161100.1	935.8463856	0.716864507	0.109347092	6.555863	5.53E-11	1.24E-10	grey	0.408343881	1.10E-07	GO:0003676	AT1G55310.1	ATSCL33,SCL33,SR33	SC35-like splicing factor 33	NA
Sapur.007G046000.1	590.7814047	-0.346436799	0.052847448	-6.55541	5.55E-11	1.25E-10	grey	-0.424120972	3.11E-08		AT4G37260.1	ATMYB73,MYB73	myb domain protein 73	NA
Sapur.016G103700.2	2.258411148	-1.20072024	0.183189965	-6.55451	5.58E-11	1.25E-10	grey	-0.460346554	1.31E-09	GO:0046983,GO:0003677	AT5G60440.1	AGL62	AGAMOUS-like 62	MADS-box transcription factor, putative
Sapur.016G149400.1	22.56783514	0.536456645	0.081847212	6.554367	5.59E-11	1.25E-10	grey	0.430194116	1.87E-08	GO:0006468,GO:0005524,GO:0004672	AT3G51990.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.010G049600.1	108.4315996	0.851918518	0.130011514	6.552639	5.65E-11	1.27E-10	grey	0.417231917	5.45E-08	GO:0005515	AT2G29420.1	ATGSTU7,GST25,GSTU7	glutathione S-transferase tau 7	glutathione S-transferase GST
Sapur.016G207800.1	4.119583629	-0.991863032	0.15145142	-6.54905	5.79E-11	1.30E-10	grey	-0.436226156	1.12E-08		AT3G01810.1			EEIG1/EHBP1 protein amino-terminal domain protein
Sapur.009G021100.3	5.047681204	-0.787647715	0.120290188	-6.5479	5.84E-11	1.31E-10	grey	-0.366639786	2.33E-06		AT3G46450.2		SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	CRAL/TRIO domain protein
Sapur.001G135400.1	1546.920597	-0.551814745	0.084273984	-6.54787	5.84E-11	1.31E-10	grey	-0.451654067	2.90E-09	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT3G14310.1	ATPME3,PME3	pectin methylesterase 3	NA
Sapur.003G098800.4	17.041889	0.697363865	0.106536394	6.545781	5.92E-11	1.33E-10	grey	0.237467524	0.002747698	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT5G41610.1	ATCHX18,CHX18	cation/H+ exchanger 18	cation/H(+) antiporter
Sapur.005G048600.2	1.558287375	1.663743534	0.254183162	6.545451	5.93E-11	1.33E-10	grey	0.462655191	1.06E-09	GO:0016624,GO:0008152	AT5G09300.1		Thiamin diphosphate-binding fold (THDP-binding) superfamily protein	2-oxoisovalerate dehydrogenase alpha subunit, putative
Sapur.018G108500.1	41.32596961	-0.884841693	0.13519957	-6.54471	5.96E-11	1.34E-10	grey	-0.48301983	1.48E-10	GO:0046983	AT4G29930.3		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH protein
Sapur.006G228200.1	138.7749779	0.695087008	0.106227369	6.543389	6.01E-11	1.35E-10	grey	0.450033125	3.35E-09	GO:0008152,GO:0003824	AT5G65940.1	CHY1	beta-hydroxyisobutyryl-CoA hydrolase 1	3-hydroxyisobutyryl-CoA hydrolase
Sapur.016G172300.1	62.74336246	0.434596738	0.066423619	6.542804	6.04E-11	1.35E-10	grey	0.468180649	6.29E-10	GO:0005515,GO:0008144,GO:0016773	AT1G50030.1	TOR	target of rapamycin	Serine/Threonine-kinase TOR
Sapur.016G113200.11	2.177720397	-1.320793149	0.201881813	-6.54241	6.05E-11	1.36E-10	grey	-0.19465257	0.014569235	GO:0007275	AT1G08465.1	YAB2	Plant-specific transcription factor YABBY family protein	transcription factor YABBY2
Sapur.016G272200.3	19.27582104	0.626666191	0.095792701	6.541899	6.07E-11	1.36E-10	grey	0.026722915	0.739722542	GO:0016491	AT4G27270.1		Quinone reductase family protein	quinone oxidoreductase, putative
Sapur.008G068600.2	3.782539927	-1.105985651	0.169075868	-6.54136	6.10E-11	1.37E-10	grey	-0.487031682	9.93E-11	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT1G14205.1		Ribosomal L18p/L5e family protein	ribosomal protein L18
Sapur.018G059000.2	12.6944318	0.596537415	0.091209054	6.540331	6.14E-11	1.37E-10	grey	0.407780993	1.15E-07		AT2G20120.1	COV1	Protein of unknown function (DUF502)	Cov1
Sapur.010G111000.1	6.71412855	1.821040922	0.278432527	6.540331	6.14E-11	1.37E-10	grey	0.433625505	1.40E-08					NA
Sapur.013G091100.1	1.332824631	-1.6518753	0.252580972	-6.53998	6.15E-11	1.38E-10	grey	-0.432834878	1.50E-08	GO:0008033,GO:0004809,GO:0003723	AT3G56330.1		N2,N2-dimethylguanosine tRNA methyltransferase	N2,N2-dimethylguanosine tRNA methyltransferase
Sapur.019G084300.2	174.4694183	-0.566114604	0.086580685	-6.53858	6.21E-11	1.39E-10	grey	-0.310865932	7.41E-05	GO:0046933,GO:0015986	AT4G09650.1	ATPD	ATP synthase delta-subunit gene	ATP synthase F1, delta subunit
Sapur.001G003600.1	5.448609122	1.423812907	0.217762821	6.538365	6.22E-11	1.39E-10	grey	0.434386224	1.32E-08	GO:0006355,GO:0003700	AT2G47520.1	HRE2	Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.T122400.1	0.749342338	2.149132963	0.32877564	6.536777	6.29E-11	1.41E-10	grey	0.395695063	2.91E-07		AT5G17020.1	ATCRM1,ATXPO1,HIT2,XPO	exportin 1A	NA
Sapur.011G012500.1	1349.761217	0.307377169	0.047028916	6.535919	6.32E-11	1.42E-10	grey	0.430683863	1.80E-08	GO:0016787	AT4G22300.1	SOBER1	carboxylesterases	acyl-protein thioesterase
Sapur.005G204500.1	956.3886543	-0.384693721	0.058858628	-6.53589	6.32E-11	1.42E-10	grey	-0.427770414	2.30E-08		AT1G42550.1	PMI1	plastid movement impaired1	plastid movement impaired protein, putative
Sapur.016G247700.3	80.40316543	-0.301450551	0.046143981	-6.53282	6.45E-11	1.44E-10	grey	-0.29568165	0.000170121		AT3G14830.1			hypothetical protein
Sapur.008G161300.1	5.014452585	-1.077354158	0.164931799	-6.53212	6.48E-11	1.45E-10	grey	-0.478836318	2.25E-10	GO:0005515	AT3G06880.2		Transducin/WD40 repeat-like superfamily protein	transducin family protein, putative
Sapur.15WG005200.1	282.357362	0.410031141	0.062773209	6.531945	6.49E-11	1.45E-10	grey	0.418889631	4.76E-08	GO:0009733	AT4G00880.1		SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.014G073200.1	29.18554428	0.556401975	0.085193195	6.531061	6.53E-11	1.46E-10	grey	0.460234772	1.32E-09	GO:0006355,GO:0003700	AT2G46310.1	CRF5	cytokinin response factor 5	AP2/ERF domain transcription factor
Sapur.006G100400.1	16.65556922	-0.851903489	0.130452809	-6.53036	6.56E-11	1.47E-10	grey	-0.421500747	3.85E-08		AT3G53200.1	AtMYB27,MYB27	myb domain protein 27	Myb DNA-binding domain protein, putative
Sapur.017G096400.1	72.59766149	0.392733454	0.060146113	6.529656	6.59E-11	1.47E-10	grey	0.439462623	8.50E-09		AT5G16160.1			NA
Sapur.003G006100.1	0.847888707	2.020000117	0.309448456	6.527743	6.68E-11	1.49E-10	grey	0.414547616	6.75E-08	GO:0003677				B3 DNA-binding domain protein
Sapur.017G110300.1	1.232517454	1.828716723	0.280190298	6.526695	6.72E-11	1.50E-10	grey	0.402964162	1.67E-07		AT5G23530.1	AtCXE18,CXE18	carboxyesterase 18	arylacetamide deacetylase, putative
Sapur.001G189000.2	2.088955089	-1.315283028	0.201682818	-6.52154	6.96E-11	1.56E-10	grey	-0.466664254	7.26E-10	GO:0005525	AT5G39960.1		GTP binding;GTP binding	GTP-binding protein EngA, putative
Sapur.T159100.1	10.69018971	0.752728108	0.115433504	6.520881	6.99E-11	1.56E-10	grey	0.472121937	4.31E-10		AT1G56120.1		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.008G061400.1	10.38599463	-0.58288866	0.089424724	-6.51828	7.11E-11	1.59E-10	grey	-0.456278642	1.91E-09		AT1G65420.1	NPQ7	Protein of unknown function (DUF565)	antigen receptor, putative
Sapur.016G102500.1	37.36440521	-0.631323819	0.096862316	-6.51774	7.14E-11	1.60E-10	grey	-0.435161947	1.23E-08	GO:0006351,GO:0005634,GO:0003700	AT5G01380.1		Homeodomain-like superfamily protein	transcription factor, putative
Sapur.019G006500.1	3.36179884	1.71233416	0.262720242	6.517709	7.14E-11	1.60E-10	grey	0.434764908	1.27E-08		AT4G15093.1		catalytic LigB subunit of aromatic ring-opening dioxygenase family	NA
Sapur.008G142100.1	103.8054069	0.788560194	0.120992021	6.517456	7.15E-11	1.60E-10	grey	0.392331331	3.74E-07	GO:0005515	AT3G09270.1	ATGSTU8,GSTU8	glutathione S-transferase TAU 8	tau class glutathione transferase GSTU19
Sapur.15ZG057000.1	0.793648621	2.13979796	0.328372507	6.516374	7.20E-11	1.61E-10	grey	0.383632988	7.06E-07		AT1G75290.1		NAD(P)-binding Rossmann-fold superfamily protein	NA
Sapur.005G074500.1	37.2679957	0.814198643	0.124947221	6.516341	7.20E-11	1.61E-10	grey	-0.010064579	0.900441035	GO:0006468,GO:0005524,GO:0004672	AT3G13530.1	MAP3KE1,MAPKKK7	mitogen-activated protein kinase kinase kinase 7	MAP3K epsilon kinase
Sapur.T140900.1	0.400936466	2.104165791	0.322936146	6.515733	7.23E-11	1.62E-10	grey	0.544353502	1.72E-13					NA
Sapur.013G137400.2	7.848475621	-0.903398297	0.138677128	-6.5144	7.30E-11	1.63E-10	grey	-0.458574967	1.54E-09	GO:0043565,GO:0006355,GO:0003700	AT2G38470.1	ATWRKY33,WRKY33	WRKY DNA-binding protein 33	WRKY transcription factor
Sapur.001G051700.2	1.093763373	-1.715787117	0.263441409	-6.51297	7.37E-11	1.65E-10	grey	-0.466087047	7.66E-10	GO:0006355,GO:0005634,GO:0003677,GO:0009725	AT5G62000.1	ARF1-BP,ARF2,HSS,ORE14	auxin response factor 2	auxin response factor
Sapur.019G011400.1	332.9411427	0.279071195	0.042851482	6.512521	7.39E-11	1.65E-10	grey	0.480495727	1.91E-10	GO:0055114,GO:0016491,GO:0008270	AT5G63620.2		GroES-like zinc-binding alcohol dehydrogenase family protein	NA
Sapur.002G103300.1	8.364938427	-1.225850954	0.188240011	-6.51217	7.41E-11	1.65E-10	grey	-0.425526674	2.77E-08	GO:0005509				EF hand protein
Sapur.001G082000.1	31.81383786	-0.543004077	0.083396105	-6.51114	7.46E-11	1.67E-10	grey	-0.475997857	2.96E-10		AT5G41470.1		Nuclear transport factor 2 (NTF2) family protein	SnoaL-like domain protein
Sapur.15WG015000.1	0.765625682	-1.837329321	0.282198276	-6.51077	7.48E-11	1.67E-10	grey	-0.52053028	2.79E-12		AT3G50120.1		Plant protein of unknown function (DUF247)	NA
Sapur.15WG114900.1	25.15808112	0.581168067	0.089269803	6.510242	7.50E-11	1.68E-10	grey	0.460093524	1.34E-09	GO:0005515	AT5G50640.1		CBS / octicosapeptide/Phox/Bemp1 (PB1) domains-containing protein	meiotically up-regulated protein
Sapur.017G064200.5	5.837611039	-0.841932939	0.129337653	-6.50957	7.54E-11	1.68E-10	grey	-0.452614322	2.66E-09		AT3G28700.1		Protein of unknown function (DUF185)	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.017G091000.1	5.577629834	1.22467966	0.188139636	6.509419	7.54E-11	1.68E-10	grey	0.415203527	6.41E-08					hypothetical protein
Sapur.009G068600.1	0.626577536	2.151363572	0.330622524	6.507008	7.67E-11	1.71E-10	grey	0.443222797	6.13E-09	GO:0005515	AT4G35270.1		Plant regulator RWP-RK family protein	PB1 domain protein
Sapur.005G068700.1	2.432571591	-1.374562484	0.211287206	-6.50566	7.74E-11	1.73E-10	grey	-0.480641402	1.88E-10	GO:0008270	AT4G24630.1		DHHC-type zinc finger family protein	zinc finger protein, putative
Sapur.002G126800.2	11.8436003	-0.616082452	0.094708048	-6.50507	7.77E-11	1.73E-10	grey	-0.420613534	4.14E-08		AT3G61180.1		RING/U-box superfamily protein	E3 ubiquitin-protein ligase, putative
Sapur.016G283100.1	0.746052107	-2.552142997	0.392382559	-6.50422	7.81E-11	1.74E-10	grey	-0.511566433	7.55E-12	GO:0003677,GO:0000786	AT5G10400.1		Histone superfamily protein	NA
Sapur.010G096100.1	1684.721577	-0.37801145	0.058118989	-6.5041	7.82E-11	1.74E-10	grey	-0.499378144	2.78E-11	GO:0016747,GO:0008610,GO:0016020,GO:0006633	AT1G68530.1	CER6,CUT1,G2,KCS6,POP1	3-ketoacyl-CoA synthase 6	3-ketoacyl-CoA synthase
Sapur.15WG124700.1	6.323682013	-0.848508914	0.130476076	-6.50318	7.86E-11	1.75E-10	grey	-0.449592316	3.49E-09		AT5G45480.1		Protein of unknown function (DUF594)	NA
Sapur.15WG079200.1	28.85832998	0.491638673	0.075605546	6.50268	7.89E-11	1.76E-10	grey	0.511129441	7.91E-12					hypothetical protein
Sapur.017G092000.1	430.6655605	-0.214181999	0.032961829	-6.49788	8.15E-11	1.82E-10	grey	-0.475481786	3.12E-10		AT5G38600.1		Proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein	nucleic acid-binding protein, putative
Sapur.017G120800.1	1.408984372	-1.394933717	0.214764309	-6.49518	8.29E-11	1.85E-10	grey	-0.489824208	7.48E-11					NA
Sapur.011G096200.1	11.86015018	-0.803704015	0.123774761	-6.49328	8.40E-11	1.87E-10	grey	-0.443830074	5.81E-09		AT3G20640.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH123
Sapur.T177500.1	0.552113195	1.966483234	0.303053344	6.488901	8.65E-11	1.93E-10	grey	0.479639106	2.08E-10		AT4G15110.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3	NA
Sapur.016G003100.1	2.909460322	-1.284644823	0.198011723	-6.48772	8.71E-11	1.94E-10	grey	0.078548531	0.32814497		AT5G47800.1		Phototropic-responsive NPH3 family protein	BTB/POZ domain protein
Sapur.15WG047100.4	0.553046422	-2.463930173	0.379836802	-6.48681	8.77E-11	1.95E-10	grey	-0.514218983	5.64E-12	GO:0055085,GO:0016021	AT1G73590.1	ATPIN1,PIN1	Auxin efflux carrier family protein	auxin efflux carrier component 1
Sapur.018G042200.4	3.780116979	0.972658546	0.150006793	6.484097	8.93E-11	1.99E-10	grey	0.078548531	0.32814497		AT1G19110.1		inter-alpha-trypsin inhibitor heavy chain-related	inter-alpha-trypsin inhibitor heavy chain, putative
Sapur.001G166600.2	11.33985574	-0.611161051	0.094264283	-6.48348	8.96E-11	2.00E-10	grey	-0.429275769	2.02E-08	GO:0006351,GO:0005634,GO:0003899,GO:0003677	AT3G13940.1		DNA binding;DNA-directed RNA polymerases	A49-like RNA polymerase I associated factor
Sapur.T024600.1	0.875241152	-2.698524176	0.416239097	-6.48311	8.99E-11	2.00E-10	grey	-0.41499921	6.51E-08		AT3G60470.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.002G060200.1	0.84102191	2.305284348	0.355668561	6.481552	9.08E-11	2.02E-10	grey	0.359133127	3.86E-06	GO:0030247,GO:0006468,GO:0004672	AT1G21240.1	WAK3	wall associated kinase 3	tyrosine kinase family protein
Sapur.019G073900.1	1.425165883	1.681831523	0.259491701	6.481254	9.10E-11	2.03E-10	grey	0.424978272	2.89E-08		AT2G24670.1		Domain of unknown function (DUF313)	DUF313 domain protein
Sapur.014G138900.1	4.72278646	0.895814746	0.138223852	6.480898	9.12E-11	2.03E-10	grey	0.496920736	3.60E-11	GO:0015074	AT4G12680.1			NA
Sapur.005G147200.2	7.126359309	-0.794650661	0.122626396	-6.48026	9.16E-11	2.04E-10	grey	-0.181800821	0.022680229		AT1G48880.1	TBL7	TRICHOME BIREFRINGENCE-LIKE 7	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.002G176200.4	4.900678015	-1.422192852	0.219582984	-6.47679	9.37E-11	2.09E-10	grey	-0.505591793	1.44E-11					NA
Sapur.018G048900.1	973.3296129	0.245200201	0.037861552	6.476232	9.40E-11	2.09E-10	grey	0.420974825	4.02E-08		AT4G29520.1			DUF3456 domain protein
Sapur.014G131500.1	2.533591774	-1.303506838	0.201327852	-6.47455	9.51E-11	2.12E-10	grey	-0.454762239	2.19E-09		AT2G44310.1		Calcium-binding EF-hand family protein	calcium ion-binding protein, putative
Sapur.014G123800.1	3.229732156	1.120235467	0.1730401	6.473849	9.55E-11	2.13E-10	grey	0.456099827	1.94E-09		AT3G59300.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing-like protein
Sapur.016G215700.1	2.075767731	1.515330396	0.23408722	6.473358	9.58E-11	2.13E-10	grey	0.404360562	1.50E-07					NA
Sapur.006G142800.1	3.486497633	-1.122314237	0.173380694	-6.47312	9.60E-11	2.14E-10	grey	-0.458926763	1.49E-09					NA
Sapur.005G194800.1	1565.754705	0.239526361	0.037012308	6.471533	9.70E-11	2.16E-10	grey	0.45134115	2.98E-09	GO:0006511	AT1G75950.1	ASK1,ATSKP1,SKP1,SKP1A,U	S phase kinase-associated protein 1	SKP1-like protein
Sapur.003G142600.1	28.45918061	0.569897438	0.088077551	6.470405	9.77E-11	2.17E-10	grey	-0.010096611	0.900125816	GO:0031047	AT5G23570.1	ATSGS3,SGS3	XS domain-containing protein / XS zinc finger domain-containing protein-related	NA
Sapur.010G008300.1	0.728997031	-2.367000513	0.365902204	-6.46894	9.87E-11	2.20E-10	grey	-0.482571668	1.55E-10		AT3G06890.1			transmembrane protein, putative
Sapur.010G007200.2	27.06781277	0.504815424	0.078051047	6.46776	9.95E-11	2.21E-10	grey	0.494257494	4.75E-11	GO:0016746,GO:0008152	AT3G06850.1	BCE2,DIN3,LTA1	2-oxoacid dehydrogenases acyltransferase family protein	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase, putative
Sapur.003G094400.1	3.356800647	-1.129810428	0.174693111	-6.4674	9.97E-11	2.22E-10	grey	-0.466690031	7.24E-10	GO:0005515	AT5G41380.1		CCT motif family protein	CCT motif protein
Sapur.016G069900.1	1.710659183	-1.4415453	0.222902763	-6.46715	9.99E-11	2.22E-10	grey	-0.477182306	2.64E-10		AT3G11550.1		Uncharacterised protein family (UPF0497)	casparian strip membrane protein
Sapur.012G021900.1	14.85010801	-1.065694621	0.164795879	-6.46676	1.00E-10	2.23E-10	grey	-0.482031253	1.64E-10	GO:0055114,GO:0050660,GO:0016491	AT1G30760.1		FAD-binding Berberine family protein	NA
Sapur.013G060000.1	71.81734696	0.350522399	0.054206797	6.466392	1.00E-10	2.23E-10	grey	0.425883605	2.69E-08		AT5G37480.1			NA
Sapur.019G074400.1	3.229828221	1.424036374	0.220226364	6.466239	1.00E-10	2.23E-10	grey	0.366613222	2.33E-06	GO:0055114,GO:0050661,GO:0050660,GO:0004499	AT1G19250.1	FMO1	flavin-dependent monooxygenase 1	NA
Sapur.017G053600.1	208.8413903	-0.293899464	0.045463694	-6.46449	1.02E-10	2.26E-10	grey	-0.47957038	2.09E-10		AT5G41070.1	DRB5	dsRNA-binding protein 5	double-stranded RNA-binding protein
Sapur.005G012200.1	8.33184076	-1.790544921	0.27699128	-6.46426	1.02E-10	2.26E-10	grey	-0.51361638	6.03E-12	GO:0004527,GO:0003676	AT5G45775.2		Ribosomal L5P family protein	NA
Sapur.T035300.1	3.925162021	0.870230501	0.134672436	6.461831	1.03E-10	2.30E-10	grey	0.467311304	6.83E-10		AT1G09320.1		agenet domain-containing protein	NA
Sapur.005G126900.1	99.50960658	-0.350013681	0.054173021	-6.46103	1.04E-10	2.31E-10	grey	-0.475467208	3.12E-10		AT2G39260.1		binding;RNA binding	NA
Sapur.003G004900.3	5.766234375	-0.8801001	0.136238659	-6.45999	1.05E-10	2.33E-10	grey	0.019287602	0.810513192	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G15220.1		Ribosomal protein L27 family protein	ribosomal protein L27
Sapur.013G086700.1	306.23789	0.512440669	0.079334043	6.459278	1.05E-10	2.34E-10	grey	0.436686977	1.08E-08	GO:0055085,GO:0016020,GO:0006810,GO:0005215,GO:0006863,GO:0005345	AT3G10960.1	ATAZG1,AZG1	AZA-guanine resistant1	adenine/guanine permease AZG2
Sapur.004G116300.2	4.761383269	-0.817503937	0.126573664	-6.45872	1.06E-10	2.35E-10	grey	-0.43787322	9.76E-09	GO:0006468,GO:0004672	AT2G16250.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.002G125000.1	35.97994453	-0.469962899	0.072793277	-6.45613	1.07E-10	2.39E-10	grey	-0.478503537	2.32E-10		AT1G01840.1			plant/T1N6-19 protein, putative
Sapur.006G170800.1	3.33042674	1.368305226	0.211985529	6.454711	1.08E-10	2.41E-10	grey	0.433712467	1.39E-08		AT5G17580.1		Phototropic-responsive NPH3 family protein	BTB/POZ domain protein
Sapur.002G149000.2	7.094046082	-0.764593321	0.118513224	-6.45154	1.11E-10	2.46E-10	grey	-0.461935253	1.13E-09		AT2G46170.2		Reticulon family protein	reticulon-like protein
Sapur.T013200.1	26.96683699	0.568227913	0.088084308	6.450955	1.11E-10	2.47E-10	grey	0.388879572	4.82E-07		AT2G28580.1		Plant protein of unknown function (DUF247)	NA
Sapur.T185500.1	2.767269918	-0.95983871	0.148801892	-6.45045	1.12E-10	2.48E-10	grey	-0.497011432	3.57E-11		AT4G35730.1		Regulator of Vps4 activity in the MVB pathway protein	NA
Sapur.002G071200.1	393.58635	-0.2003388	0.031065382	-6.44894	1.13E-10	2.50E-10	grey	-0.461716853	1.15E-09		AT4G08500.1	ARAKIN.ATMEKK1.MAPKKK	MAPK/ERK kinase kinase 1	NA
Sapur.004G162300.1	47.88946902	-0.660631836	0.10244051	-6.44893	1.13E-10	2.50E-10	grey	-0.4720126	4.36E-10		AT5G57620.1	AtMYB36,MYB36	myb domain protein 36	transcription factor MYBJ7, putative
Sapur.004G116500.1	0.814066986	1.969863918	0.305459412	6.448857	1.13E-10	2.50E-10	grey	0.397433512	2.55E-07					NA
Sapur.011G047200.1	426.7856295	-0.345591833	0.053594458	-6.44828	1.13E-10	2.51E-10	grey	-0.466434025	7.42E-10	GO:0005515,GO:0006468,GO:0004672	AT5G45800.1	MEE62	Leucine-rich repeat protein kinase family protein	NA
Sapur.001G133900.2	5.214823682	0.82156169	0.127415733	6.447883	1.13E-10	2.52E-10	grey	0.442177471	6.72E-09	GO:0042578,GO:0036092,GO:0007033	AT3G14205.1		Phosphoinositide phosphatase family protein	phosphoinositide phosphatase
Sapur.010G065300.1	1.894693829	1.30126119	0.20181986	6.447637	1.14E-10	2.52E-10	grey	0.431444643	1.69E-08	GO:0016021,GO:0015116,GO:0008272,GO:0055085,GO:0016020,GO:0008271	AT3G51895.1	AST12,SULTR3;1	sulfate transporter 3;1	sulfate/bicarbonate/oxalate exchanger and transporter sat-1
Sapur.006G195800.1	16.03020358	-0.742401541	0.115160757	-6.44665	1.14E-10	2.54E-10	grey	-0.46833423	6.20E-10		AT4G32870.1		Polyketide cyclase/dehydrase and lipid transport superfamily protein	polyketide cyclase/dehydrase and lipid transporter
Sapur.017G030400.1	13.24706358	-0.639054016	0.099149365	-6.44537	1.15E-10	2.56E-10	grey	-0.450643222	3.17E-09		AT2G32280.1		Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.008G020600.1	213.8258554	0.344787751	0.05350735	6.443746	1.17E-10	2.58E-10	grey	0.430824435	1.78E-08		AT5G02420.1			cyclin-dependent kinase inhibitor siamese protein, putative
Sapur.002G128000.1	257.9907426	-0.970807495	0.150666059	-6.44344	1.17E-10	2.59E-10	grey	-0.466981522	7.04E-10	GO:0016491,GO:0008152	AT3G61220.1		NAD(P)-binding Rossmann-fold superfamily protein	(+)-neomenthol dehydrogenase
Sapur.016G152300.3	35.19393764	-0.451137985	0.070025523	-6.44248	1.18E-10	2.61E-10	grey	-0.383942835	6.91E-07	GO:0006457	AT3G21640.1	ATFKBP42.FKBP42.TWD1.U	FKBP-type peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase
Sapur.018G049600.2	1.88842974	-1.275296868	0.197952982	-6.44242	1.18E-10	2.61E-10	grey	-0.486977311	9.98E-11	GO:0005975,GO:0004553	AT5G56590.1		O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase
Sapur.017G049500.1	177.3581783	-0.217573608	0.03377601	-6.44166	1.18E-10	2.62E-10	grey	-0.412657106	7.85E-08		AT5G43490.1			hypothetical protein
Sapur.T066000.1	5.056708626	2.243222987	0.34823958	6.441608	1.18E-10	2.62E-10	grey	0.47229517	4.24E-10					NA
Sapur.011G008800.2	2.958071418	-1.177916693	0.182864544	-6.44147	1.18E-10	2.62E-10	grey	-0.458668705	1.53E-09	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G22130.1	SRF8	STRUBBELIG-receptor family 8	strubbelig family receptor kinase, putative
Sapur.018G004000.1	15.9290042	-0.527972658	0.081965825	-6.44138	1.18E-10	2.62E-10	grey	-0.472320607	4.23E-10					NA
Sapur.002G074900.1	1.299281519	2.004553685	0.311230254	6.440742	1.19E-10	2.63E-10	grey	0.380246724	9.01E-07					NA
Sapur.006G001200.1	41.76211727	-0.945655197	0.146861668	-6.43909	1.20E-10	2.66E-10	grey	-0.408287594	1.11E-07	GO:0046872,GO:0030001	AT4G05030.1		Copper transport protein family	heavy metal-associated domain protein
Sapur.014G107200.1	7.750307801	1.309759345	0.203435333	6.43821	1.21E-10	2.68E-10	grey	0.408433924	1.09E-07	GO:0045454,GO:0015035,GO:0009055	AT1G03020.1		Thioredoxin superfamily protein	monothiol glutaredoxin-S6 protein
Sapur.007G041800.1	3.377004121	-1.45686021	0.226302481	-6.43767	1.21E-10	2.69E-10	grey	-0.452974017	2.57E-09	GO:0046983	AT5G67060.1	HEC1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.T183000.1	8.80900067	0.672307021	0.104437568	6.437406	1.22E-10	2.69E-10	grey	0.457616085	1.69E-09		AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO	exportin 1A	NA
Sapur.007G123500.1	0.707130339	2.633597166	0.409193693	6.436065	1.23E-10	2.72E-10	grey	0.429517083	1.98E-08		AT5G44265.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	NA
Sapur.019G067700.1	122.0480404	0.613562048	0.095336775	6.435733	1.23E-10	2.72E-10	grey	0.419417565	4.56E-08	GO:0006355,GO:0003700	AT5G25810.1	tny	Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.T178400.1	7.900250398	-0.831269286	0.129179114	-6.43501	1.23E-10	2.73E-10	grey	-0.445124535	5.19E-09					NA
Sapur.15WG013400.1	11.20943612	-1.152611578	0.179225873	-6.43106	1.27E-10	2.81E-10	grey	-0.463297119	9.96E-10	GO:0030247,GO:0008270,GO:0005515	AT5G53110.1		RING/U-box superfamily protein	NA
Sapur.016G037700.1	9.236178259	-1.077446689	0.167544479	-6.43081	1.27E-10	2.81E-10	grey	-0.448977871	3.68E-09		AT3G50160.1		Plant protein of unknown function (DUF247)	NA
Sapur.006G147600.1	13.87786818	-0.706838797	0.109921515	-6.4304	1.27E-10	2.82E-10	grey	-0.471015246	4.80E-10		AT4G30700.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.005G161200.1	178.1969361	0.703161841	0.109424507	6.426	1.31E-10	2.90E-10	grey	0.370345124	1.80E-06	GO:0006508,GO:0004190	AT3G59080.1		Eukaryotic aspartyl protease family protein	basic 7S globulin 2 small subunit, putative
Sapur.004G073500.1	0.517548659	-2.477461465	0.385605239	-6.42486	1.32E-10	2.92E-10	grey	-0.546928434	1.26E-13		AT1G13680.1		PLC-like phosphodiesterases superfamily protein	phospholipase C, putative
Sapur.014G106000.2	1.883854752	1.46013933	0.227277257	6.424485	1.32E-10	2.93E-10	grey	0.541750057	2.36E-13		AT3G62770.3	AtATG18a	Transducin/WD40 repeat-like superfamily protein	WD repeat phosphoinositide-interacting protein
Sapur.017G102800.1	2.282967738	-1.596188579	0.248468508	-6.42411	1.33E-10	2.93E-10	grey	-0.48516158	1.20E-10		AT3G02645.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.012G009100.1	26.92067361	0.767646681	0.119503994	6.423607	1.33E-10	2.94E-10	grey	0.399087136	2.25E-07	GO:0005524	AT2G46620.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	chaperone BCS1
Sapur.T151800.1	1.943900428	1.169737297	0.182125714	6.422692	1.34E-10	2.96E-10	grey	0.515613094	4.84E-12					NA
Sapur.003G167200.1	60.48026713	0.659721427	0.102755669	6.420292	1.36E-10	3.01E-10	grey	0.342204747	1.15E-05	GO:0016592,GO:0006357,GO:0001104	AT1G55325.2	GCT	RNA polymerase II transcription mediators	mediator of RNA polymerase II transcription subunit 13
Sapur.017G128400.1	0.836256456	-2.083545022	0.32455829	-6.41963	1.37E-10	3.02E-10	grey	-0.436276475	1.12E-08	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G73340.1		Cytochrome P450 superfamily protein	cytochrome P450 family 720 protein
Sapur.011G062000.1	22.73657286	-0.646250635	0.100684402	-6.41858	1.38E-10	3.04E-10	grey	-0.240528493	0.002410097	GO:0016021	AT1G78620.1		Protein of unknown function DUF92, transmembrane	integral membrane family protein
Sapur.002G009700.2	0.879368472	2.197963747	0.342472452	6.417929	1.38E-10	3.05E-10	grey	0.045926488	0.567891042	GO:0043169,GO:0005975,GO:0003824,GO:0005509,GO:0004556	AT1G76130.1	AMY2,ATAMY2	alpha-amylase-like 2	alpha-amylase
Sapur.016G084000.1	284.0345043	-0.916607349	0.142835903	-6.41721	1.39E-10	3.07E-10	grey	-0.459522701	1.41E-09	GO:0008168,GO:0008152	AT3G53400.1			NA
Sapur.002G158000.1	388.8309156	0.361053763	0.056269756	6.41648	1.39E-10	3.08E-10	grey	0.421677438	3.80E-08		AT4G02370.1		Protein of unknown function, DUF538	DUF538 family protein
Sapur.006G189300.1	5565.937959	-0.409258712	0.063788935	-6.41583	1.40E-10	3.10E-10	grey	-0.455195665	2.10E-09	GO:0055114,GO:0006546,GO:0004375	AT4G33010.1	AtGLDP1,GLDP1	glycine decarboxylase P-protein 1	glycine dehydrogenase [decarboxylating] protein
Sapur.014G111100.1	629.4639063	0.174296105	0.027169302	6.415185	1.41E-10	3.11E-10	grey	0.456744324	1.83E-09	GO:0008270,GO:0005634,GO:0003677	AT3G63030.1	MBD4	methyl-CPG-binding domain 4	methyl-CpG-binding domain protein
Sapur.008G050700.1	1.514846449	-1.767052455	0.27548534	-6.41432	1.41E-10	3.13E-10	grey	-0.34546085	9.38E-06					NA
Sapur.15WG113000.1	23.021621	-0.614469703	0.095800322	-6.41407	1.42E-10	3.13E-10	grey	-0.472601157	4.12E-10	GO:0016787	AT5G50400.1	ATPAP27,PAP27	purple acid phosphatase 27	purple acid phosphatase
Sapur.002G174500.1	12.83727558	-0.526787498	0.082147812	-6.41268	1.43E-10	3.14E-10	grey	-0.46365526	9.83E-10		AT3G55170.1		ribosomal protein L30 family protein	ribosomal protein L30
Sapur.006G206100.1	5.377899893	-1.202898629	0.187608463	-6.41175	1.44E-10	3.16E-10	grey	-0.432791443	1.51E-08	GO:0005524,GO:0003676	AT5G60990.1		DEA(D/H)-box RNA helicase family protein	DEAD-box ATP-dependent RNA helicase
Sapur.004G157000.1	16.73286399	-0.806619601	0.125808608	-6.41148	1.44E-10	3.16E-10	grey	-0.442523331	6.25E-09	GO:0008270,GO:0005515	AT4G38170.1	FRS9	FAR1-related sequence 9	FAR1-related sequence protein
Sapur.006G107100.1	2169.680328	0.225588842	0.038304557	6.411478	1.44E-10	3.16E-10	grey	0.433985956	1.36E-08	GO:0006355,GO:0005634,GO:0003677	AT2G37120.1		S1FA-like DNA-binding protein	DNA-binding protein S1FA
Sapur.006G155500.1	7.670186203	-0.989866439	0.1544068	-6.41077	1.45E-10	3.17E-10	grey	-0.446685506	4.52E-09		AT1G52140.1			NA
Sapur.018G085300.1	7.60082591	1.58109001	0.246645041	6.410386	1.45E-10	3.17E-10	grey	0.293773491	0.000188239	GO:0006468,GO:0004672	AT4G23240.1	CRK16	cysteine-rich RLK (RECEPTOR-like protein kinase) 16	tyrosine kinase family protein
Sapur.006G130100.1	102.3217158	-0.386796243	0.060346615	-6.41036	1.46E-10	3.18E-10	grey	-0.460919281	1.24E-09	GO:0008270	AT5G18650.1		CHY-type zinc finger family protein	DHHC-type zinc finger family protein
Sapur.006G142700.1	0.915844718	2.459924119	0.383814446	6.409149	1.46E-10	3.19E-10	grey	0.384932651	5.62E-07	GO:0005515	AT1G67480.1		Galactose oxidase/kelch repeat superfamily protein	kelch repeat F-box protein
Sapur.008G037800.1	3.664577419	-0.880317825	0.137361526	-6.40877	1.47E-10	3.24E-10	grey	-0.473615697	3.74E-10	GO:0005634,GO:0003676	AT3G55200.1		Cleavage and polyadenylation specificity factor (CPSF) A subunit protein	Splicing factor 3B subunit 3
Sapur.015G108300.1	378.6657662	0.316477649	0.049392132	6.407451	1.48E-10	3.27E-10	grey	0.44180057	7.82E-09		AT3G21865.1	PEX22	peroxin 22	peroxin, putative
Sapur.016G218500.1	3.169990246	1.297299335	0.202480273	6.406984	1.48E-10	3.28E-10	grey	0.440403554	7.84E-09		AT5G63090.1	LOB	Lateral organ boundaries (LOB) domain family protein	elongated petiole protein
Sapur.013G109200.1	4.729335517	0.909905973	0.142024838	6.406668	1.49E-10	3.28E-10	grey	0.433989839	1.36E-08	GO:0016757,GO:0016020	AT1G33250.1		Protein of unknown function (DUF604)	beta-1%2C3-N-acetylglucosaminyltransferase radical fringe protein, putative

Sapur.012G000400.1	212.4842264	2.60344561	0.04920747	6.405882	1.50E-10	3.30E-10	grey	0.38842751	4.98E-07		ATSG24680.1	LSU2	response to low sulfur 2	hypothetical protein
Sapur.T030400.1	4.94681735	2.14801987	0.33537004	6.404925	1.50E-10	3.32E-10	grey	0.43202798	1.75E-08					NA
Sapur.005G000800.1	684.0669035	0.57004096	0.08916027	6.403224	1.50E-10	3.36E-10	grey	0.38412207	3.94E-08	GO:0055114,GO:0016491	ATSG51240.1	F3'H,F3H,TT6	flavanone 3-hydroxylase	NA
Sapur.017G035800.1	81.8954513	-0.63034341	0.09987642	-6.40134	1.54E-10	3.40E-10	grey	-0.43857832	9.18E-09	GO:0016757	ATSG43630.1			transmembrane protein, putative
Sapur.006G000100.1	730.4519816	0.32009083	0.05607283	6.401146	1.54E-10	3.40E-10	grey	0.44567285	8.84E-10					hypothetical protein
Sapur.001G029600.1	50.3042585	-0.36609183	0.05720702	-6.39936	1.56E-10	3.44E-10	grey	-0.45249073	2.69E-09					NA
Sapur.016G038100.1	102.7842	0.64780142	0.10125026	6.399085	1.56E-10	3.45E-10	grey	0.43418159	1.34E-08		ATSG70700.1		Mitochondrial substrate carrier family protein	substrate carrier family protein
Sapur.012G000900.1	23.23454577	-0.49420266	0.07724760	-6.39885	1.57E-10	3.45E-10	grey	0.40724619	1.20E-07	GO:0005515	ATSG07760.1		Sterile alpha motif (SAM) domain-containing protein	downward leaf curling protein, putative
Sapur.010G025100.1	38.51574601	-0.44755274	0.06991038	-6.39751	1.58E-10	3.48E-10	grey	-0.45227087	2.76E-09		ATSG40460.1			hypothetical protein
Sapur.006G034000.1	2.78542868	3.52E-192	7.7979E-09	6.24598E+13	2.96E-01	3.96E-01	grey	0.44091923	2.50E-09	GO:0005975,GO:0004553	ATSG72240.1	BG3	beta-1,3-glucanase 3	glucan endo-1%2C3-beta-glucosidase
Sapur.004G068900.1	7.54540435	1.23603869	0.20710963	6.384874	1.61E-10	3.54E-10	grey	0.37785809	1.07E-06	GO:0055085,GO:0016020,GO:0006811,GO:0005216	ATSG15410.2	ATCNGC2,CNGC2,DND1	Cyclic nucleotide-regulated cation channel 2	NA
Sapur.010G176100.1	26.58916157	0.75787194	0.11854725	6.39127	1.62E-10	3.58E-10	grey	0.39732876	2.46E-07		ATSG20600.1	UBC19	ubiquitin conjugase 19	ubiquitin
Sapur.004G118300.1	43.3532044	-0.40243919	0.06298374	-6.38944	1.66E-10	3.67E-10	grey	-0.46603715	7.65E-10		ATSG66440.1			transmembrane protein, putative
Sapur.001G135100.1	111.1370897	0.61175479	0.09582728	6.38743	1.67E-10	3.69E-10	grey	0.48226288	6.80E-10	GO:0003700,GO:0009058	ATSG7330.1	ALAAT2	alanine aminotransferase 2	alanine aminotransferase
Sapur.159G148800.1	4.60812187	0.88120893	0.13790212	6.387384	1.68E-10	3.72E-10	grey	0.43591051	1.15E-08	GO:0007264,GO:0005525	ATSG22950.1	ARFC1,ATARFC1	ADP-ribosylation factor C1	ADP-ribosylation factor(Arf)/Arf-like (Arl) small GTPase family protein
Sapur.018G006300.1	76.50956218	0.75356401	0.11949763	6.287091	1.68E-10	3.73E-10	grey	0.39816892	2.41E-07		ATSG60695.1			hypothetical protein
Sapur.T035100.1	3.95057842	0.85266375	0.13556635	6.384286	1.72E-10	3.76E-10	grey	0.46216139	1.08E-09		ATSG69320.1		agenet domain-containing protein	NA
Sapur.009G075000.1	188.5590712	0.40336089	0.06318785	6.383211	1.73E-10	3.82E-10	grey	0.41930426	6.71E-09	GO:0008270	ATSG14830.2		Regulator of Ipx4 activity in the MVB pathway protein	histone deacetylase
Sapur.009G054500.1	6.70463993	-0.62802823	0.14101815	-6.38245	1.74E-10	3.84E-10	grey	-0.42374235	1.20E-07	GO:0005515	ATSG19280.1		Rho GTPase activation protein (RhoGAP) with PH domain	Rho GTPase-activating protein
Sapur.001G147000.1	31.0164885	0.51484519	0.08063186	6.382122	1.75E-10	3.85E-10	grey	0.42311874	3.37E-08					NA
Sapur.010G051300.6	1.01327918	0.46187584	0.07238603	6.38	1.75E-10	3.85E-10	grey	0.3161652	2.5E-05	GO:0055124,GO:0003676	ATSG27880.1		DEAD/DEAH box RNA helicase family protein	ATP-dependent DNA helicase RecQ
Sapur.005G125300.1	7.27282905	0.73104368	0.11458375	-6.38129	1.76E-10	3.87E-10	grey	-0.41383789	8.38E-09	GO:0043565,GO:0006355,GO:0003700	ATSG42240.1	ATWRKY7,WRKY7	WRKY DNA-binding protein 7	WRKY transcription factor
Sapur.006G047000.1	9.83747797	0.68735688	0.10702569	6.379338	1.78E-10	3.92E-10	grey	0.48811749	9.90E-11	GO:0005515	ATSG07620.1	ATBPM2,BPM3	BTB/POZ/MATH-domain containing protein	speckle-type POZ protein, putative
Sapur.008G156700.3	8.42053934	0.75097344	0.11763726	-6.37891	1.78E-10	3.93E-10	grey	-0.11586619	0.14907403		ATSG70730.1		5'-AMP-activated protein kinase-related	5'-AMP-activated kinase-like protein, putative
Sapur.002G098000.4	1.28974767	0.61175479	0.09582728	6.378146	1.79E-10	3.93E-10	grey	0.44366466	6.00E-09	GO:0016020	ATSG46150.1		Uncharacterized protein family (UPF0016)	transmembrane protein TPA6, putative
Sapur.013G032100.1	41.91020877	-0.77234921	0.0905039	-6.37822	1.79E-10	3.94E-10	grey	-0.49320923	5.29E-11		ATSG41070.1	DRB5	dsRNA-binding protein 5	hypothetical protein
Sapur.005G077700.1	816.8670922	0.36020324	0.05426587	6.37809	1.79E-10	3.94E-10	grey	-0.45937884	1.43E-09		ATSG76660.1			NA
Sapur.013G124500.1	18.74849842	0.67572928	0.10601269	6.37716	1.80E-10	3.96E-10	grey	-0.44772242	4.10E-08		ATSG20720.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR domain protein
Sapur.004G007300.1	1.79891651	1.36876435	0.21465437	6.37652	1.81E-10	3.99E-10	grey	-0.47662854	7.76E-09	GO:0006355,GO:0005739,GO:0003690	ATSG75900.1		Mitochondrial transcription termination factor family protein	NA
Sapur.005G185300.1	10.72552234	0.68035261	0.10695149	6.37568	1.82E-10	4.01E-10	grey	-0.46631495	7.50E-10		ATSG72581.1	ATMRT8,MRT8	myb domain protein 79	MYB transcription factor, putative
Sapur.015G052400.4	252.0869405	-0.49825267	0.07819406	-6.37544	1.82E-10	4.01E-10	grey	0.06201929	0.452988213	GO:0060983,GO:0003677,GO:0006355,GO:0005634,GO:0003700	ATSG18960.1	AG	K-box region and MADS-box transcription factor family protein	MADS-box transcription factor
Sapur.005G154500.1	109.4783889	-0.58532916	0.09181917	-6.37517	1.82E-10	4.01E-10	grey	-0.06916216	0.38936868	GO:0005515	ATSG47730.1	ATCOTL4,TIGGTF8,GSTA.GO	glutathione S-transferase ph 8	Phi class glutathione S-transferase
Sapur.007G130000.1	16.94513127	0.95197842	0.14950148	6.374262	1.84E-10	4.04E-10	grey	0.41145047	8.85E-08	GO:0016779,GO:0009058	ATSG05630.1	APS2	ADP-glucose pyrophosphorylase small catalytic subunit 2	glucose-1-phosphate adenylyltransferase
Sapur.009G028900.1	0.76005494	-2.54221441	0.3988025	-6.37282	1.86E-10	4.08E-10	grey	0.50658055	1.16E-11	GO:0003677,GO:0006306	ATSG04600.1		Histone superfamily protein	NA
Sapur.003G069300.1	61.86961899	0.40672572	0.06382515	6.372435	1.86E-10	4.09E-10	grey	0.41466167	5.79E-08	GO:0055085,GO:0016020,GO:0006810,GO:0015171,GO:0003333	ATSG31830.1		Amino acid permease family protein	amino acid transporter, putative
Sapur.159G151800.1	779.4416601	0.18863146	0.03000567	6.292182	1.87E-10	4.12E-10	grey	0.45268464	1.16E-08	GO:0016491,GO:0055114	ATSG43430.2		Nucleotide-binding/Rossmann-fold superfamily protein	short-chain dehydrogenase TIC 32
Sapur.016G092900.1	36.74240641	0.66548835	0.10463942	6.370463	1.88E-10	4.14E-10	grey	0.02689505	0.737209904	GO:0006468,GO:0005134,GO:0016627	ATSG37840.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.016G080400.1	756.785245	0.25768783	0.04043455	6.368016	1.91E-10	4.21E-10	grey	-0.47382166	3.67E-10	GO:0055114,GO:0050660,GO:0016491,GO:0003824	ATSG06580.1		FAD-linked oxidases family protein	D-lactate dehydrogenase (cytochrome)
Sapur.006G139700.1	200.1115609	0.66588376	0.10463874	6.367774	1.91E-10	4.21E-10	grey	0.41323951	7.50E-08		ATSG46410.1			AT5BT12, putative
Sapur.005G089400.1	253.7679239	0.36053259	0.05663708	6.367232	1.92E-10	4.23E-10	grey	0.43476556	1.27E-08		ATSG35980.1			hypothetical protein
Sapur.010G088900.1	4.20053473	1.22180702	0.19217567	6.36704	1.93E-10	4.24E-10	grey	0.42057299	4.04E-08	GO:0003926	ATSG25120.1	AK-A/N-Inv/L/INV-C	alkaline/neutral invertase	alkaline/neutral invertase
Sapur.005G011100.1	177.2325481	0.38482244	0.06043854	-6.36703	1.93E-10	4.23E-10	grey	-0.43730963	1.02E-08		ATSG08320.1		Pentatricopeptide repeat (PPR-like) superfamily protein	PPR containing plant protein
Sapur.005G130400.1	24.34148488	0.52485452	0.08249147	6.364718	1.94E-10	4.26E-10	grey	-0.12122586	0.07579433	GO:0016567,GO:0006462,GO:0006488,GO:0005524,GO:0004672	ATSG45910.1		U-box domain-containing protein family protein	receptor kinase, putative
Sapur.018G096800.1	115.2464711	0.30862988	0.04848184	6.363888	1.94E-10	4.27E-10	grey	0.43524015	1.21E-08					hypothetical protein
Sapur.009G000100.1	58.5418771	-0.40686212	0.06420419	-6.36204	1.95E-10	4.30E-10	grey	-0.46223025	7.57E-10	GO:0008270	ATSG01275.2		RING/FYVE/PHD zinc finger superfamily protein	membrane-associated RING-finger protein 1%2C8, putative
Sapur.001G053700.1	4.30086662	1.03252198	0.16230933	-6.35936	2.03E-10	4.45E-10	grey	-0.41984238	4.41E-08	GO:0016020,GO:0006810,GO:0005215	ATSG13400.1		Major facilitator superfamily protein	peptide transporter, putative
Sapur.006G121600.1	24.88616	0.67109154	0.10546439	6.359077513	2.03E-10	4.45E-10	grey	0.45268343	2.36E-09		ATSG30880.1		Kinase interacting (KIP1-like) family protein	KIP1-like protein
Sapur.T020700.1	0.55022548	2.08710194	0.32828408	6.357602	2.05E-10	4.50E-10	grey	0.44300875	6.25E-09		ATSG15130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3	NA
Sapur.014G060400.2	29.89317339	0.80346361	0.09450022	6.357419	2.05E-10	4.50E-10	grey	0.32099472	6.15E-05		ATSG03553.3			transmembrane protein, putative
Sapur.016G035000.1	32.21254898	0.50438934	0.07935886	6.354524	2.08E-10	4.56E-10	grey	0.46478831	1.42E-08		ATSG18130.1			transmembrane protein, putative
Sapur.009G060300.1	3.69856706	0.91113908	0.14340611	6.353758	2.10E-10	4.61E-10	grey	0.43580609	1.16E-08					hypothetical protein
Sapur.005G011200.1	64.4087619	0.57236167	0.09008906	6.353179	2.11E-10	4.63E-10	grey	0.3953818	3.97E-07		ATSG43150.1			NA
Sapur.016G257000.1	0.95069925	-2.13344012	0.33581609	-6.35312	2.11E-10	4.63E-10	grey	-0.42532816	2.81E-08					NA
Sapur.016G138300.1	3.91522854	-0.62838152	0.10962245	-6.35292	2.11E-10	4.63E-10	grey	-0.44832105	3.70E-09		ATSG43240.3		Protein of unknown function (DUF674)	DUF674 family protein
Sapur.016G107700.1	3.75015975	-1.79883284	0.28317116	-6.35246	2.12E-10	4.65E-10	grey	-0.42417307	3.56E-08	GO:0016747,GO:0008610,GO:0016020,GO:0006633	ATSG26640.1	KCS11	3-ketoacyl-CoA synthase 11	NA
Sapur.T035800.1	1.30353904	1.18329334	0.24756187	6.352426	2.12E-10	4.65E-10	grey	0.45738631	2.75E-09		ATCHM1,ATHPO1,HT2,XPO	exportin 1A	Importin beta family protein	type I nucleolar 17%2C18%2C19%2C28%2C5-phosphatase
Sapur.015G094800.1	27.12013212	0.85897252	0.13523346	6.351777	2.13E-10	4.67E-10	grey	-0.44159828	7.12E-09	GO:0004674,GO:0048544,GO:0006468,GO:0004672	ATSG27290.1		S-locus lectin protein kinase family protein	Serine/Threonine-kinase
Sapur.010G065300.1	91.38367262	0.35870873	0.05478165	6.351461	2.13E-10	4.68E-10	grey	0.45825491	3.18E-09	GO:0055085,GO:0009922,GO:0000226	ATSG06695.3			transmembrane protein, putative
Sapur.009G021800.1	167.793552	0.57329544	0.08916297	6.350605	2.14E-10	4.70E-10	grey	0.27988049	0.00038841	GO:0016567,GO:0006462,GO:0005515	ATPUB13,PUB13	ATPUB13,PUB13	plant U-box 13	spotted leaf protein, putative
Sapur.013G092100.1	0.98422649	-1.77507243	0.27958258	-6.34952	2.18E-10	4.76E-10	grey	-0.47981586	2.04E-10		ATSG21280.1			Copia-like polyprotein/retrotransposon
Sapur.010G085400.1	7.76392185	0.58174268	0.09175	6.349471	2.16E-10	4.74E-10	grey	0.44596381	4.01E-09	GO:0005515	ATSG27320.1		F-box/RNI-like/FBD-like domains-containing protein	NA
Sapur.003G111000.1	22.08705134	0.65811046	0.10368784	6.347109	2.18E-10	4.81E-10	grey	0.43726741	1.01E-08	GO:0006355,GO:0003677	ATSG43000.1	anac042,NAC042	NAC domain containing protein 42	NAC transcription factor G30
Sapur.015G015200.1	120.8185252	0.63750487	0.10058395	6.34683	2.20E-10	4.85E-10	grey	-0.36591748	2.44E-06		ATSG01881.1	AIMP3DD,AIP3DD	myb-domain protein	R2R3-MYB transcription factor, putative
Sapur.015G095800.1	334.0603053	-0.22727157	0.03580077	-6.34682	2.20E-10	4.82E-10	grey	-0.45809597	1.62E-09	GO:0055515,GO:0008236,GO:0006508	ATSG46390.2		Peptidase S41 family protein	carboxyl-terminal-processing protease
Sapur.016G082800.1	63.68613301	0.67291154	0.10603257	6.345687	2.21E-10	4.85E-10	grey	0.44907604	1.61E-09		ATSG20581.1			hypothetical protein
Sapur.003G102700.1	2.07854362	-3.05021704	0.48073373	-6.34505	2.22E-10	4.87E-10	grey	-0.43546305	1.20E-08		ATSG15910.1		cryptdin protein-related	transmembrane protein, putative
Sapur.003G046400.1	0.61778128	2.81180096	0.44387407	6.344867	2.23E-10	4.88E-10	grey	0.44485051	5.01E-09		ATSG21380.1			NA
Sapur.016G270300.1	437.28297	0.49936481	0.07876095	6.344605	2.23E-10	4.88E-10	grey	0.43756274	1.00E-08	GO:0048544,GO:0006468,GO:0004672	ATSG21380.1	ARK3,RK3	receptor kinase 3	Serine/Threonine-kinase
Sapur.016G076500.1	1344.901631	0.38247831	0.06029582	6.342884	2.25E-10	4.94E-10	grey	0.41452743	6.76E-08		ATSG46290.1			transmembrane protein, putative
Sapur.006G128700.1	11.46705826	-0.52488966	0.19957816	-6.34201	2.27E-10	4.97E-10	grey	-0.45079139	1.25E-09		ATSG20960.1			hypothetical protein
Sapur.008G095700.1	32.78847774	-0.51778679	0.08164745	-6.34188	2.27E-10	4.97E-10	grey	-0.45713082	1.76E-09		ATSG13330.1	AHP2	Arabidopsis Hop2 homolog	NA
Sapur.T085500.1	5.86395541	-0.28191267	0.20219552	-6.34172	2.27E-10	4.98E-10	grey	-0.46142143	1.19E-09		ATSG34151.1	ATPAL,PL1	Pleckstrin homology (PH) domain-containing protein	NA
Sapur.009G041200.1	114.4668915	0.35717629	0.05636245	6.338091	2.33E-10	5.09E-10	grey	0.45816377	1.92E-09	GO:0008080	ATSG17780.1		Acyl-CoA N-acyltransferases (NAT) superfamily protein	amino-terminal acetyltransferase complex ARD1 subunit-like protein
Sapur.015G138000.4	2.72405654	-0.18529304	0.03187787	-6.33608	2.33E-10	5.10E-10	grey	-0.32047005	0.010988466		ATSG51581.1	ERA3	Endosomal farnesylation protein family protein	type I nonaitin 17%2C18%2C19%2C28%2C5-phosphatase
Sapur.015W0101000.1	257.3349884	0.34956104	0.05117918	6.331852	2.36E-10	5.17E-10	grey	0.44764418	4.23E-09	GO:0006468,GO:0004672	ATSG24740.1	AFC2,AMEL1,FC2	FUS3-complementing gene 2	NA
Sapur.004G205800.1	460.1924313	0.27625353	0.04048926	6.33474	2.38E-10	5.20E-10	grey	0.41899849	4.72E-08	GO:0022857,GO:0016021	ATSG07880.1		Major facilitator superfamily protein	phosphoinositol/choline transporter, putative
Sapur.017G021300.1	1.92769539	1.57201154	0.24107929	6.334625	2.38E-10	5.21E-10	grey	0.4484485	4.45E-09	GO:0003247,GO:0006468,GO:0055124,GO:0004672	ATSG38240.1		Protein kinase superfamily protein	tyrosine kinase family protein
Sapur.017G054500.1	50.76385157	-0.67020805	0.10727232	-6.33429	2.38E-10	5.22E-10	grey	-0.49284783	5.49E-11		ATSG40960.1		Protein of unknown function (DUF 3339)	transmembrane protein, putative
Sapur.003G026200.1	271.8630154	-0.47406466	0.07428607	-6.33367	2.39E-10	5.23E-10	grey	-0.40604705	1.15E-07		ATSG15620.1	UVR3	DNA photolyase family protein	6-4, DNA photolyase
Sapur.004G001300.1	2.94033584	-1.30408425	0.19904327	-6.33125	2.43E-10	5.32E-10	grey	-0.3482657	9.75E-06	GO:0005515	ATCOP1,COP1,DET340,EMB	Transducin/WD40 repeat-like superfamily protein		ubiquitin ligase COP1
Sapur.010G071200.1	4.88506760	0.91358237	0.14424087	6.328857	2.47E-10	5.40E-10	grey	0.44227226	7.46E-09	GO:0006488,GO:0004672	CRK14	cysteine-rich RLK (RECEPTOR-like protein) kinase14	cysteine-rich RLK (RECEPTOR-like protein) kinase	NA
Sapur.T028600.1	212.5823653	0.87365718	0.13801584	6.32866	2.47E-10	5.41E-10	grey	0.47485801	1.31E-10		ATSG07810.1		SNF2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing pr	NA
Sapur.005G166400.1	499.9736615	0.37280974	0.05850469	6.327954	2.48E-10	5.42E-10	grey	0.42498752	2.86E-08		ATSG41420.1			seven transmembrane domain protein
Sapur.002G049900.5	2.76437399	-1.00409975	0.17400015	-6.32448	2.54E-10	5.56E-10	grey	-0.28649601	0.00027643		ATSG06690.1		NADP(H)-linked oxidoreductase superfamily protein	aldo/keto reductase family protein
Sapur.009G154000.1	1.15861994	-0.56285537	0.2672021	-6.32423	2.54E-10	5.56E-10	grey	-0.44432204	1.57E-09		ATSG16000.1	MFP1	MAR binding filament-like protein	MAR binding filament-like protein
Sapur.006G114600.1	6839.974649	-0.47128524	0.07453584	-6.32293	2.57E-10	5.61E-10	grey	-0.43634072	1.40E-08	GO:0003476	ATSG39260.3	ATGRP8,CCR1,GR-RBP8,GRI	cold, circadian rhythm, and RNA binding 1	RNA-binding protein 42 (RBM42)-like RNA recognition motif protein
Sapur.159G028300.2	21.76513423	0.66718149	0.10463874	6.321852	2.58E-10	5.63E-10	grey	-0.47368945	1.31E-08	GO:0006468,GO:0004672	ATSG27850.1		Protein kinase superfamily protein	Serine/Threonine-kinase domain protein
Sapur.016G038500.1	430.3661512	0.41437955	0.06554768	6.321604	2.58E-10	5.66E-10	grey	0.45863865	1.62E-09	GO:0005515	ATSG41370.1	BOP2	Ankyrin repeat family protein / BTB/POZ domain-containing protein	BOP/NPR1/NIM1-like regulatory protein
Sapur.006G227700.1	3.17588642	-0.11291918	0.17606437	-6.32099	2.60E-10	5.68E-10	grey	-0.45432447	2.32E-09					hypothetical protein
Sapur.159G031000.2	10.06222954	0.61588479	0.09745556	-6.3195	2.62E-10	5.73E-10	grey	-0.41702247	1.26E-08	GO:0016021,GO:0006810	ATSG24170.1		Golt/SFt2-like vesicle transport protein family	vesicle transporter SFT2A, putative
Sapur.005G068400.1	2.36002486	3.35863497	0.21005125	-6.31914	2.63E-10	5.75E-10	grey	-0.50515786	1.51E-11		ATSG39180.2			WRKY DNA-binding protein protein
Sapur.003G188800.1	6.57929459	0.81878315	0.12957024	6.31607	2.64E-10	5.76E-10	grey	-0.45527543	2.44E-09	GO:0043565,GO:0006355,GO:0003700	ATSG42670.1	ATWRKY2,WRKY2	WRKY DNA-binding protein 2	NA
Sapur.016G137100.3	14.52123936	0.57244175	0.09060145	6.318241	2.65E-10	5.78E-10	grey	0.07854531	0.32814467	GO:0016787	ATSG38640.1	TOPP4	type one serine/threonine protein phosphatase 4	serine/threonine-protein phosphatase PP1
Sapur.015G035100.1	2.34285594	1.50380746	0.23798504	6.31816	2.66E-10	5.79E-10	grey	-0.47724845	1.20E-07	GO:0055085,GO:0016020,GO:0015299,GO:0006812	ATSG05230.1	ATNHX2,NHX2	sodium hydrogen exchanger 2	sodium/hydrogen exchanger
Sapur.010G099900.1	238.4157984	0.57611578	0.09127815	-6.31513	2.70E-10	5.90E-10	grey	-0.43685221	1.07E-08	GO:0009955	ATSG20570.1	AENDOLS,EN DDL9	early rodulin-like protein 9	plantacyanin-like domain protein
Sapur.009G033700.1	19.65002833	0.43468222	0.06874461	-6.3129	2.72E-10	5.94E-10	grey	-0.42582772	6.69E-08	GO:0016020,GO:0008375	ATSG15050.1	Cor+-2/1-branching beta-1,6-N-acetylglucosaminyltransferase family protein		glycosyltransferase family 14 protein
Sapur.013G076000.1	2.06070333	1.76082041	0.27889074	6.313657	2.73E-10	5.95E-10	grey	-0.23850497	0.00262591					NA
Sapur.014G071100.1	19.40482204	0.66236217	0.10508214	6.31087	2.75E-10	5.99E-10	grey	0.38415142	6.80E-07		ATSG41420.1			NA
Sapur.010G014300.1	226.7513575	0.79468916	0.12590632	6.31184	2.76E-10	6.02E-10	grey	0.44371071	5.87E-09		ATSG20340.1			protein-coding nuclear receptor coactivator protein
Sapur.006G088400.1	102.870305	-0.46026784	0.07292489	-6.31145	2.76E-10	6.06E-10	grey	-0.4254384	1.20E-08		ATSG08820.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing protein, putative
Sapur.006G137600.1	5.55383607	-0.74814709	0.11854148	-6.31069	2.77E-10	6.05E-10	grey	-0.41274658	1.16E-08		ATSG28600.1	NPGR2	no pollen germination related 2	O-linked N-acetylglucosamine transferase, ogt protein%2C putative
Sapur.003G045300.1	108.3879408	0.46386379	0.07353714	6.308471	2.82E-10	6.15E-10	grey	0.44900941	3.68E-09		ATSG16680.1		Nucleotide-diphosphe-sugar transferases superfamily protein	glycosyltransferase, putative
Sapur.003G094600.1	7.70114994	0.35795861	0.05677425	6.308323	2.82E-10	6.16E-10	grey	0.44449876	6.76E-08	GO:0000062	ATCBF,ACBP6	acyl-CoA-binding protein	acyl-CoA-binding protein(ACBP)	acyl-CoA-binding protein
Sapur.004G098000.1	2.94208559	-1.05437592	0.16748904	-6.30769	2.83E-10	6.18E-10	grey	-0.45409563	2.20E-09	GO:0004045	ATSG38290.2		Peptidyl-tRNA hydrolase family protein	group III intron splicing facilitator CRS2
Sapur.005G091000.1	31.91852149	0.50369185	0.08076523	-6.30766	2.84E-10	6.19E-10	grey	-0.12622704	0.11404574		ATSG08930.1	UBP24	ubiquitin-specific protease 24	ubiquitin carboxyl-terminal hydrolase
Sapur.017G059600.1	3.03457584	0.28019883	0.31804936	6.307384	2.84E-10	6.19E-10	grey	0.44808043	7.51E-09	GO:0071805,GO:0016020,GO:0015079	ATSG35060.2	KLP11	K+ uptake permease 11	NA
Sapur.013G050000.1	4.81679867	-1.09803658	0.17630725	-6.30701	2.84E-10	6.21E-10	grey	-0.37538344	1.27E-06		ATSG18340.1	ATO	splicing factor family protein	NA
Sapur.010G192600.1	3448.320593	-1.09001945	0.19010422	-6.30696	2.85E-10	6.21E-10	grey	-0.50472583	1.66E-11		ATSG10080.1		RmlC-like cupins superfamily protein	oxalate oxidase, putative
Sapur.007G037700.1	1.69865021	1.26217613	0.28007043	6.306704	2.85E-10	6.22E-10	grey	0.39264605	8.01E-07	GO:0003700,GO:0009058	ATSG11810.1	ALD1	AGD2-like defense response protein 1	D-alanine/proline aminotransferase
Sapur.005G147100.1	2.80127434	0.82084564	0.76565168	6.306503	2.85E-10	6.23E-10	grey	0.32214513	3.88E-05		ATSG19980.1			NA
Sapur.001G125700.1	0.85197775	-1.87606312	0.29745361	-6.3062	2.88E-10	6.26E-10	grey	-0.47992958	2.00E-10					NA
Sapur.008G040200.1	0.07741483	0.68522457	0.10779279	6.305851	2.87E-10	6.25E-10	grey	0.36479306	1.11E-07	GO:0055114,GO:0016616,GO:0006994,GO:0003854	ATSG28760.1	UXS6	UDP-XYL synthase 6	UDP-glucuronate decarboxylase
Sapur.T040100.1	4.52067332	2.24873269	0.19806569	-6.30462	2.88E-10	6.30E-10	grey	-0.49138569	8.38E-11	GO:0006412,GO:0005840,GO:0005622,GO:0003735	ATSG23740.1	RPS11-BETA	ribosomal protein S11-beta	POPTR/ORDRAT-57861418 protein
Sapur.016G097500.1	279.3713826	0.50830723	0.08062719	6.304625	2.89E-10	6.31E-10	grey	-0.42438936	7.26E-08		ATSG26080.1		Uncharacterized protein family (UPF0497)	CAAP-like protein POPTR/ORDRAT-578614 protein
Sapur.013G017800.8	1.39489048	-1.38217261	0.21928331	-6.30305	2.92E-10	6.36E-10	grey	-0.48608795	1.09E-10	GO:000896,GO:0000077,GO:0006281,GO:0000075	ATSG5480.3	ATRAD5,RAD9	cell cycle checkpoint control protein family	Rad9 protein
Sapur.004G084600.1	25.66663237	0.66188455	0.10854148	6.302983	2.93E-10	6.46E-10	grey	-0.47009758	1.16E-08		ATSG40870.1		phosphoinositide binding	FYVE zinc finger protein, putative
Sapur.014G002200.2	1.19330565	1.02960386	0.32188055	6.299583	2.98E-10	6.51E-10	grey	0.41945786	4.55E-08	GO:0006508,GO:0004222	ATSG65420.1		Zincin-like metalloproteases family protein	oligopeptidase A
Sapur.006G132500.1	0.10593948	1.14375379	0.18184506	6.298859	2.99E-10	6.54E-10	grey	0.40583803	1.46E-08		ATSG13120.1		Uncharacterized protein (UPF0121/Gut2_ vIMA	NA
Sapur.006G149400.1	70.89515223	0.89636158	0.14285618	-6.29751	3.02E-10	6.59E-10	grey	-0.39162089	3.94E-07		ATSG15680.1		NAD(P)-binding Rossmann-fold superfamily protein	short chain alcohol dehydrogenase, putative
Sapur.006G060800.1	38.79559502	1.08299382	0.17197807	6.297417	3.03E-10	6.60E-10	grey	-0.40824203	1.11E-07					NA
Sapur.017G280300.1	45.23685537	-0.8719308	0.13848246	-6.29679	3.04E-10	6.62E-10	grey	-0.42089103	1.02E-08		ATSG37670.1		HSP20-like chaperones superfamily protein	persistent small heat shock protein
Sapur.T081700.1	7.34050848	-0.86241409	0.13709214	-6.29456	3.08E-10	6.72E-10	grey	-0.43508455	1.19E-

Sapur.005G075600.1	151.3228828	27.01740703	0.043827702	6.183412	6.27E-10	1.35E-09	grey	0.415323042	6.35E-08			ATSG08320.1					NA
Sapur.005G078000.1	124.180737	0.446097819	0.072301097	6.182177	6.32E-10	1.36E-09	grey	0.406014146	1.32E-07	GO:0005515		AtSG15470.1	PIRL4			plant intracellular ras-group-related LRR 4	
Sapur.005G081100.1	171.8140778	0.241466681	0.030604559	6.18199	6.33E-10	1.36E-09	grey	0.445622218	9.36E-08			AtSG18630.1				sequence-specific DNA binding transcription factors	
Sapur.006G219400.2	12.30401823	0.564593823	0.091333424	6.181618	6.34E-10	1.37E-09	grey	0.420688255	4.12E-08	GO:0045747;GO:0007049;GO:0006221		AtSG10830.1	ATER;ER			enhancer of rudimentary-like protein	enhancer of rudimentary-like protein
Sapur.005G080400.1	187.163411	0.355557888	0.041461224	6.18167	6.34E-10	1.37E-09	grey	0.418664811	9.27E-08			AtSG78100.1				F-box family protein	F-box-like protein
Sapur.017G020900.1	1.174653622	1.843426324	0.298228273	6.181259	6.36E-10	1.37E-09	grey	0.378164205	1.05E-06	GO:0003677		AtSG01570.1	RGA;RGA1			GRAS family transcription factor family protein	GRAS domain protein
Sapur.013G121200.1	3.390378519	-1.362339419	0.204263134	6.17986	6.41E-10	1.38E-09	grey	-0.3734672	1.45E-06	GO:0009607;GO:0006952		AtSG24020.1	MLP423			MLP-like protein 423	pathogenesis-related protein Bet V I family protein
Sapur.019G067004.4	1.571275152	1.727307425	0.281134977	-6.1797	6.42E-10	1.38E-09	grey	-0.449789403	1.42E-09	GO:0055515;GO:0045531		AtSG27220.1				NB-ARC domain-containing disease resistance protein	NA
Sapur.003G094900.1	3.78655272	0.994614499	0.160551574	6.178346	6.48E-10	1.39E-09	grey	0.432662751	1.52E-08			AtSG47510.1				Sec14p-like phosphatidylinositol transfer family protein	CRAL/TRIO, amino-terminal domain protein
Sapur.005G170900.4	0.913843868	1.05608629	0.170287167	-6.17819	6.48E-10	1.40E-09	grey	-0.38217151	1.64E-07	GO:0003676		AtSG05160.1				CCCH-type zinc fingerfamily with RNA-binding domain	zinc finger CCCH domain protein, putative
Sapur.001G063400.1	73.47142417	0.574478344	0.093028567	-6.17817	6.49E-10	1.40E-09	grey	-0.437394132	1.02E-08	GO:0016021;GO:0006952		AtSG24250.1	ATMLO13;MLO13			Seven transmembrane MLO family protein	NA
Sapur.005G103000.1	151.1692604	0.315790461	0.051114201	6.178116	6.49E-10	1.40E-09	grey	0.440319268	5.64E-08	GO:0004872		AtSG30580.1				DREB/A-interactome gene 2	ring/finger protein, putative
Sapur.010G100800.1	120.8858842	0.284787082	0.046103602	6.177071	6.53E-10	1.40E-09	grey	0.472309966	3.88E-10			AtSG25682.1				Family of unknown function (DUF572)	NA
Sapur.T007400.1	590.6600	0.71487	0.116876879	6.175369	6.71E-10	1.41E-09	grey	0.44671133	3.38E-09			AtSG07260.1	ATUBC2;UBC2			ubiquitin-conjugating family 2 protein	NA
Sapur.019G033300.1	523.1829282	0.342756177	0.055504674	-6.17527	6.61E-10	1.42E-09	grey	-0.352824318	5.97E-06			AtSG39050.1				hydroxyproline-rich glycoprotein family protein	hypothetical protein
Sapur.006G198600.1	86.28983802	0.432320806	0.070028988	-6.17391	6.68E-10	1.42E-09	grey	-0.366150654	2.41E-06	GO:0005852;GO:0005737;GO:0003743		AtSG25723.1				RNA polymerase I-associated factor PAF67	eukaryotic translation initiation factor 3 subunit L
Sapur.010G049500.1	24.20192946	1.631391757	0.264243904	6.17381	6.67E-10	1.43E-09	grey	0.427870086	4.01E-10			AtSG09270.1	ATGSTU8;GSTU8			glutathione S-transferase TAU 8	NA
Sapur.005G163100.1	7.167348095	1.718788217	0.278410529	6.173575	6.68E-10	1.44E-09	grey	0.395393313	0.014190966			AtSG17370.1	UBP1B			oligoutylate binding protein 1B	oligoutylate-binding protein 1B
Sapur.005G132500.2	8.019692752	1.642908783	0.112113205	6.172327	6.75E-10	1.44E-09	grey	-0.272293386	1.44E-03	GO:0003676		AtSG33051.1				F-box family protein	hypothetical protein
Sapur.016G291900.1	3.778851523	-1.051509977	0.167110537	-6.17262	6.72E-10	1.44E-09	grey	-0.452061479	2.79E-09			AtSG30551.1				hypothetical protein	hypothetical protein
Sapur.005G131100.1	6.800928077	1.7183615	0.273618108	6.171671	6.73E-10	1.44E-09	grey	-0.401497538	2.97E-07	GO:0030244;GO:0016798;GO:0016820		AtSG18190.1	ATCLD4;CLD4			cellulose synthase like D4	cellulose synthase D-like protein
Sapur.013G309500.1	1.060161587	1.855147989	0.300730982	6.168885	6.88E-10	1.48E-09	grey	0.439453825	8.51E-09			AtSG31130.1					NA
Sapur.019G264500.1	5.476683956	1.517184664	0.184395051	6.16852	6.97E-10	1.50E-09	grey	0.418015001	1.11E-08			AtSG09190.1	ATCSN7;COP15;CSN7;FUSS			Proteasome component (PCI) domain protein	hypothetical protein
Sapur.017G013900.1	4.029413976	1.384375215	0.20837271	-6.1668	6.97E-10	1.50E-09	grey	-0.377861759	1.07E-06			AtSG28580.1				Plant protein of unknown function (DUF247)	NA
Sapur.011G055600.3	1.637677842	1.324801182	0.201486629	-6.16567	7.08E-10	1.51E-09	grey	-0.418946415	6.59E-08	GO:0005975;GO:0004553		AtSG08370.1				O-Glycosyl hydrolase family 17 protein	glucan endo-1N2C3-beta-glucosidase
Sapur.012G054800.1	1042.078665	-0.205691298	0.033369911	-6.16564	7.02E-10	1.51E-09	grey	-0.462280403	1.02E-09			AtSG17190.1				Oligosaccharyltransferase complex/magnesium transporter family protein	dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 3, putative
Sapur.016G190200.1	3.850657554	0.551601423	0.251730461	-6.16372	7.11E-10	1.53E-09	grey	-0.41326684	6.38E-08			AtSG31160.1				Ankyrin repeat family protein	NA
Sapur.007G069000.1	19.45616153	0.707988822	0.132723305	6.163245	7.13E-10	1.53E-09	grey	-0.379278084	4.01E-07			AtSG04190.1	PK54			phytochrome kinase substrate 4	hypothetical protein
Sapur.T023900.1	45.47013028	-1.943645685	0.315458851	-6.16175	7.19E-10	1.54E-09	grey	-0.443214895	6.13E-10			AtSG24370.1				Plant protein of unknown function (DUF247)	DUF247 domain protein
Sapur.019G100000.1	101.1243008	0.238867461	0.038477564	6.16169	7.20E-10	1.54E-09	grey	-0.461743222	5.16E-09			AtSG03150.1					hypothetical protein
Sapur.006G045300.1	13.54554032	0.698526072	0.113375634	-6.16117	7.22E-10	1.55E-09	grey	-0.39948774	2.18E-07	GO:0055114;GO:0020037;GO:0016705;GO:0005506		AtSG30490.1	ATC4H;CAH;CYP73A5;REF3			cinnamate-4-hydroxylase	cytochrome P450 family 73 cinnamate 4-hydroxylase
Sapur.006G139100.1	23.24564139	0.705275162	0.122964611	-6.15743	7.29E-10	1.56E-09	grey	-0.430017528	1.90E-08	GO:0071944		AtSG28440.1	SQE1;AT1			squalene monooxygenase family protein	squalene epoxidase
Sapur.008G072400.1	5884.60028	0.194527864	0.031602705	6.155418	7.48E-10	1.61E-09	grey	-0.40060547	2.01E-07	GO:0045905;GO:0045901;GO:0004332;GO:0003746;GO:0003723		AtSG11570.1	ATEUTSA-1;EIF-5A;EIF5A;EU			eukaryotic elongation factor 5A-1	eukaryotic translation initiation factor 5A
Sapur.006G146100.1	132.7901834	0.825604197	0.134138784	6.154931	7.51E-10	1.61E-09	grey	-0.42071501	4.11E-08	GO:0046355		AtSG44120.1	ATCAL1;CAL;CRU1			RmlC-like cupins superfamily protein	Rv 5 Y.0101 allergen 101.globulin precursor, putative
Sapur.T123700.1	6.893447328	0.961810581	0.15631903	-6.15287	7.61E-10	1.63E-09	grey	-0.402075536	1.79E-07	GO:0080270;GO:0008023;GO:0006625;GO:0005779		AtSG04460.1	APM4;ATPDX12;PDX12			pentatin-12	NA
Sapur.013G053200.1	6.788664838	1.272401182	0.185764738	6.152824	7.61E-10	1.63E-09	grey	-0.484605652	1.26E-10			AtSG27320.1					transmembrane protein, putative
Sapur.017G016000.3	4.51197527	-0.782609297	0.127273455	-6.1514	7.68E-10	1.64E-09	grey	-0.11562048	0.149306826			AtSG30700.1					hypothetical protein
Sapur.I59G011100.1	0.757607119	1.967832875	0.319019949	6.150805	7.71E-10	1.65E-09	grey	0.401214124	1.91E-07			AtSG04940.1	FLA12			FASCICLIN-like arabinogalactan-protein 12	fasciclin-like AGP protein
Sapur.008G064300.1	0.91519565	1.860684631	0.31126171	6.149386	7.78E-10	1.67E-09	grey	-0.373022899	1.00E-06	GO:0055114;GO:0020037;GO:0006979;GO:0004601		AtSG08370.1				Peroxidase superfamily protein	peroxidase
Sapur.013G052400.1	329.623705	-0.496600093	0.081156193	-6.14902	7.88E-10	1.67E-09	grey	-0.445019806	8.04E-09			AtSG13540.1	ATMYB95;MYB95			myb domain protein 5	MYB transcription factor
Sapur.T155600.1	6.477164271	-1.450982753	0.136767529	-6.14759	7.87E-10	1.68E-09	grey	-0.428682374	2.14E-08			AtSG34750.1					NA
Sapur.T063300.1	2.426143644	1.600100226	0.260310004	6.146903	7.90E-10	1.69E-09	grey	0.414612309	6.72E-08			AtSG03320.1				RNA-binding ASCH domain protein	NA
Sapur.006G142300.1	112.4456263	0.788109207	0.129663554	6.146227	7.98E-10	1.71E-09	grey	0.447874747	4.07E-09			AtSG04240.1				ELMO/CED-12 domain family	ELMO/CED-12 domain protein
Sapur.006G208600.4	17.69446625	-0.499177156	0.081235459	-6.14512	7.99E-10	1.71E-09	grey	-0.448416693	3.87E-09			AtSG29230.1				Alba DNA/RNA-binding protein	alba protein
Sapur.008G058500.1	781.1867923	0.355201005	0.161087839	6.026430209	8.14E-10	1.74E-09	grey	0.432238656	2.26E-08			AtSG05700.1				Drought-response family protein	protein dehydration-induced-like protein
Sapur.003G119000.1	1.586693952	1.548717317	0.252058433	6.144257	8.03E-10	1.72E-09	grey	0.408878716	1.05E-07	GO:0004857		AtSG00080.1	UNE11			Plant invertase/pectin methylesterase inhibitor superfamily protein	pectin methylesterase inhibitor, putative
Sapur.005G043800.2	3.155256849	0.987117011	0.160811883	6.141984	8.04E-10	1.72E-09	grey	-0.067308087	0.236127752	GO:0005198;GO:0016272;GO:0006457		AtSG28780.1	AIP1;PFD4			ABD-interacting protein 1	prefoldin subunit 4, putative
Sapur.011G034100.1	544.0496601	0.337906967	0.055008513	6.14623	8.11E-10	1.74E-09	grey	-0.447427239	4.23E-09	GO:0030133;GO:0030138;GO:0016192;GO:0006886;GO:0005198		AtSG20760.1				Clathrin light chain protein	clathrin light chain
Sapur.016G144000.2	15.91247716	0.701375824	0.114479462	6.142375	8.13E-10	1.74E-09	grey	0.242261175	0.002140466	GO:0005515		AtSG12400.1				DNA binding;zinc ion binding;DNA binding	PHD-Finger and DNA-binding domain protein, putative
Sapur.005G243300.2	385.2173268	0.257291995	0.041881639	6.140164	8.15E-10	1.75E-09	grey	0.414266562	5.32E-08			AtSG18990.1	TXN19			thioredoxin domain-containing protein	thioredoxin-like ATP-binding protein
Sapur.006G133600.1	4.491430013	-0.028208028	0.167420357	-6.14148	8.18E-10	1.75E-09	grey	-0.454264389	2.29E-09	GO:0009968		AtSG19930.1				RNA-dependent RNA polymerase family protein	NA
Sapur.010G054800.1	17.10414143	0.750802757	0.12624272	-6.13899	8.30E-10	1.78E-09	grey	-0.429365544	4.18E-08	GO:0004648;GO:0005524;GO:0004672		AtSG30080.1				AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	NA
Sapur.003G148800.1	1.399362757	-1.514767788	0.246782246	-6.13809	8.35E-10	1.79E-09	grey	-0.412517893	7.94E-08								NA
Sapur.003G082500.2	1.424867568	-1.512375124	0.250663556	-6.13796	8.36E-10	1.79E-09	grey	-0.025403686	0.701315364			AtSG11790.1	NDL2			N-MYC downregulated-like 2	NA
Sapur.004G022300.1	5939.817826	-0.343221822	0.056509781	-6.13656	8.43E-10	1.81E-09	grey	-0.447882682	4.06E-09			AtSG33850.1					hypothetical protein
Sapur.003G072000.1	336.492399	-0.263813174	0.043009543	-6.13614	8.45E-10	1.81E-09	grey	-0.418520708	4.90E-08			AtSG31550.1	CIN4;COP1;ELMB144;FUSI			Ubiquitin-conjugating enzyme family protein	ubiquitin-conjugating enzyme E2, putative
Sapur.003G153600.1	11.0135256	-0.590004235	0.096159281	-6.1357	8.48E-10	1.82E-09	grey	-0.45929664	1.44E-09			AtSG59560.1	SIR1			sensitivity to red light reduced protein (SRR1)	sensitivity TO RED LIGHT reduced protein
Sapur.007G012500.1	5.985649561	0.984206857	0.160406611	-6.1357	8.49E-10	1.82E-09	grey	-0.386957073	5.51E-07	GO:0009017;GO:0007018;GO:0005524;GO:0003777;GO:0005871		AtSG19150.2				ATP binding microtubule motor family protein	kinesin motor domain protein
Sapur.008G085200.1	0.886663567	1.205164492	0.196511459	6.126319954	8.61E-10	1.84E-09	grey	0.119608842	0.157094502	GO:0007049;GO:0005634		AtSG30025.1				Terminins protein family (TPR)-like superfamily protein	NA
Sapur.013G109200.1	7.360099906	0.686396794	0.111896613	6.124205	8.56E-10	1.83E-09	grey	0.463942708	1.13E-09	GO:0016757;GO:0016020		AtSG32510.1				Protein of unknown function (DUF604)	beta-1?2?3-N-acetylglucosaminyltransferase radical fringe protein, putative
Sapur.007G054300.1	20.70837757	0.687102197	0.112084128	6.123748	8.57E-10	1.83E-09	grey	-0.420034378	4.31E-08			AtSG37230.1				ABC transporter G family member 11	ABC transporter family protein
Sapur.004G076000.3	20.43956325	0.548529391	0.089450124	6.1325	8.65E-10	1.85E-09	grey	0.423052182	3.09E-08	GO:0016020;GO:0006886		AtSG39510.1	ATVTI11;ATVTI1A;SGR4;VTI			Vesicle transport v-SNARE protein	vesicle transport V-SNARE protein
Sapur.003G139000.1	6.335391276	0.958879131	0.156382121	6.1321	8.66E-10	1.85E-09	grey	0.420257928	1.98E-07			AtSG28710.1				Nucleotide-diphospho-sugar transferase family protein	nucleotide-diphospho-sugar transferase
Sapur.013G093000.1	116.1689696	-0.641397353	0.104606216	-6.13154	8.70E-10	1.86E-09	grey	-0.454163613	2.31E-09			AtSG27680.1					hypothetical protein
Sapur.006G122300.1	84.01736163	0.699425994	0.112869449	6.129864	8.85E-10	1.89E-09	grey	0.425288338	1.39E-08			AtSG22120.1	MED19A			Transcriptional mediator complex subunit 19a family protein	RNA-binding protein, putative
Sapur.008G130900.1	1.060204277	1.279165857	0.205611516	6.127914	8.90E-10	1.90E-09	grey	0.326373689	3.02E-05			AtSG14780.1				MAC/Perforin domain-containing protein	MAC/perforin domain protein
Sapur.011G045700.1	207.7391375	0.614868893	0.100703125	6.12712	8.94E-10	1.91E-09	grey	-0.437660014	1.01E-08			AtSG30882.1				alpha/beta-hydrolases superfamily protein	esterase/lipase domain protein
Sapur.009G002000.3	1.896687034	1.420756262	0.231958778	-6.12562	9.03E-10	1.93E-09	grey	-0.203310387	0.015182362	GO:0006412;GO:0005840;GO:0005622;GO:0003735		AtSG44890.1	RPL9			ribosomal protein L9	50S ribosomal protein L9
Sapur.014G021000.1	1.178107398	1.706178122	0.27873364	6.123274	9.17E-10	1.96E-09	grey	-0.429462213	1.96E-08			AtSG28161.1				Protein of unknown function, DUF538	DUF538 family protein
Sapur.010G068700.1	26.6250164	0.502809268	0.102838564	-6.1231	9.18E-10	1.96E-09	grey	-0.447381186	4.32E-09	GO:0005515;GO:0005634		AtSG37420.1				indole-3-acetic acid inducible 28 protein	indole-3-acetic acid inducible protein
Sapur.007G125800.1	10.47045554	-1.653343669	0.270071669	-6.12187	9.25E-10	1.98E-09	grey	-0.456208754	1.83E-09								NA
Sapur.013G058200.1	2.780668891	-1.413828717	0.230661409	-6.12063	9.33E-10	1.99E-09	grey	-0.414836416	4.96E-08			AtSG05950.1				RmlC-like cupins superfamily protein	RuvB/ATP receptor, putative
Sapur.017G017400.1	6.339282635	-0.151323574	0.165878358	-6.12089	9.33E-10	1.99E-09	grey	-0.431867108	2.82E-07			AtSG37650.1	SGR7;SGR			GRAS family transcription factor	NA
Sapur.006G134400.1	5.538613967	0.111897541	0.189059219	6.120388	9.34E-10	2.00E-09	grey	-0.432620398	1.46E-08			AtSG26160.1				NAD+ ADP-ribosyltransferase	poly (ADP-ribose) polymerase
Sapur.006G089500.1	703.4688724	0.186917209	0.030543151	6.119772	9.37E-10	2.00E-09	grey	-0.419392234	4.57E-08	GO:0006351;GO:0005634;GO:0003677;GO:0008270;GO:0003676		AtSG38560.1	TFIIS			transcript elongation factor IIS	transcription elongation factor S-II, putative
Sapur.006G162700.1	115.3125406	0.267409926	0.051232214	6.119324	9.40E-10	2.01E-09	grey	-0.422934762	2.64E-08	GO:0016887;GO:0016020;GO:0015079		AtSG14120.1	ATHAK5;HAK5			high affinity K+ transporter 5	NA
Sapur.013G072600.1	9.462315233	-0.765791762	0.121859798	-6.11847	9.45E-10	2.02E-09	grey	-0.443817711	5.86E-09	GO:0005885;GO:0016020;GO:0051297;GO:0051328;GO:0006855		AtSG06320.1				MATE efflux family protein	NA
Sapur.I59G001400.1	0.897881487	1.708695193	0.279256679	-6.11801	9.48E-10	2.02E-09	grey	-0.42770869	9.90E-09			AtSG25381.1	PATL2			PATELLIN 2	patellin, putative
Sapur.007G075800.1	1331.192897	-0.317360182	0.051879451	-6.11785	9.48E-10	2.02E-09	grey	-0.451654152	2.07E-09	GO:0016887;GO:0005524		AtSG44640.1	ATGCN;GCN5			general control non-repressible 5	ABC transport family protein
Sapur.016G241900.1	131.7940192	0.543375	0.088837474	6.117462	9.51E-10	2.03E-09	grey	-0.395005563	2.56E-07	GO:0055114;GO:0016491		AtSG26400.1	ATGA2OX1;GA2OX1			Arabidopsis thaliana gibberellin 2-oxidase 1	gibberellin 2-oxidase
Sapur.I59G008001.1	111.8285994	0.549860654	0.233368025	-6.1161	9.51E-10	2.03E-09	grey	-0.482276953	5.11E-10	GO:0004531		AtSG27830.1				LRR and NB-ARC domain-containing disease resistance protein	NA
Sapur.008G009800.1	1.550861772	1.140276135	0.349880221	-6.11736	9.51E-10	2.03E-09	grey	-0.456093532	3.18E-09								NA
Sapur.005G126000.1	21.71993653	1.764857705	0.285246381	6.117024	9.53E-10	2.04E-09	grey	0.445027741	3.41E-09	GO:0006355;GO:0005634;GO:0003700;GO:0046983;GO:0003677		AtSG05370.1	AGL69;AGL4;MADF4			K-box region and MADS-box transcription factor family protein	MADS-box transcription factor
Sapur.011G111300.1	159.5405279	-0.465750751	0.076795081	-6.11684	9.54E-10	2.04E-09	grey	-0.412964617	7.66E-08	GO:0055114;GO:0016491		AtSG10500.1				2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase, putative
Sapur.006G148800.1	836.0208313	0.107416158	0.032291102	6.113651	9.74E-10	2.08E-09	grey	-0.415175175	5.42E-08			AtSG17150.1					transmembrane protein
Sapur.016G166300.1	3.145284979	-0.734297061	0.283739278	-6.11329	9.82E-10	2.10E-09	grey	-0.429201266	2.04E-08	GO:0016758;GO:0008152		AtSG30150.1				UDP-Glycosyltransferase superfamily protein	NA
Sapur.008G134800.2	3.928630007	-0.864079864	0.154614446	-6.10991	9.97E-10	2.13E-09	grey	-0.418632162	3.82E-08			AtSG45580.1				Nucleotide-diphospho-sugar transferase family protein	nucleotide-diphospho-sugar transferase
Sapur.016G082900.3	22.63868382	0.42656662	0.069815242	6.109312	1.00E-09	2.14E-09	grey	-0.395242906	3.01E-07	GO:0005543		AtSG01600.1	EN/TH;ANTH;VHS superfamily protein				clathrin assembly protein, putative
Sapur.013G007000.1	8.363814668	0.778372938	0.127419321	-6.10876	1.00E-09	2.14E-09	grey	-0.419457641	7.37E-08			AtSG18610.1	Galactose oxidase/kelch repeat superfamily protein				kelch motif protein
Sapur.010G197500.1	70.51461299	0.370564331	0.060637945	6.107507	1.01E-09	2.16E-09	grey	-0.418847194	1.10E-07			AtSG17600.1					EIF(iG)/HIF1 protein;amino-terminal domain protein
Sapur.003G136200.1	63.64468839	0.729201857	0.119423209	6.106869	1.02E-09	2.17E-09	grey	-0.38860734	2.32E-07			AtSG21105.1				cytochrome-c oxidase;electron carriers	acytochrome-C oxidase/electron carrier protein
Sapur.007G017800.1	607.6517174	0.353780829	0.057936006	6.106388	1.02E-09	2.17E-09	grey	-0.424167671	2.19E-08	GO:0043565;GO:0008270;GO:0003700;GO:0006355	GATA5	AtSG04320.1	GATA5	GATA5		GATA transcription factor	GATA transcription factor
Sapur.017G091400.1	1.038375539	1.780363452	0.291573292	6.106058	1.02E-09	2.18E-09	grey	-0.429671298	1.91E-08								hypothetical protein
Sapur.006G158400.1	11.24164674	-0.507974277	0.097074955	-6.10459	1.03E-09	2.19E-09	grey	-0.422777204	2.61E-08	GO:0005815;GO:0009523;GO:0000226;GO:0007020;GO:0005856		AtSG26680.1	ATGCP1;ATSPC98;GCP3;SPC			spindle pole body component 98	gamma-tubulin complex component, putative
Sapur.003G098800.1	0.7014343	0.986656863	0.325182665	-6.10185	1.05E-09	2.24E-09	grey	-0.456713066	3.67E-11	GO:0016020		AtSG64150.1				Uncharacterized protein family (UPF0016)	transmembrane protein TPA81, putative
Sapur.006G208300.1	1.646724274	1.550991031	0.254194804	-6.10115	1.05E-09	2.24E-09	grey	-0.339973556	1.62E-05	GO:0003677		AtSG05480.1	ANAC008;SOG1			NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC transcription factor
Sapur.010G085300.2	6.412918516	1.139610283	0.186817514	6.100126	1.06E-09	2.26E-09	grey	-0.42945784	1.99E-08	GO:0042398;GO:0004357		AtSG23100.1	ATECS1;CAD2;GSHL;GSHLA;P			glutamate-cysteine ligase	glutamate-cysteine ligase
Sapur.010G085400.1	16.36558839	-0.616323428	0.101524	-6.09909	1.09E-09	2.27E-09	grey	-0.43528803	1.22E-08								transmembrane protein, putative
Sapur.015G185800.1	15.6376341	1.876426203	0.307618844	6.099245	1.07E-09	2.27E-09	grey	-0.461609966	1.22E-09	GO:0045454;GO:0015035;GO:0006662		AtSG15030.1	ATTRX H1;ATTRX1;TRX1			thioredoxin H-type 1	NA
Sapur.007G025500.1	187.1863925	0.414795842	0.068015779	6.098524	1.07E-09	2.28E-09	grey	-0.414966127	6.52E-08								cytoplasmic protein of eukaryotic or (EG) protein, putative
Sapur.I59G057200.1	0.88817525	-0.607806562	0.170728266	-6.09735	1.08E-09	2.30E-09	grey	-0.458516602	5.20E-09	GO:0004648;GO:0006672		AtSG08930.1	ATNEK2;NEK2			NIMA-related kinase 2	Serine/Threonine kinase domain protein
Sapur.T012100.1	5.28076056	0.897465876	0.147281612	-6.09405	1.10E-09	2.35E-09	grey	-0.445472451	5.03E-09								NA
Sapur.016G012000.1	2.132660963	1.163194254	0.190912851	6.093802	1.11E-09	2.36E-09	grey	0.446017387	7.06E-08	GO:0016787		AtSG18300.1	atnudt9;NUDT4			nudix hydrolase homolog 4	NA
Sapur.016G161500.1	3.339615395	1.363517381	0.223862173	6.091057	1.12E-09	2.39E-09	grey	0.379015065	9.80E-07	GO:0004648;GO:0005524;GO:0004672		AtSG70530.1	CRK3			cysteine-rich RLK (RECEPTOR-like protein kinase) 3	cysteine-rich receptor-like kinase
Sapur.007G054400.1	121.1273852	-0.614593704	0.109649756	-6.09084	1.12E-09	2.40E-09	grey	-0.445437724	1.61E-08			AtSG45270.1	EMB2763			ribosomal family protein	NA
Sapur.014G021000.1	3.014590047	1.144623217	0.187042491	6.090316	1.13E-09	2.40E-09	grey	-0.42304678	3.39E-08			AtSG24870.1				Helicase/SANT-associated, DNA binding protein	NA
Sapur.I59G000100.1	23.49457618	1.061224308	0.176230485	6.089692	1.13E-09	2.41E-09	grey	-0.506060307	2.31E-09			AtSG49040.1	SCD1			cromatin collection 1 (SCD1) protein (SCD1)	NA
Sapur.018G060700.2	6.125148822	-0.85791341	0.140868661	-6.08944	1.13E-09	2.41E-09	grey	-0.414160696	6.96E-08			AtSG29100.1				basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor, putative
Sapur.008G139800.1	4.931527172	0.925886475	0.152863648	-6.08881	1.14E-09	2.42E-09	grey	-0.28997297	2.02E-07	GO:0005975;GO:0004650		AtSG06770.2				Pectin lyase-like superfamily protein	NA
Sapur.007G028700.1	74.41614973	0.402854586	0.066122293	6.0885	1.14E-09	2.43E-09	grey	-0.43573555	6.07E-08			AtSG37180.1				Homeodomain-like superfamily protein	NA
Sapur.T143000.1	3.948934887	0.879235865	0.144609464	6.088423	1.14E-09	2.43E-09	grey	-0.46880281	5.35E-10			AtSG26700.2	ATFIM1;FIM1			fimbrin 1	NA
Sapur.016G021000.3	1.334620761	1.066387197	0.246646869	-6.08746	1.15E-09	2.46E-09	grey	-0.301718592	0.000122916			AtSG05080.2	ATUBC2;UBC22			ubiquitin-conjugating enzyme 22	ubiquitin-conjugating enzyme E2
Sapur.006G164900.1	10.37528317	0.709880771	0.116634158	6.086474	1.15E-09	2.46E-09	grey	0.407755681	1.01E-07			AtSG11380.1				PLACE family protein	NA
Sapur.I10G047001.1	78.76013336	0.576310385	0.094666593	6.08564	1.16E-09	2.47E-09	grey	-0.419135645	4.07E-08	GO:0006810;GO:0005622		AtSG15170.2	NTL1			NTF2-like	nuclear transport factor 2
Sapur.004G080900.1	52.03514172	0.316324586	0.052018629	6.084831	1.17E-09	2.48E-09	grey	-0.48357268	1.40E-10			AtSG47140.3	SWEETIE			HEAT repeat-containing protein	NA
Sapur.006G082000.1	1.578393007	1.552805179	0.255618188	6.083917	1.17E-09	2.50E-09	grey	-0.418374723	3.82E-07								hypothetical protein
Sapur.I59G031000.1	47.43877306	0.981852362	0.161492037	6.081871	1.18E-09	2.52E-09	grey	-0.390676212	4.22E-07	GO:0005515		AtSG29440.1	ATGSTU4;GST22;GSTU4			glutathione S-transferase tau 4	glutathione S-transferase GST
Sapur.005G080300.1	1.452181449	0.901888845	0.158916135	6.078924	1.19E-09	2.53E-09	grey	-0.407884603	1.44E-07			AtSG12770.1

Sapur.01G0181700.8	19.87819165	-0.45135842	0.075561015	-5.97343	2.12E-09	4.89E-09	grey	-0.018270455	0.820332269	GO:0008270;GO:0003676	zinc finger CCHC-type and RNA-binding motif protein
Sapur.01G0945500.11	5.717985182	0.726831331	0.121698823	5.972402	2.34E-09	4.92E-09	grey	0.414887504	5.60E-08		UV radiation resistance-associated protein, putative
Sapur.0I0G0282900.1	1115.977727	0.312264412	0.052350216	-5.97176	2.35E-09	4.93E-09	grey	-0.457531664	7.90E-09	GO:0005975;GO:0004553	beta-hexosaminidase
Sapur.0I3G0957500.9	160.2942392	0.402802177	0.067408201	5.970352	2.37E-09	4.98E-09	grey	-0.068234562	0.395836375	GO:0005515;GO:0003924	Transducin/WD40 repeat-like superfamily protein
Sapur.0I6G1280500.1	886.0363831	0.213683306	0.03578504	-5.969	2.38E-09	5.02E-09	grey	-0.452703884	2.66E-09	GO:0003924	Tubulin/FtsZ family protein
Sapur.0I6G2363600.1	130.3621213	-0.474124234	0.079432569	-5.96888	2.39E-09	5.02E-09	grey	-0.422306315	3.70E-08		Plant protein of unknown function (DUF247)
Sapur.1S2G231200.1	5.047894105	-3.343196407	0.5250682811	-5.9681	2.40E-09	5.06E-09	grey	-0.441768979	6.96E-09	GO:0016851;GO:0005975	DNA-damage-repair/toleration protein (DRT102)
Sapur.0I9G0220001.1	633.2372907	-0.202331045	0.041945958	-5.968	2.40E-09	5.05E-09	grey	-0.435535451	1.16E-08		Rib3 ortholog 1 in Arabidopsis thaliana
Sapur.0I6G1574000.1	20.78875535	-0.501195294	0.08400771	-5.96606	2.43E-09	5.11E-09	grey	-0.431851881	1.63E-08		WRC protein
Sapur.0I0G1437900.1	61.07545549	0.290251171	0.04870317	5.96407	2.45E-09	5.15E-09	grey	-0.412511961	5.82E-08		hypothetical protein
Sapur.0I3G0290600.1	10.46595113	-0.821382171	0.137739156	-5.96416	2.46E-09	5.17E-09	grey	-0.419383523	2.16E-08	RUS2,WKR1	Protein of unknown function, DUF647
Sapur.0I3G0280200.1	70.46168316	-0.455808882	0.093135436	-5.96152	2.47E-09	5.19E-09	grey	-0.464763416	1.68E-10	GO:0046872;GO:0030001	Heavy metal transport/detoxification superfamily protein
Sapur.0I3G0838800.1	64.14045661	-0.981065177	0.164563707	-5.96172	2.52E-09	5.24E-09	grey	-0.338157313	1.48E-05	GO:0055114;GO:0016491	leucoanthocyanidin dioxygenase
Sapur.0I5G1884000.1	42.99130003	0.398241984	0.051762229	5.960471	2.52E-09	5.28E-09	grey	-0.357580864	3.30E-07	GO:0003676	Nucleic acid binding, OB-fold-like protein
Sapur.0I9G0393200.1	588.8159312	-0.193462492	0.032476571	-5.95828	2.55E-09	5.35E-09	grey	-0.447076466	4.36E-09		Protein of unknown function (DUF3411)
Sapur.0I4G0137200.1	5.018976545	-0.110188612	0.186435751	-5.95817	2.55E-09	5.35E-09	grey	-0.408287513	1.32E-07		Cysteine/histidine-rich C1 domain protein
Sapur.0I1G0924000.1	402.0300073	-0.448916016	0.075364838	-5.95657	2.58E-09	5.41E-09	grey	-0.428728897	2.12E-08	GO:0043531	NB-ARC domain-containing disease resistance protein
Sapur.0I1G0112500.1	2090.03462	0.232062216	0.038973926	5.954039	2.62E-09	5.49E-09	grey	0.407314915	1.21E-07	GO:0006950	Adenine nucleotide alpha hydrolases-like superfamily protein
Sapur.0I3G0258800.5	2.504230379	-0.203358203	0.181436175	-5.95393	2.62E-09	5.49E-09	grey	-0.124069608	0.019966968		Peptidase M20/M20/M2 family protein
Sapur.0I6G2484000.1	646.0686369	0.322321596	0.054148002	5.952604	2.64E-09	5.54E-09	grey	0.417464979	5.35E-08		serine-rich protein-related
Sapur.0I4G0930300.1	1.024554174	-5.641364459	0.958502122	-5.9507	2.66E-09	5.58E-09	grey	-0.476032424	2.61E-10	GO:0005881;GO:0003196;GO:0003387	ARM-repeat superfamily protein
Sapur.0I7G1019000.1	13.39109697	0.535225019	0.089926767	5.951798	2.65E-09	5.56E-09	grey	0.445278867	4.90E-09	GO:0046983;GO:0003677	AGAMOUS-like 62
Sapur.0I8G0000100.1	6.205262645	0.778851495	0.130854197	-5.95178	2.65E-09	5.56E-09	grey	-0.459204373	5.40E-11	GO:0005515	
Sapur.0I0G1357500.1	0.6553842	1.891988451	0.317890635	5.951696	2.65E-09	5.57E-09	grey	0.383218867	9.02E-07		
Sapur.0I6G1748800.1	11.53878021	0.575780252	0.096735138	5.950497	2.68E-09	5.64E-09	grey	0.348258604	1.32E-07	GO:0005524;GO:0004035;GO:0000103	Nucleic acid binding, OB-fold-like protein
Sapur.7I1S4000.1	1.970721776	-1.2507439	0.210234007	-5.94929	2.68E-09	5.64E-09	grey	-0.3869621	2.65E-07		low-molecular-weight cysteine-rich 68
Sapur.0I6G2790900.1	12.02593673	1.105068858	0.194218494	5.947261	2.73E-09	5.72E-09	grey	0.331823656	2.21E-05	GO:0004674;GO:0048544;GO:0006468;GO:0004672	receptor kinase 3
Sapur.0I9G0940000.1	0.893937798	3.101830479	0.52152294	5.946682	2.74E-09	5.76E-09	grey	0.349531836	7.22E-06	GO:0006629	phosphatidylcholine 2A
Sapur.0I1G0097000.1	4792.399188	-0.242480611	0.040777156	-5.94648	2.74E-09	5.76E-09	grey	-0.467339664	6.81E-10	GO:0006296;GO:0003872	Phosphofructokinase family protein
Sapur.0I1G0208800.1	2.064019535	-0.103278984	0.17388879	-5.94513	2.76E-09	5.79E-09	grey	-0.459140125	1.47E-09		
Sapur.1S9G0676300.1	15.25438836	-0.698401884	0.117531371	-5.94216	2.81E-09	5.90E-09	grey	-0.417499962	5.31E-08		Protein kinase superfamily protein
Sapur.0I1G0117600.1	1.118576532	1.517384573	0.255388573	5.941651	2.82E-09	5.91E-09	grey	-0.432681662	1.52E-08		
Sapur.0I6G0384000.1	197.9768842	0.390889522	0.065790364	5.941244	2.83E-09	5.93E-09	grey	-0.429135276	2.01E-08	BOP2	Ankyrin repeat family protein (BTB/POZ domain-containing protein
Sapur.0I6G2610100.2	27.88493015	0.464228872	0.078140381	5.940973	2.84E-09	5.94E-09	grey	0.440604765	7.66E-09		Pathogenesis-related thaumatin-superfamily protein
Sapur.0I0G1562300.1	190.9583979	0.721801207	0.121499665	5.940796	2.84E-09	5.94E-09	grey	0.403398653	1.62E-07		cadmium tolerant 4
Sapur.7I1I3000.1	68.68436115	0.718429763	0.121000579	5.939573	2.86E-09	5.98E-09	grey	-0.403508664	1.97E-07	AT1CDT1,ATRIP,ATLIP7,ATLIP7,XPO	ARM-repeat superfamily protein
Sapur.7I0I1300.1	23.73179676	0.642204154	0.108175583	5.938067	2.88E-09	6.04E-09	grey	0.43193038	1.46E-08		emb2734
Sapur.0I8G0978800.1	29.26439966	1.118701513	0.188401129	5.937971	2.88E-09	6.05E-09	grey	-0.394854641	3.92E-07		Exostosin family protein
Sapur.0I3G0950500.1	333.2143773	0.341502757	0.041503141	5.935147	2.94E-09	6.15E-09	grey	0.44823007	3.94E-09		Uncharacterized conserved protein (DUF2215)
Sapur.0I5G1997500.1	10.49110507	-0.729021353	0.122832461	-5.93509	2.94E-09	6.15E-09	grey	-0.451477675	2.95E-09	GO:0055085;GO:0016020	mechanosensitive channel of small conductance-like 6
Sapur.1S9G0607300.1	306.3834057	-0.104279233	0.176825549	-5.94143	2.96E-09	6.20E-09	grey	-0.457531042	9.14E-09		Yippee family putative zinc binding protein, putative
Sapur.0I6G1051000.1	266.5872964	0.711575109	0.119920567	5.933715	2.96E-09	6.20E-09	grey	0.37189856	1.62E-06	GO:0016020;GO:0008810;GO:0005215	plasma membrane intrinsic protein PIP2 2
Sapur.0I9G0947000.1	446.9370604	-0.410692863	0.075118836	-5.93127	2.99E-09	6.26E-09	grey	-0.432707996	1.39E-08		plasma membrane intrinsic protein PIP2 2
Sapur.0I6G0602000.4	16.58043544	0.630578945	0.106282318	5.930062	2.97E-09	6.22E-09	grey	-0.178625363	0.025200381		glycine tumor suppressor-region protein, putative
Sapur.0I3G0810000.1	525.4468269	0.973181717	0.164501103	5.93219	2.99E-09	6.26E-09	grey	-0.383079007	7.35E-07	GO:0009116;GO:0003824	amino acid transporter, putative
Sapur.0I1G0017000.1	12.20767273	0.58238883	0.09885238	5.930953	3.01E-09	6.30E-09	grey	0.425344474	2.76E-08	GO:0003723	Phosphotyrase superfamily protein
Sapur.0I0G0367000.1	2.775631277	0.968821027	0.162943664	5.929323	3.04E-09	6.37E-09	grey	0.405534609	1.07E-07	GO:0009378;GO:0006310;GO:0006281	pumilio 12
Sapur.7I1I7100.1	5.557100555	1.03092304	0.173872657	5.929184	3.04E-09	6.37E-09	grey	0.453823843	2.38E-09		AAA-type ATPase family protein
Sapur.0I8G1094000.1	2152.684825	0.233554896	0.039393723	5.929087	3.05E-09	6.38E-09	grey	0.410475201	9.31E-08	GO:0045454;GO:0015035;GO:0009055	Glutaredoxin family protein
Sapur.0I5G1330200.1	42.36472689	0.855363287	0.14092389	5.929006	3.05E-09	6.38E-09	grey	0.342956503	1.12E-05	GO:0009731	Gck-like auxin-responsive protein family
Sapur.0I4G1427000.1	4.904242423	-1.807134727	0.304804357	-5.92883	3.05E-09	6.38E-09	grey	-0.496809694	3.58E-11		Expressed protein
Sapur.0I6G1350600.1	29.49778638	0.715301556	0.120611278	5.928476	3.06E-09	6.39E-09	grey	0.395752	2.91E-07		Protein of unknown function (DUF3511)
Sapur.0I1G0867000.1	15.14474126	-0.703415293	0.123718539	-5.92848	3.06E-09	6.40E-09	grey	-0.424310685	3.88E-08	GO:0043565;GO:0006355;GO:0003700	DUF3511 domain protein
Sapur.0I6G2074000.1	6.264445502	-0.618824694	0.108036146	-5.92756	3.08E-09	6.41E-09	grey	-0.439392253	8.55E-08		leucine aminopeptidase 1
Sapur.0I2G0871000.1	103.1138672	0.375061405	0.063472122	5.926503	3.09E-09	6.47E-09	grey	0.384963643	6.59E-07		B2P family protein
Sapur.0I3G1861000.1	9.968093236	-0.654908117	0.111712165	-5.92595	3.10E-09	6.49E-09	grey	-0.416106574	3.26E-08	GO:0005515;GO:0000160	Uncharacterized protein family SERF
Sapur.0I4G0273000.1	4.050527003	0.849319976	0.143355326	-5.92332	3.15E-09	6.60E-09	grey	-0.425103586	2.86E-08		pseudo-response regulator 5
Sapur.0I7G0127000.1	165.2321284	0.217446035	0.036722279	5.921381	3.16E-09	6.68E-09	grey	-0.467793884	6.52E-10	GO:0007165;GO:0005155;GO:0000160	AHK4,ATHK1,HK3
Sapur.0I8G0945000.1	12.04561512	-0.567257462	0.160104255	-5.92083	3.20E-09	6.71E-09	grey	-0.429017041	4.04E-08	GO:0006508;GO:0004196	Eukaryotic aspartyl protease family protein
Sapur.0I3G0920000.1	18.32319905	0.770892194	0.130213828	5.920202	3.23E-09	6.72E-09	grey	0.410931669	9.00E-08	GO:0004618;GO:0000166;GO:0005524;GO:0004812	ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases
Sapur.0I0G0200000.1	111.5995432	0.359110169	0.07180441	5.919858	3.25E-09	6.76E-09	grey	0.405534609	1.07E-07	GO:0009378	Transducin/WD40 repeat-like superfamily protein
Sapur.0I9G0923000.1	411.4667574	0.5363674	0.090675153	5.915524	3.31E-09	6.91E-09	grey	0.428743928	2.12E-08	GO:0016747;GO:0008610;GO:0016020;GO:0006633	3-ketoacyl-CoA synthase 4
Sapur.0I4G0000500.1	2.403805153	-1.002557977	0.18302828	-5.91489	3.32E-09	6.94E-09	grey	-0.191498622	0.052625818		hypothetical protein
Sapur.0I4G0324000.1	5.070437011	1.100671579	0.186172078	5.913708	3.34E-09	6.99E-09	grey	0.303267075	0.000116587		transmembrane protein, putative
Sapur.0I7G0980200.1	535.1832846	0.267107269	0.050886625	5.910189	3.40E-09	7.14E-09	grey	0.402470429	1.61E-07		Transducin family protein
Sapur.0I6G1930600.1	536.6912712	0.172617303	0.029213607	5.909002	3.44E-09	7.19E-09	grey	0.426691851	4.11E-08	GO:0003723;GO:0008408;GO:0016635;GO:0003676	β(1-6)/ exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing p
Sapur.0I6G1350600.1	5.459195182	-0.152063383	0.1350646	-5.91066	3.46E-09	7.21E-09	grey	-0.419258884	4.08E-08		Protein of unknown function (DUF3511)
Sapur.7I1T2500.1	157.3615224	-0.473016918	0.080068091	-5.90768	3.47E-09	7.25E-09	grey	-0.428318961	2.19E-08	GO:0009116	phosphorthioyl pyrophosphate (PRPP) synthase 3
Sapur.0I3G1361000.1	686.8854872	0.309422686	0.052337325	5.90757	3.47E-09	7.25E-09	grey	0.402576691	1.72E-07		
Sapur.0I1G0947000.1	28.12359854	-0.267391056	0.045664125	-5.90719	3.48E-09	7.27E-09	grey	-0.429342029	2.01E-08	GO:0003824;GO:0006470;GO:0004722	Protein phosphatase 2C family protein
Sapur.0I8G1511000.9	2.343832448	-0.056023527	0.178909519	-5.90596	3.51E-09	7.32E-09	grey	0.018331167	0.819743392		HD domain-containing metal-dependent phosphohydrolase family protein
Sapur.0I1G0261800.1	674.0404801	-0.13887493	0.22622566	-5.90403	3.54E-09	7.38E-09	grey	-0.462672027	1.03E-09	GO:0006629	alpha/beta-hydrolases superfamily protein
Sapur.0I1G0625200.1	5.480301091	0.750404027	0.127132851	5.903769	3.55E-09	7.42E-09	grey	-0.40683881	2.66E-07	GO:0005524	AAA-ATPase 1
Sapur.0I1G0207100.1	17.66216176	0.674896539	0.080228877	5.902169	3.56E-09	7.46E-09	grey	-0.450790402	3.16E-08		Protein of unknown function (DUF1644)
Sapur.0I6G1937000.1	766.7078561	-0.194064735	0.032892496	-5.90116	3.61E-09	7.54E-09	grey	-0.409240917	1.03E-07		Protein of unknown function (DUF3411)
Sapur.0I4G0700800.1	33.75224811	-0.657882179	0.091146613	-5.89954	3.67E-09	7.66E-09	grey	-0.448026124	2.01E-08	GO:0005524	CHR42
Sapur.0I5G0771000.1	4.595163827	-0.870874761	0.147659554	-5.89786	3.68E-09	7.68E-09	grey	-0.420934472	4.03E-08	GO:0005515	ASML2
Sapur.0I5G1512000.1	325.6958818	0.45452225	0.077098489	5.895352	3.74E-09	7.80E-09	grey	-0.419217239	4.64E-08		AT-GT2,GT2
Sapur.0I8G0979500.2	12.55651348	-0.624616666	0.105959226	-5.8949	3.76E-09	7.85E-09	grey	-0.436182768	1.68E-08	GO:0016787	Duplicated homeodomain-like superfamily protein
Sapur.0I4G1268000.3	42.9106582	0.414475398	0.070325711	5.893651	3.78E-09	7.88E-09	grey	0.25674262	0.001170902		SPT2 chromatin protein
Sapur.0I5G1763400.1	1.633647541	1.489887491	0.252907504	5.89143	3.81E-09	7.94E-09	grey	0.41051681	9.60E-08		
Sapur.0I5G0514000.1	83.60027934	-0.34683822	0.05887389	-5.89121	3.83E-09	8.00E-09	grey	-0.216918806	0.006355848	GO:0006355;GO:0003713;GO:0003677	sulDNA-binding transcriptional regulator
Sapur.0I5G0972200.1	2.031731556	-0.288686379	0.049267184	-5.88966	3.85E-09	8.02E-09	grey	0.277409207	0.006615258	GO:0008270	RING/FYVE/PHD zinc finger superfamily protein
Sapur.0I6G0946300.1	13.73162428	0.529576683	0.089819829	5.88989	3.84E-09	8.06E-09	grey	0.393982393	3.84E-07	GO:0008270;GO:0003677	A20/AN1-like zinc finger family protein
Sapur.0I6G0000400.1	5.023573207	0.833584333	0.141604138	5.889619	3.87E-09	8.07E-09	grey	0.431116024	1.73E-08	GO:0003724;GO:0006468;GO:0004672	Protein kinase family protein
Sapur.0I7G0225500.1	16.7174747	0.231377856	0.200092965	-5.88914	3.88E-09	8.09E-09	grey	-0.455214023	2.10E-09	GO:0005515;GO:0043531	LRR and NB-ARC domains-containing disease resistance protein
Sapur.0I6G1351000.1	837.4816663	0.267008779	0.045367365	-5.88921	3.88E-09	8.09E-09	grey	-0.415505054	2.24E-08		NAD(P)H oxidoreductase family protein
Sapur.0I9G0539000.1	4.783092006	-0.081294479	0.183697745	-5.88627	3.95E-09	8.21E-09	grey	-0.353778924	5.49E-06	AtCRT3,CRT3,ERS2,PSL1	calreticulin 3
Sapur.1S9G0680600.1	1.99029786	-0.119035517	0.190134947	-5.8861	3.95E-09	8.24E-09	grey	-0.411133899	8.86E-08	GO:0031047	IQN2,RDM12
Sapur.0I6G0347400.1	3.490873126	-1.362816166	0.231577427	-5.88476	3.96E-09	8.26E-09	grey	-0.389202128	4.70E-07		
Sapur.0I1G1891000.2	2.472276369	1.298600188	0.220527217	5.885487	3.97E-09	8.27E-09	grey	0.399407667	2.20E-07	GO:0005662;GO:0003824	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.0I7G0872000.1	2.923638438	0.998832775	0.169634429	5.884922	3.98E-09	8.30E-09	grey	-0.416349869	5.82E-08	GO:0004683;GO:0005524;GO:0004672	receptor serine/threonine kinase, putative
Sapur.0I7G0675500.1	4.981504886	1.050840794	0.180138896	5.88353	4.02E-09	8.37E-09	grey	0.396284847	2.76E-07		
Sapur.0I0G0991500.1	6.931938933	0.814848585	0.13851293	5.88128	4.05E-09	8.44E-09	grey	0.393637651	3.66E-07		
Sapur.1S9G1215000.1	1.386286374	1.42177255	0.241740508	5.881273	4.07E-09	8.48E-09	grey	0.434401079	1.31E-08		Histone superfamily protein
Sapur.0I7G0298800.1	58.37297924	0.295277618	0.050207843	-5.88111	4.08E-09	8.49E-09	grey	-0.414763861	6.66E-08	GO:0016301;GO:0006468	MKS1
Sapur.0I5G0231000.1	77.10557876	0.385061275	0.065475471	5.881	4.08E-09	8.49E-09	grey	0.388303876	5.03E-07		Transport protein particle (TRAPP) component
Sapur.0I1G0853000.2	10.14766216	-0.270467528	0.123515745	-5.88063	4.09E-09	8.51E-09	grey	0.052432276	0.514377705		Transmembrane protein, putative
Sapur.0I1G0805500.1	1245.10291	0.292762406	0.049788523	5.880118	4.10E-09	8.54E-09	grey	0.400756415	1.99E-07	GO:0016021	Low temperature and salt responsive protein family
Sapur.0I6G1340000.1	11.72910343	0.562532853	0.095677028	5.879499	4.12E-09	8.57E-09	grey	0.40692682	1.27E-07	GO:0043565;GO:0006355;GO:0003700	stress-induced hydrophobic peptide protein
Sapur.0I6G0947500.1	192.1254168	-0.369457318	0.062848169	-5.87857	4.14E-09	8.62E-09	grey	-0.431873624	2.17E-08		WRKY transcription factor, putative
Sapur.0I8G0118000.1	3.546086679	-0.976296457	0.166189313	-5.8746	4.24E-09	8.83E-09	grey	-0.405026242	1.41E-07		flavin-containing monooxygenase, putative
Sapur.0I6G2011000.1	160.3924991	0.758079927	0.129078628	5.875015	4.28E-09	8.91E-09	grey	0.416946138	5.97E-08	GO:0016020;GO:0006886;GO:0006605	bZIP protein, putative
Sapur.0I1G1310800.1	108.0667245	-0.370791701	0.063145588	-5.87201	4.31E-09	8.96E-09	grey	-0.417182217	5.47E-08		sec23/sec24-gamma protein transport protein
Sapur.0I7G0590000.1	8.008800247	-1.250011124	0.212008774	-5.87038	4.35E-09	9.05E-09	grey	-0.432818268	1.50E-08		hypothetical protein
Sapur.0I8G1020600.1	9.381999104	0.972741633	0.165703361	-5.87038	4.35E-09	9.05E-09	grey	-0.437517841	1.04E-08		
Sapur.7I0I1300.1	2.301164542	0.920883576	0.158090388	5.870383	4.35E-09	9.05E-09	grey	0.454287708	3.95E-09	ATCBM1,ATRIPO1,HET2,XPO	fasciclin-like arabinogalactan protein
Sapur.0I7G0640500.5	5.901231498	0.769283467	0.131061753	-5.86963	4.37E-09	9.09E-09	grey	-0.033271134	0.679116439	GO:0004681;GO:0016020	exportin 1A
Sapur.0I2G1941000.1	196.9470886	-0.018348519	0.105381315	-5.86962	4.37E-09	9.09E-09	grey	-0.424935333	3.09E-08		CLPS3
Sapur.0I3G1817000.1	10.02401878	-0.637387079	0.108623506	-5.86694	4.44E-09	9.24E-09	grey	-0.423986101	3.30E-08	GO:0005515	Calcium-dependent lipid-binding (CaLB domain) family protein
Sapur.1S9G1229000.1	7.068967044	0.799269518	0.136247419	-5.86616	4.46E-09	9.28E-09	grey	-0.42114281	3.66E-08		Regulator of chromosome condensation (RCC1) family protein
Sapur.0I1G1423500.1	1.221415534	1.389473128	0.236948213	5.865828	4.46E-09	9.29E-09	grey	-0.325195607	1.80E-08	GO:0016021	Auxin-responsive family protein
Sapur.0I7G0053000.1	191.7160940	-0.073329611	0.18101331	-5.8636	4.53E-09	9.42E-09	grey	-0.408873873	1.06E-07	GO:0005017;GO:0004144	O-acyltransferase WSD1-like family protein
Sapur.0I6G1240400.1	19.73413375	0.507463344	0.1010865	-5.86286	4.54E-09	9.46E-09	grey	-0.458213713	2.13E-09		WRKY family transcription factor
Sapur.0I0G0977800.1	2.299710182	1.173651981	0.200206716	5.862201	4.57E-09	9.50E-09	grey	0.422269709	3.62E-08		
Sapur.0I7G0871000.1	1.565862343	1.614342618	0.242948825	5.862079	4.58E-09	9.51E-09	grey	0.399774462	2.14E-07	GO:0003247;GO:0006468;GO:0005524;GO:0004672	Protein kinase superfamily protein
Sapur.0I1G1973000.1	16.62748359	0.489196765	0.083462419	5.861382	4.58E-09	9.55E-09	grey	-0.443257758	2.86E-09		
Sapur.0I1G0948000.1	138.0670087	0.710153767	0.121517018	5.860908	4.60E-09	9.57E-09	grey	-0.456093271	4.57E-09	GO:0005524	SNF2 domain-containing protein / helicase domain-containing protein / RING-type E3 ubiquitin transferase (RING finger)
Sapur.0I1G1352800.1	557.043567	-0.242902776	0.041467829	-5.86045	4.62E-09	9.60E-09	grey	-0.433783524	1.38E-08		Chlorophyll A-B binding family protein
Sapur.0I8G0119000.1	0.781037804	-0.465004189	0.429838906	-5.85986	4.63E-09	9.63E-09	grey	-0.382015118	3.94E-07		RING/U-box superfamily protein with ARM repeat domain
Sapur.0I6G1231000.1	60.28911063	-0.481782018	0.065152202	-5.85954	4.64E-09	9.65E-09	grey	-0.417534482	2.01E-08		Pyridine nucleotide-disulphide oxidoreductase family protein
Sapur.0I4G1232000.1	33.92712252	1.055881406	0.197188859	5.859474	4.64E-09	9.65E-09	grey	0.349822558	7.09E-06		
Sapur.0I1G0857000.1	0.614866421	1.452222222	0.252488889	5.859	4.66E-09	9.69E-09	grey	-0.448413897	1.87E-09		Homeodomain-like superfamily protein
Sapur.0I0G0014000.1	1.008361872	2.160517986	0.368767528	5.85753	4.66E-09	9.69E-09	grey	0.334561663	1.85E-05	GO:0005509;GO:0016021;GO:0004676;GO:0030247	Wall-associated kinase family protein
Sapur.0I4G0000300.1	7.183319245	0.769373156	0.127969097	5.856778	4.68E-09	9.72E-09	grey	-0.011264697	0.850906013		ubiquitin-specific protease 9X
Sapur.0I6G0721000.1	1.6586794	3.708913498	0.29685642	5.857759	4.68E-09	9.75E-09	grey	0.353617556	6.85E-06	GO:0009611;GO:0004867	Serine protease inhibitor, potato inhibitor I-type family protein
Sapur.0I6G1422200.2	5.791008835	0.802490117	0.137829949	5.85637	4.70E-09	9.77E-09	grey	0.397304201	2.58E-07	GO:0008270;GO:0005515	SPX (SYG1/Pho81/XPR1) domain-containing protein / zinc finger (C3HC4-type RING finger) protein-related
Sapur.0I3G0420000.1	1.082515221	-1.668804161	0.284975438	-5.85596	4.74E-09	9.85E-09	grey	-0.447201622	5.88E-09		
Sapur.0I1G1918000.1	4.392216749	0.742862418	0.126891082	-5.85403	4.79E-09	9.95E-09	grey	-0.418627996	4.85E-08		
Sapur.0I6G1422000.2	-5.96241127	-0.760247625	0.131314869	-5.85267	4.80E-09	9.98E-09	grey	-0.40245475	1.40E-07		
Sapur.0I4G0100800.1	13.31046223	0.894867199	0.152937411	-5.85185	4.84E-09	1.01E-08	grey	-0.523351277	2.03E-12		Chaperonne Dnaj-domain superfamily protein
Sapur.0I5G0870000.1	3904.742834	0.100580816	0.032583931	5.848868	4.95E-09	1.03E-08	grey	0.383615448	2.98E-07	GO:0006511	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 family protein
Sapur.0I6G2190900.1	84.38739847	0.425391653	0.072738968	5.848195	4.97E-09	1.03E-08	grey	0.37242233	1.56E-06		
Sapur.0I9G0949000.1	9.88847279	0.681512369	0.116524444	5.847759	4.98E-09	1.04E-08	grey	0.483216218	1.45E-10		ATCBM1,ATRIPO1,HET2,XPO
Sapur.0I1G1094000.1	11.75795233	0.89507533	0.153075654	5.847351	4.99E-09	1.04E-08	grey	0.388008845	5.11E-07	GO:0006468;GO:0004672	
Sapur.0I5G0887000.1	57.24619025	1.464868767	0.250501661	5.846247	5.02E-09	1.05E-08	grey	0.448828483	3.78E-09	GO:0009733	
Sapur.0I1G1461200.1	44.22161881	0.628576487	0.107523983	-5.84592	5.04E-09	1.05E-08	grey	-0.419463179	4.56E-08	GO:0046983	
Sapur.0I6G0200500.2	2.766028946	0.850581541	0.145267599	-5.84514	5.06E-09	1.06E-08	grey	-0.432608015	1.30E-08		
Sapur.7I0I4100.1	2.764923663	1.251750567	0.214189757	5.84412	5.08E-09	1.06E-08	grey	0.446676604	5.40E-09		
Sapur.0I6G1991000.2	0.518727787	-2.23358695	0.38829695	-5.84405	5.09E-09	1.06E-08	grey	-0.506353949	1.33E-11		
Sapur.0I9G1929300.1	101.4661644	-0.4621864	0.079059556	5.843687	5.11E-09	1.06E-08	grey	0.392012344	4.91E-07		
Sapur.7I0I2600.1	5.10159707	1.016185397	0.1739032	-5.8434	5.11E-09	1.06E-08	grey	-0.378832092	9.96E-07		
Sapur.7I0I7500.1	2.387115588	1.563884425	0.2678833	5.83639	5.13E-09	1.07E-08	grey	0.384566663	8.70E-07		
Sapur.0I7G0366000.1	13.72606002	-0.461027569	0.078920675	-5.84166	5.17E-09	1.07E-08	grey	-0.440193669	7.98E-09	GO:0006468;GO:0005524;GO:0004672	
Sapur.0I8G0519000.1	0.088838649	2.054064645	0.348588227	5.841678	5.18E-09	1.08E-08	grey	-0.410388526	1.56E-07	GO:0005515;GO:0003676;GO:0003677	
Sapur.0I1G0987000.2	0.782636374	1.880839241	0.32204661	5.840275	5.21E-09	1.08E-08	grey	0.363384911	2.36E-06	GO:0005515;GO:0043531	
Sapur.0I1G0284000.1	32.48897161	0.587566572	0.100675125	5.839932	5.22E-09	1.08E-08	grey

Sapur.009G331500.1	1360.84485	0.4982752	0.5860588831	5.759268	8.45E-09	1.76E-08	grey	0.37279033	1.52E-06	GO:0005507;GO:0055114;GO:0016491	AT2G38080.1	ATLMCO4;IRX12;LAC4;LMCO4	Laccase/Diphenol oxidase family protein	laccase 1a
Sapur.013G104600.2	4.76053863	0.75894794	0.13176047	7.758749	8.47E-09	1.76E-08	grey	0.41237907	8.02E-08	GO:0004468;GO:0006472	AT1G55670.1	ATCDPK2;ATCPK11;CDPK2;C	calcium-dependent protein kinase 2	calcium-dependent kinase
Sapur.013G166800.1	91.08810127	0.40207852	0.06993125	7.75584	8.51E-09	1.75E-08	grey	0.40868962	1.07E-07		AT5G62480.2		Protein of unknown function (DUF674)	NA
Sapur.15WG031900.1	1.90353888	1.04328047	0.18119094	5.75792	8.51E-09	1.75E-08	grey	0.44360153	5.78E-09	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP81D8	cytochrome P450, family 81, subfamily D, polypeptide 4	cytochrome P450 family protein	NA
Sapur.009G080800.1	6.52364323	1.19383368	0.20746778	5.75784	8.51E-09	1.75E-08	grey	0.39253112	3.68E-07	GO:0071251;GO:0005515;GO:0043531			Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.001G037000.1	0.56319224	2.17887167	0.37842027	5.757174	8.51E-09	1.76E-08	grey	0.41274859	7.79E-08	GO:0055062;GO:0003824	AT1G15950.1	ATCCRL1;CCR1;IRX4	cinnamoyl coa reductase 1	cinnamoyl-CoA reductase
Sapur.013G185300.3	7.23927644	0.92923783	0.16140724	7.75686	8.51E-09	1.76E-08	grey	-0.06029846	0.93787622	GO:0006351;GO:0005739;GO:0003690	AT4G08620.1		Mitochondrial transcription termination factor family protein	transcription termination factor family protein, putative
Sapur.005G095900.2	7.64418224	1.14523255	0.1994809	5.75613	8.61E-09	1.77E-08	grey	0.40899967	1.05E-07		AT5G7588.1	CPuORF5	conserved peptide upstream open reading frame 5	BZIP transcription factor AT82
Sapur.017G028200.1	0.78960391	3.0120338	0.52333569	5.755497	8.64E-09	1.78E-08	grey	0.375508821	1.25E-06	GO:0005515	AT3G32350.1		Ubiquitin-like superfamily protein	ubiquitin, putative
Sapur.003G202600.2	12.7117883	0.68178431	0.11526788	5.752388	8.66E-09	1.78E-08	grey	-0.39149741	3.78E-08		AT1G16120.1	UVR3	DNA photolyase	6-4, DNA photolyase
Sapur.001G154000.3	2.26034992	0.92847644	0.16136197	-5.754	8.72E-09	1.79E-08	grey	-0.32084753	4.59E-05		AT5G16010.1		Pentatricopeptide repeat (PPR-like) superfamily protein	PPR containing plant protein
Sapur.011G042800.2	1.00066134	0.91382416	0.15672683	-5.75337	8.75E-09	1.80E-08	grey	-0.45129765	1.90E-07		AT4G08920.1		Family of unknown function (DUF568)	DUF568 family protein
Sapur.014G142700.1	11.8549601	-0.75388055	0.13018308	-5.75313	8.76E-09	1.80E-08	grey	-0.44607141	4.76E-09	GO:0016021	AT4G05730.1		Cytochrome b561/ferric reductase transmembrane with DOMON related domain	dopamine beta-monooxygenase, putative
Sapur.T001400.1	1.53428317	0.98812167	0.16947613	5.75292	8.77E-09	1.80E-08	grey	-0.44308116	1.08E-07		AT2G40010.1	ATCIRK1;ATKPCI;HIT2;XPO	exportin 1a	NA
Sapur.010G060300.1	13.60138695	0.58505046	0.10109011	5.752199	8.81E-09	1.81E-08	grey	0.38465581	6.65E-07		AT3G32130.2	HSP70T-2	heat-shock protein 70T-2	heat shock 70 kDa protein
Sapur.003G184600.1	476.3538281	0.65338345	0.11308345	5.08605148	8.85E-09	1.81E-08	grey	-0.37236527	2.06E-06	GO:0045454;GO:0010035;GO:0009055	AT5G64580.1		Gluteredoxin family protein	electron transporter, putative
Sapur.013G111900.1	319.395249	0.32306726	0.05617525	5.751249	8.88E-09	1.82E-08	grey	0.39523426	3.01E-07		AT5G35530.1		Optic atrophy 3 protein (OPA3)	optic atrophy 3 protein
Sapur.010G205200.1	12.07531603	0.59870347	0.10410624	-5.75102	8.87E-09	1.82E-08	grey	-0.43894659	8.88E-09	GO:0003170;GO:0009058	AGAT2;GGT2	alanine-2-oxoglutarate aminotransferase 2	alanine-2-oxoglutarate aminotransferase	alanine-2-oxoglutarate aminotransferase
Sapur.006G042000.1	6.07791934	0.92140481	0.16024881	-5.7427	8.91E-09	1.82E-08	grey	0.38187338	8.08E-07	GO:0005524;GO:0004552			Sulfotrxn family protein	NA
Sapur.003G076700.1	50.09015248	-0.45130458	0.07850158	-5.74977	8.94E-09	1.83E-08	grey	-0.42842807	2.17E-08		AT5G57680.1			plant/P14407-9 protein
Sapur.016G270300.1	0.52843204	2.07245744	0.36051816	-5.74888	8.98E-09	1.84E-08	grey	-0.41274122	2.24E-08	GO:0048544;GO:0006468;GO:0004672	AT4G27290.1		S-locus lectin protein kinase family protein	Serine/Threonine kinase domain protein
Sapur.009G108000.1	783.2239427	0.17286515	0.03006569	5.748876	8.98E-09	1.84E-08	grey	0.39937884	2.20E-07		AT3G16800.1		high-affinity nickel-transport family protein	high-affinity nickel-transport family protein, putative
Sapur.004G000900.1	106.1870989	0.74078852	0.12881821	5.748641	9.00E-09	1.84E-08	grey	0.33184353	2.18E-05					hypothetical protein
Sapur.002G017700.2	1.13077422	2.48654141	0.43182473	-5.74787	9.04E-09	1.85E-08	grey	-0.43294258	1.49E-08	GO:0008168;GO:0008152	AT4G31790.2		Tetrapyrrole (Corrin/Porphyrin) Methylases	diphthine synthase
Sapur.016G260600.1	40.09513943	0.53502016	0.09307112	-5.75078	9.04E-09	1.86E-08	grey	-0.42180477	2.50E-08	GO:0019538	AT5G24480.1		Double Cys-His motif containing P-loop nucleoside triphosphate hydrolases superfamily protein	heat shock protein, putative
Sapur.003G091700.1	0.52569912	2.08780451	0.36322769	-5.74758	9.05E-09	1.86E-08	grey	-0.4527609	2.62E-09		AT4G11450.1		Protein of unknown function (DUF3237)	DUF3237 domain protein
Sapur.001G038500.1	33.3523904	0.45025685	0.07834241	-5.74744	9.06E-09	1.86E-08	grey	-0.41728312	5.46E-08					F-box protein, putative
Sapur.006G414200.2	0.44379327	2.08238156	0.34853276	-5.74718	9.07E-09	1.86E-08	grey	0.30541686	0.00103012		AT3G44820.1		Phototropic-responsive NPH3 family protein	BTB/POZ domain protein
Sapur.004G124300.1	6.25023466	1.14728409	0.19666243	5.746039	9.14E-09	1.87E-08	grey	0.33685379	1.40E-05	GO:0009731	AT3G18840.1		SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.004G163000.1	4.07777759	0.94188192	0.16481611	-5.7447	9.21E-09	1.88E-08	grey	-0.39849635	2.36E-07	GO:0006468;GO:0004672;GO:0005515	AT5G16250.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.15WG041500.1	38.87581675	-0.39763435	0.06924846	-5.74244	9.33E-09	1.91E-08	grey	-0.42078152	4.31E-08		AT5G12300.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.009G037800.1	387.10456	0.61461331	0.07287682	5.7417	9.36E-09	1.91E-08	grey	-0.43803007	6.52E-08	GO:0016773;GO:0005975;GO:0005524;GO:0046835;GO:0005536;GO:0004396;GO:0005167	AT4H1;LHR1		hexokinase 1a	hexokinase
Sapur.007G057800.1	3.62311576	0.75148791	0.12638541	5.741426	9.39E-09	1.92E-08	grey	0.50972786	9.22E-12		AT3G44880.1		Helicase/SANT-associated, DNA binding protein	high-affinity nickel-transport family protein, putative
Sapur.006G139900.1	39.62765114	-0.08502606	0.01430195	-5.74029	9.45E-09	1.92E-08	grey	-0.34709252	8.46E-06	GO:0055114;GO:0006260;GO:0005524;GO:0004748	AT5N8R1;LISB;RL8N8R1		ribonucleotide reductase 1	NA
Sapur.012G107300.1	1.42157041	1.62316048	0.28276683	5.740381	9.45E-09	1.94E-08	grey	0.35995162	3.65E-06		AT5G62065.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	nonspecific lipid-transfer protein, putative
Sapur.010G281000.1	0.51928294	1.94364189	0.34061401	-5.74021	9.46E-09	1.94E-08	grey	-0.46516239	3.38E-10		AT5G19315.1		Stigma-specific Stig1 family protein	Stig1 stigma-specific protein
Sapur.012G074100.1	109.1267914	0.41050359	0.07158148	5.739852	9.48E-09	1.94E-08	grey	-0.44827081	-4.22E-09		AT4G24500.1			NA
Sapur.016G227400.1	20.52858741	-0.41059398	0.07154381	-5.7394	9.50E-09	1.95E-08	grey	-0.00432984	0.95741965	GO:0008641	AT5G51130.1	CNX5;SIR1	co-factor for nitrate, reductase and xanthine dehydrogenase 5	adenylyltransferase and sulfurtransferase MOCS3
Sapur.009G132100.1	50.61661013	-0.77664799	0.13585886	-5.73876	9.54E-09	1.96E-08	grey	-0.46281687	1.04E-09		AT4G35320.1		Double Cys-His motif containing P-loop nucleoside triphosphate hydrolases superfamily protein	plant/P28212-120 protein, putative
Sapur.017G007700.1	6.68072531	-0.93279492	0.17299379	-5.73849	9.55E-09	1.96E-08	grey	-0.41529754	6.12E-08	GO:0003676;GO:0045292;GO:0005846;GO:0000339	AT4G24200.1	CAF30;CSP30	CAP-binding protein 20	nuclear Cap-binding protein
Sapur.006G051500.2	2.95383884	1.07304553	0.19302256	5.737674	9.60E-09	1.97E-08	grey	0.07519365	0.34950778		AT5G20280.1	AT5PGS1;SPS1F	sucrose phosphate synthase 1F	sucrose phosphate synthase
Sapur.014G082900.1	1.88897481	1.30936711	0.23526195	5.736296	9.68E-09	1.98E-08	grey	0.37785768	1.07E-06		AT3G19130.1			hypothetical protein
Sapur.004G091100.1	2.67222797	0.98812167	0.17759223	5.735427	9.73E-09	1.98E-08	grey	0.41265671	7.82E-08					NA
Sapur.004G014400.2	21.61338995	0.50755761	0.08840571	5.73593	9.70E-09	1.99E-08	grey	0.36733856	2.23E-06	GO:0005515;GO:0006629			phospholipase;galactosylgenes	calcium-independent phospholipase A2-gamma
Sapur.003G075100.1	2.01284142	0.51826725	0.1458442	5.732604	9.80E-09	2.01E-08	grey	-0.42038242	1.84E-08	GO:0005515	AT3G1 PS1		forkhead-associated (FHA) domain-containing protein	NA
Sapur.017G059900.1	1247.873034	0.16328187	0.02847548	5.734172	9.80E-09	2.01E-08	grey	0.39036172	4.32E-07	GO:0051603;GO:0005839;GO:0004298	AT5G45580.1	PBB2	20S proteasome beta subunit PBB2	proteasome subunit beta type protein
Sapur.016G199300.1	456.6350758	0.10185281	0.01775488	5.73375	9.88E-09	2.02E-08	grey	-0.43543613	1.23E-08		AT5T5B08.1		Pathogenesis-related thaumatin superfamily protein	Bridger Pro-thio protein, putative
Sapur.010G101000.1	7.21003289	-0.70568034	0.12311571	-5.73184	9.93E-09	2.03E-08	grey	-0.40587965	1.34E-07		AT5G05150.1	ATHAM3;HAM3	GRAS family transcription factor	GRAS family transcription factor
Sapur.006G089900.1	1763.641145	0.62785282	0.10958526	5.729349	1.01E-08	2.06E-08	grey	0.39139542	4.01E-07					hypothetical protein
Sapur.009G085800.1	227.7193659	0.27924624	0.04873517	5.73024	1.01E-08	2.06E-08	grey	0.36810327	7.08E-07		AT3G15910.2		CSL zinc Finger domain-containing protein	diphthamide biosynthesis protein
Sapur.014G087500.1	684.9671554	0.45288045	0.07905149	5.728866	1.01E-08	2.07E-08	grey	0.37360942	1.54E-06		AT3G62030.1	GLP10	Germin family protein	germin-like protein
Sapur.004G070400.2	1.83705751	1.18379336	0.20676068	5.727026	1.02E-08	2.08E-08	grey	0.04754235	0.54432619		AT5G10960.2	AKN10;AKN10;SNRK1.1	SNF1-related kinase catalytic subunit alpha KIN10	SNF1-related kinase catalytic subunit alpha KIN10
Sapur.15WG021500.1	2.61072836	-2.24587313	0.21208696	-5.72701	1.02E-08	2.09E-08	grey	-0.42437101	3.26E-08		AT5G19180.1	ARC6H;ATCDP1;CDP1;PARC	paralog of ARC6	plastid division protein CDP1, putative
Sapur.004G090100.1	187.8806114	-0.32744309	0.05718485	-5.72676	1.03E-08	2.09E-08	grey	-0.41837891	4.88E-08	GO:0016787;GO:0008152	AT5G19190.1		alpha/beta-hydrolases superfamily protein	CXE carboxylesterase
Sapur.005G084800.1	1.01242285	1.63443185	0.28540059	5.72675	1.02E-08	2.10E-08	grey	0.39148266	3.98E-07	GO:0005515	AT4G14730.1	AtRLP13;RLP13	receptor like protein 13	NA
Sapur.015G013200.1	0.74146675	2.15046524	0.37532261	5.726369	1.03E-08	2.10E-08	grey	0.34154063	1.20E-05		AT4G27410.1		Domain of unknown function (DUF213)	hypothetical protein
Sapur.012G098800.1	140.18894	0.90068912	0.10322791	5.724895	1.03E-08	2.12E-08	grey	0.38234529	7.81E-07	GO:0055085	AT2G27730.1	ATOPT6;OPT6	oligopeptide transporter 1	oligopeptide transporter OPT family protein
Sapur.012G099100.1	1351.194989	0.20882766	0.03649529	5.723585	1.04E-08	2.13E-08	grey	0.3995781	2.17E-07	GO:0005515	AT5G27480.1		Galactose oxidase/kelch repeat superfamily protein	kelch repeat F-box protein
Sapur.T002600.1	2.01121945	-0.88087826	0.15338239	-5.72264	1.05E-08	2.15E-08	grey	-0.42052614	4.17E-08		AT3G47502.3			NA
Sapur.012G045500.1	0.72585035	1.82611769	0.31918569	5.721143	1.06E-08	2.17E-08	grey	0.38561732	6.12E-07					NA
Sapur.006G148800.1	22.30994802	0.72154124	0.12614462	-5.72105	1.06E-08	2.17E-08	grey	-0.37381499	1.46E-06		AT2G27740.1		Family of unknown function (DUF662)	transcriptional activator
Sapur.010G045500.2	3.30018577	1.05433073	0.18434869	5.720404	1.08E-08	2.17E-08	grey	0.39828863	2.39E-07		AT1G67120.1	ATCSN7;COP15;CSN7;FUS5	Proteasome component (PCI) domain protein	hypothetical protein
Sapur.004G085200.2	4.85473984	0.73571411	0.12728151	5.719914	1.08E-08	2.18E-08	grey	0.38261476	9.07E-07		AT5G15150.1		ubiquitin-associated (UBA)/TS-N domain-containing protein	NA
Sapur.016G092100.1	38.00523939	-0.47456242	0.08305444	-5.7199	1.07E-08	2.18E-08	grey	-0.40804556	1.13E-07					hypothetical protein
Sapur.016G097500.1	112.3374877	0.20862128	0.03515485	5.719026	1.07E-08	2.19E-08	grey	0.37352283	1.45E-06	GO:0005085;GO:0016020;GO:0016020;GO:0006810;GO:0005215	AT3T7B1;PTR1		peptide transporter 1	peptide transporter, putative
Sapur.002G054100.1	0.66232042	2.55853185	0.44704479	5.717436	1.08E-08	2.21E-08	grey	0.43645675	1.00E-08	GO:0008121;GO:0006122	AT5G15120.1		Ubiquinol-cytochrome C reductase hinge protein	NA
Sapur.015G106500.1	17.53645636	0.51004688	0.08764945	5.716616	1.09E-08	2.22E-08	grey	0.44643656	1.31E-08	GO:0009058;GO:0003824	PECT1	phosphorylethanolamine cytidylyltransferase 1	ethanolamine-phosphate cytidylyltransferase	ethanolamine-phosphate cytidylyltransferase
Sapur.016G174100.1	11.10377802	1.11795646	0.19556501	-5.71658	1.09E-08	2.22E-08	grey	-0.36362499	2.85E-06		AT4G33800.1			hypothetical protein
Sapur.007G052100.2	5.18260783	0.86807473	0.15180356	5.716241	1.09E-08	2.23E-08	grey	0.41482174	6.61E-08	GO:0055085	AT1G07700.1	ATOPT7;OPT7	oligopeptide transporter 7	oligopeptide transporter OPT family protein
Sapur.013G204500.1	6.17944854	-0.64238537	0.11197572	-5.7486	1.12E-08	2.24E-08	grey	-0.41229124	8.08E-08		AT5G10210.1	DJ73	Photosynthetic stress protein	NA
Sapur.014G077700.2	32.88697674	0.43812723	0.07668545	5.713322	1.11E-08	2.27E-08	grey	0.40754807	1.17E-07	GO:0007275;GO:0006511;GO:0005634	AT5G17790.1		Protein with RING/U-box and TRAF-like domains	E3 ubiquitin-protein ligase SINAT3
Sapur.007G011000.1	189.1755021	0.17616402	0.03083709	5.71243	1.11E-08	2.28E-08	grey	-0.42208604	1.67E-08		AT5G19610.1		Zinc finger C-x8-C-x5-H type family protein	hypothetical protein
Sapur.003G071000.2	1.83218409	-1.18295429	0.20715158	-5.7114	1.12E-08	2.29E-08	grey	-0.45267265	2.65E-09		AT5G15730.1		Uncharacterized conserved protein (UCP012943)	hypothetical protein
Sapur.T000300.1	2.42288727	0.93592795	0.16462202	5.710347	1.13E-08	2.30E-08	grey	0.30703443	2.02E-07	GO:0048544;GO:0006468;GO:0004672	AT5G11461.1		S-locus lectin protein kinase family protein	NA
Sapur.15WG101400.4	65.96889946	0.40576363	0.07106881	5.709329	1.13E-08	2.32E-08	grey	0.45364978	2.42E-09	GO:0006468;GO:0006672	AT4G24740.2	AFC2;AMSE;LFC2	FUS3-complementing gene 2	Serine/Threonine-kinase domain protein
Sapur.003G015300.1	52.11398037	0.32766152	0.05739234	5.709229	1.13E-08	2.32E-08	grey	-0.41424166	7.64E-08	GO:0015136;GO:0006605	AT4G22060.2	ATMORN2;FIBRIDIN2	MORN(Membrane Occupied Recognition Nexus) repeat-containing protein 2	acetylcholine-receptor 25-kD subunit
Sapur.018G061200.1	53.51820558	-0.35149385	0.05870438	-5.70987	1.14E-08	2.32E-08	grey	-0.39027991	4.35E-07	GO:0048046;GO:0016762;GO:0003673;GO:0005618;GO:0005975;GO:0004553	AT3G26850.1	ATXH2;XLYH3B	xyloglucan endotransglucosylase/hydrolase 26	xyloglucan endotransglucosylase/hydrolase
Sapur.016G100500.1	56.4695182	0.66380704	0.11627556	5.708965	1.14E-08	2.32E-08	grey	0.33075255	2.33E-05		AT4G03320.1	tic20-IV	translocon at the inner envelope membrane of chloroplasts 20-IV	NA
Sapur.007G061100.1	159.8954847	-0.53472636	0.09372015	-5.70538	1.15E-08	2.35E-08	grey	-0.42663499	2.54E-08		AT4G16120.1		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.014G017600.1	0.45678772	2.38203853	0.41754387	5.705239	1.16E-08	2.37E-08	grey	0.47181331	4.42E-10	GO:0016020;GO:0006470	AT3G12120.1	ATGLR2.7;GLR2.7	glutamate receptor 2.7	NA
Sapur.005G054400.1	76.3881198	0.35184145	0.05525716	5.705019	1.16E-08	2.38E-08	grey	0.36469573	2.98E-06		AT4G40510.2			transmembrane protein, putative
Sapur.004G102200.1	14.17144447	0.55597129	0.09747485	-5.70379	1.17E-08	2.39E-08	grey	-0.39596637	2.85E-07		AT3G45580.1			animal cytomegalovirus UL139 protein
Sapur.016G170900.1	246.7605522	0.19168487	0.34632284	5.703575	1.17E-08	2.40E-08	grey	0.35382275	3.68E-06		AT3G61150.1	ATPBRL;PRB1	basic pathogenesis-related protein 1	pathogenesis-related protein
Sapur.017G125400.4	6.38068155	0.69663015	0.12119655	5.701578	1.19E-08	2.42E-08	grey	0.4062586	3.30E-07	GO:0016021	AT5G37310.1		Endomembrane protein 70 protein family	transmembrane 9 family protein
Sapur.T004300.1	1814.834307	0.22588769	0.04137603	5.70119	1.19E-08	2.42E-08	grey	0.39937225	2.30E-07		AT5G42060.1			transmembrane protein, putative
Sapur.T126700.1	0.6337802	1.69336517	0.29709162	5.699732	1.20E-08	2.45E-08	grey	0.39383412	3.30E-07					NA
Sapur.010G062600.1	1.86488233	0.29988723	0.05266152	5.697969	1.21E-08	2.46E-08	grey	0.41397042	1.02E-07		AT3G50300.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.012G068200.1	674.720379	0.22423187	0.03935569	-5.6985	1.21E-08	2.47E-08	grey	0.44707263	4.37E-09		AT4G03030.2		fringe-related protein	carbohydrate-binding protein of the ER protein
Sapur.005G090900.1	1513.967398	0.59681883	0.10473518	5.69823	1.21E-08	2.47E-08	grey	0.43627835	1.07E-08	GO:0055114;GO:0016491	AT5G12140.1	F3'H;F3H;TT6	flavanone 3-hydroxylase	flavanone 3-hydroxylase
Sapur.009G202600.1	2216.109974	0.17131984	0.06018404	-5.69815	1.21E-08	2.47E-08	grey	-0.39248616	2.68E-07	GO:0016491;GO:0016616;GO:0016615;GO:0008108	AT5G18130.2		lactate/malate dehydrogenase family protein	malate dehydrogenase (NADP) protein
Sapur.006G219300.1	27.58649088	-0.60282948	0.28132755	-5.69743	1.22E-08	2.48E-08	grey	-0.37903263	1.09E-06	GO:0055085;GO:0016021	AT5G10820.1		Major facilitator superfamily protein	folate/biopterin transporter
Sapur.004G075800.1	2459.38292	0.20283275	0.03564589	5.69584	1.22E-08	2.51E-08	grey	0.3862929	2.52E-07		AT5G44130.1		cAMP-regulated phosphoprotein 19-related protein	negatively light-responsive protein
Sapur.013G072600.1	623.12217	0.55405939	0.09728748	5.695084	1.23E-08	2.52E-08	grey	0.34927238	7.35E-06		AT5G60560.1		NAD(P)-linked oxidoreductase superfamily protein	aldo/keto-reductase family protein
Sapur.15WG017100.1	56.38004005	1.50080948	0.08614237	5.69466	1.24E-08	2.52E-08	grey	0.41208009	2.31E-08	GO:0008457	AT2G21620.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	pectin methylesterase
Sapur.008G093700.1	5.20674125	0.87519942	0.15770503	-5.6911	1.26E-08	2.57E-08	grey	-0.39091957	4.22E-07					NA
Sapur.003G184300.1	30.96828316	0.52466414	0.09219109	5.690574	1.27E-08	2.58E-08	grey	0.39395426	3.40E-07		AT4G33625.1			COP1 associated protein
Sapur.016G154600.1	16.00409939	0.51587043	0.09070832	5.687356	1.29E-08	2.63E-08	grey	0.35488841	5.11E-06					transmembrane protein, putative
Sapur.013G070800.2	10.32193913	0.58501524	0.10360714	5.682497	1.31E-08	2.67E-08	grey	-0.41976182	1.46E-08	GO:0008152;GO:0003824	AT4G33180.1		AMP-dependent synthetase and ligase family protein	acyl-CoA ligase
Sapur.15WG077001.1	3834.233483	-0.21681569	0.03816807	-5.6849	1.31E-08	2.67E-08	grey	-0.46804096	7.70E-10		AT1G63355.1	SPS11	SPIRAL1-like1	hypothetical protein
Sapur.012G089800.1	8.38806242	0.80169364	0.14112149	5.684244	1.31E-08	2.68E-08	grey	0.38190118	8.00E-07		AT5G52320.1			hypothetical protein
Sapur.005G081200.1	641.3137829	0.62847675	0.07435645	5.684077	1.32E-08	2.68E-08	grey	0.37424558	1.38E-06	GO:0009055	AT5T2T28.1		Cupredoxin superfamily protein	plastocyanin-like domain protein
Sapur.006G175100.3	2.82120087	0.92677365	0.16306253	-5.68349	1.32E-08	2.69E-08	grey	-0.08126851	0.31929755	GO:0006412;GO:0005840;GO:0005622;GO:0003735	AT5G02630.1		Ribosomal L29 family protein	60S ribosomal protein L35
Sapur.006G112200.1	3.74068384	0.64882974	0.11207587	5.682594	1.33E-08	2.70E-08	grey	0.40003427	1.02E-07	GO:0003700;GO:0003677	AT5G11120.1		AP2/B3 transcription factor family protein	AP2 domain transcription factor
Sapur.15WG013300.1	85.96196855	0.35819835	0.06303276	5.679901	1.35E-08	2.75E-08	grey	0.39189908	2.98E-07					NA
Sapur.T018500.1	7.36220442	0.85140706	0.14960567	5.679661	1.35E-08	2.76E-08	grey	0.40037368	2.04E-07					NA
Sapur.003G080800.1	5.60026749	-1.83943136	0.32387631	-5.67946	1.35E-08	2.75E-08	grey	-0.24315164	0.00214022					NA
Sapur.006G094900.2	65.62180136	0.27947403	0.0491136	5.679006	1.35E-08	2.76E-08	grey	0.37088142	1.64E-06		AT3G40935.3		PLACE family protein	plant cadmium resistance protein
Sapur.010G065000.2	6.01847519	0.86618347	0.15252835	5.678847	1.36E-08	2.76E-08	grey	0.36370501	2.84E-06		AT5G47730.1		Sec14p-like phosphatidylinositol transfer family protein	pelphosphoinositide-binding protein Sih1p
Sapur.010G022600.1	7.08993618	0.95805986	0.16668589	5.677051	1.37E-08	2.79E-08	grey	0.39587873	2.91E-07	GO:0048544	AT1G11340.1		S-locus lectin protein kinase family protein	NA
Sapur.T001300.1	452.2640538	0.80767661	0.05434697	-5.6768	1.37E-08	2.79E-08	grey	-0.43738831	1.02E-08		AT2G39260.1		binding/RNA binding	NA
Sapur.014G013600.1	526.8939912	0.17436205	0.03074922	5.676791	1.37E-08	2.79E-08	grey	0.40522155	1.40E-07	GO:0005515	AT1G47056.1	VFR1	VIER F-box protein 1	F-box protein
Sapur.007G099200.1	6.42847904	0.57476197	0.10160077	5.672249	1.38E-08	2.80E-08	grey	0.38276024	7.52E-07		AT4G27730.2		RING/FYVE/PHD zinc finger superfamily protein	hypothetical protein
Sapur.003G119000.1	0.69104865	2.38635844	0.42051483	-5.67588	1.38E-08	2.81E-08	grey	-0.5200166	2.95E-12		AT4G45430.1	AHL22	AT-hook motif nuclear-localized protein 22	AT-hook motif nuclear localized protein, putative
Sapur.T013900.1	387.7540513	0.21368729	0.03770646	-5.67536	1.38E-08	2.81E-08	grey	-0.38883276	4.94E-07		AT3G46630.1		Pyridoxamine 5'-phosphate oxidase family protein	pyridoxamine 5'-phosphate oxidase
Sapur.T133900.1	2.6802659	0.99117379	0.17471586	-5.67308	1.40E-08	2.86E-08	grey	-0.44363306	5.91E-09		AT5G45275.1		Major facilitator superfamily protein	NA
Sapur.016G027700.1	2.55778116	0.94809294	0.17537864	5.673	1.40E-08	2.86E-08	grey	0.30904168	4.30E-07		AT5G20130.1		DNA/RNA helicase	HRR4 domain protein
Sapur.018G069800.1	63.89164651	0.24315156	0.04287692	-5.67269	1.41E-08	2.86E-08	grey	-0.43042988	9.35E-08		AT3G27800.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.006G230000.1	1.91656466	1.61079512	0.28398328	5.67261	1.41E-08	2.86E-08	grey	0.43003427	1.02E-08	GO:0003151;GO:0003700;GO:0003677	AT4G32460.1		AP2/B3 transcription factor family protein	AP2 domain transcription factor
Sapur.015G031100.1	196.4976689	0.21680253	0.03787829	5.670827	1.42E-08	2.89E-08	grey	0.38398738	2.08E-07		AT4G14180.2	ATBBX13;BBX-LIKE3	BREVIS RADIX-like 3	brevis radix-like protein
Sapur.T147700.1	0.53422263	1.87199774	0.33014516	5.670306	1.43E-08	2.90E-08	grey	0.41283126	7.75E-08					NA
Sapur.011G062200.1	4.02470386	1.47480586	0.25985623	5.670051	1.43E-08	2.90E-08	grey	0.30451279	0.00106307		AT4G24530.1	LSH10	Protein of unknown function (DUF640)	LSH10 family protein
Sapur.002G191500.1	2.30487598	1.48936023	0.26240924	5.660812	1.48E-08	2.91E-08	grey	0.32605614	2.59E-05	GO:0006021;GO:0016021;GO:0006621	AT5G15160.1		ER lumen protein retaining receptor family protein	ER lumen protein retaining receptor family protein
Sapur.016G288800.1	5.90699516	1.13147207	0.

Sapur.002G130000.1	3.80504031	-0.947446051	0.169000859	-5.57648	2.45E-08	4.95E-08	grey	-0.197070255	2.62E-07				hypothetical protein
Sapur.001G166400.1	127.2804658	-0.320101344	0.057416583	-5.57568	2.47E-08	4.97E-08	grey	-0.4203944	4.22E-08	GO:0005114;GO:0006616;GO:0051287;GO:0016616;GO:0008152	ATG17G8370.1		D-isomer specific 2-hydroxyacid dehydrogenase family protein
Sapur.006G203500.1	5.96819695	-0.727478958	0.129991215	-5.57465	2.48E-08	5.00E-08	grey	-0.42631023	7.28E-08		ATG20750.1		F120-ATPase inhibitor protein, putative
Sapur.004G003400.1	234.0174602	-0.341900701	0.061318839	-5.57401	2.49E-08	5.02E-08	grey	-0.414504847	6.78E-08	GO:0016597;GO:0008152	ATG65890.1	ACR1	four ACT domain ACT domain protein
Sapur.006G838800.1	41.62563103	0.46016016	0.082565514	5.572059	2.51E-08	5.06E-08	grey	-0.384460911	6.68E-07	GO:0005515	ATG19080.1		uncharacterized protein
Sapur.006G255700.1	88.50434061	-0.743802367	0.13349686	-5.57168	2.52E-08	5.08E-08	grey	-0.34853874	7.70E-06	GO:0006508;GO:0004190	ATG02230.1		upstream activation factor subunit rpa27, putative
Sapur.7044080.2	6.448575751	-0.881578398	0.123329833	-5.57164	2.52E-08	5.08E-08	grey	-0.28498502	0.000297782	GO:0051082;GO:0006457;GO:0005783;GO:0005509	ATG68492.1	AtCRT1;CRT1;ERS2;PSL1	calreticulin 3
Sapur.006G714300.1	1.987910807	-0.411881168	0.253773872	-5.57419	2.53E-08	5.09E-08	grey	-0.335157039	1.74E-05		ATG19150.1		
Sapur.017G102300.1	2.61652742	1.249277083	0.2242782	5.570212	2.54E-08	5.12E-08	grey	-0.36053805	3.51E-06	GO:0006872;GO:0030001	ATG17450.1		Heavy metal transport/detoxification superfamily protein
Sapur.006G008800.1	0.69318709	-0.507297166	0.440409028	-5.56969	2.56E-08	5.16E-08	grey	-0.368271799	2.08E-06	GO:0016747	ATG26040.1		HXXXD-type acyl-transferase family protein
Sapur.004G076200.1	85.94189457	0.394007077	0.070787327	-5.56724	2.59E-08	5.21E-08	grey	-0.17482815	0.028431201	GO:0005515	ATG38840.1		SMAD/FHA domain-containing protein
Sapur.004G204300.1	24.14851369	-0.127164148	0.2643545	-5.56651	2.60E-08	5.23E-08	grey	-0.42991927	1.92E-08				
Sapur.016G183100.4	9.561914477	-0.585656164	0.105106057	-5.56634	2.60E-08	5.24E-08	grey	-0.388727804	4.88E-07	GO:0007264;GO:0005525	ATG08650.1		Small GTP-binding protein
Sapur.002G146600.2	7.384604029	-0.658490232	0.118278236	-5.56469	2.63E-08	5.27E-08	grey	-0.394463226	3.26E-06		ATG02100.1	ADNT1	adenine nucleotide transporter 1
Sapur.010G003200.1	127.4092359	0.348409131	0.062663841	5.559971	2.70E-08	5.40E-08	grey	-0.40578185	1.83E-07		ATG57560.1	AtMYRS5;MYRS5	myb domain protein 50
Sapur.006G204100.1	303.9175869	0.564909831	0.101466357	5.556985	2.71E-08	5.46E-08	grey	-0.363809731	3.80E-06	GO:0006872;GO:0030001	ATG61880.1		Heavy metal transport/detoxification superfamily protein
Sapur.017G06300.1	196.1114477	0.226479085	0.040740839	5.559019	2.71E-08	5.46E-08	grey	-0.460617011	1.28E-09	GO:0046872	ATG42280.1	ATRING1A;RING1A	RING 1A
Sapur.15W0G1468800.1	96.62058932	0.365265335	0.065721	5.557818	2.73E-08	5.49E-08	grey	-0.37938711	1.14E-06				
Sapur.017G088200.1	95.52519937	-0.552371052	0.045561941	-5.55663	2.75E-08	5.53E-08	grey	-0.402233117	1.7E-07		ATG28730.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.7082400.1	27.48574201	-0.7403401	0.133247594	-5.55614	2.76E-08	5.55E-08	grey	-0.385690107	6.09E-07				
Sapur.005G169000.1	6.557154424	-0.562948552	0.13847863	-5.55087	2.79E-08	5.61E-08	grey	-0.419417886	5.66E-08	GO:0046872	ATG46930.1	SPT	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.018G034500.15	12.28491044	-0.621515584	0.111882783	-5.55502	2.78E-08	5.58E-08	grey	-0.417788604	5.21E-08		ATG62310.4		Ribosomal protein S5 domain 2-like superfamily protein
Sapur.007G084000.1	0.500771969	0.22175871	0.396450754	5.554727	2.78E-08	5.56E-08	grey	-0.41920647	4.72E-08		ATG02020.1		
Sapur.016G067400.1	29.06869112	-0.436459727	0.078588911	-5.5537	2.80E-08	5.62E-08	grey	-0.412618273	7.87E-08	GO:0006355;GO:0005667;GO:0003700	ATG36030.1	ATE2FA;E2F3	E2F transcription factor 3
Sapur.007G150200.1	27.01026025	-0.658490232	0.118278236	-5.55365	2.81E-08	5.62E-08	grey	-0.382836731	3.98E-07		ATG48260.1		Nodulin MtN3 family protein
Sapur.003G134900.1	75.85757569	0.530228283	0.095496622	5.552441	2.82E-08	5.66E-08	grey	-0.310967246	7.37E-05	GO:0016597;GO:0008152	ATG69040.2	ACR4	four ACT domain ACT domain protein
Sapur.006G182200.1	17.81007742	0.537398738	0.096758656	5.551945	2.83E-08	5.68E-08	grey	-0.056107583	0.485203378	GO:0016042;GO:0006629	ATG46670.1		Nono/-66-acylglycerol lipase, N-terminal;Lipase, class 3
Sapur.016G268800.1	0.637763882	-0.607807773	0.179678889	-5.55183	2.83E-08	5.68E-08	grey	-0.360317985	3.56E-06				
Sapur.7082800.1	0.957567758	-0.400325725	0.252153899	-5.55097	2.84E-08	5.71E-08	grey	-0.41333616	7.44E-08		ATG54750.1		
Sapur.005G145400.1	0.816890404	-0.5181999	0.13526382	-5.55093	2.84E-08	5.71E-08	grey	-0.375473466	1.36E-06	GO:0005525;GO:0003924	ATG46070.1		Guanylate-binding family protein
Sapur.009G045200.2	3.98161997	0.998025455	0.179846128	5.549391	2.87E-08	5.76E-08	grey	-0.16824935	0.035173197		ATG62550.2		Protein of unknown function (DUF1423)
Sapur.015G195200.1	224.4645169	0.313111569	0.056063893	5.5482	2.87E-08	5.77E-08	grey	-0.360309358	2.10E-06	GO:0006334;GO:0005634;GO:0003677;GO:0000786	ATG68620.1	HON5	high mobility group family protein
Sapur.005G159200.1	122.1614731	-0.450202352	0.081152259	-5.54899	2.87E-08	5.77E-08	grey	-0.41844898	1.42E-08		ATG42900.1		Plant basic secretory protein (BSP) family protein
Sapur.003G112200.1	1308.009439	0.380806622	0.068664977	5.546607	2.93E-08	5.89E-08	grey	-0.386348876	5.72E-07	GO:0045454;GO:0015035;GO:0009055	ATG68481.1	GRX480;rxny19	Thioredoxin superfamily protein
Sapur.019G260900.1	136.6645886	-0.467497044	0.08773369	-5.54481	2.94E-08	5.91E-08	grey	-0.402087142	1.66E-07		ATG08640.1	CID1	Chloroplast 2-like domain 1
Sapur.019G266700.1	1.457676354	-0.525187884	0.12609896	-5.54369	2.95E-08	5.93E-08	grey	-0.46574646	9.01E-10				
Sapur.005G070200.1	230.1028843	0.376724988	0.067924989	5.544008	2.96E-08	5.94E-08	grey	-0.372622948	1.60E-06	GO:0005515	ATG08150.1		GRAM domain-containing protein / ABA-responsive protein-related
Sapur.016G191500.3	69.46425647	-0.470361799	0.084924892	-5.54392	2.96E-08	5.94E-08	grey	-0.07954831	0.32814497		ATG13640.1	UNE16	Homeodomain-like superfamily protein
Sapur.003G057200.1	16.43161003	-0.704506641	0.147018719	-5.54106	2.97E-08	5.97E-08	grey	-0.269481107	0.000235757		ATG47511.1		Nodulin MtN3 family protein
Sapur.012G082000.1	7.767924083	0.754289453	0.13607857	5.543044	2.97E-08	5.97E-08	grey	-0.350840637	6.86E-06				
Sapur.016G207000.1	8.790447208	0.577760398	0.131488555	5.539928	3.04E-08	6.10E-08	grey	-0.347864024	8.07E-06		ATG50120.1		Plant protein of unknown function (DUF247)
Sapur.006G209400.1	182.7211112	0.187698284	0.033902059	5.536486	3.09E-08	6.20E-08	grey	-0.401838314	1.89E-07	GO:0016021;GO:0004252	ATG56740.1		Ubiquitin-associated (UBA) protein
Sapur.004G183000.4	2.302885126	0.043849717	0.188514627	5.53604	3.09E-08	6.21E-08	grey	-0.388891055	4.82E-07		ATG60010.1		arctin family
Sapur.003G089000.1	5.668659408	-0.857499248	0.15493341	-5.53463	3.12E-08	6.26E-08	grey	-0.419102253	4.68E-08		ATG63245.1	CLE14	CLAVATA/ESR-related 14
Sapur.006G138300.1	121.1159088	0.357967327	0.064684618	5.534047	3.12E-08	6.26E-08	grey	-0.375063311	1.79E-06	GO:0006122;GO:0005750;GO:0005743	ATG27230.1		ubiquinol-cytochrome C reductase complex protein
Sapur.003G150800.1	16.11692159	-0.440966018	0.079735523	-5.53011	3.20E-08	6.42E-08	grey	-0.427824057	2.29E-08	GO:0043565;GO:0006355;GO:0003700;GO:0006351	ATG12150.2	BZIP65;TGA6	TGACG motif-binding factor 6
Sapur.003G078800.1	17.48161216	-0.562614489	0.101746495	-5.52977	3.21E-08	6.43E-08	grey	-0.414173879	6.96E-08	GO:0004857	ATG41370.1	PME1	pectin methylesterase inhibitor 1
Sapur.015W0G01880.1	260.5296337	-0.657329294	0.04161713	-5.52979	3.21E-08	6.45E-08	grey	-0.375184014	1.29E-06	GO:0005515;GO:0007275	ATG45120.1	Transducin/WD40 repeat-like superfamily protein	transparent testa glabra protein
Sapur.003G050800.1	0.42655126	1.869709442	0.31823481	5.527945	3.24E-08	6.50E-08	grey	-0.40154865	1.87E-07	GO:0003677	ATG25730.1	EDF3	ethylene response DNA binding factor 3
Sapur.7191500.1	2.182028645	-0.611204641	0.221668272	-5.52767	3.24E-08	6.51E-08	grey	-0.347711383	8.12E-06	GO:0005515;GO:0006488;GO:0005524;GO:0006472	ATG47570.1		Nucleotide-binding protein-kinase family protein
Sapur.009G089600.1	143.8649851	0.23018877	0.041676944	5.527272	3.25E-08	6.52E-08	grey	-0.371958354	1.01E-06		ATG67230.1	HVA22K	HVA22-like protein K
Sapur.006G190300.1	7.953311444	-0.557464488	0.148035887	-5.51569	3.28E-08	6.57E-08	grey	-0.368507707	2.50E-06		ATG60640.1	PHS1-like 2	abscisic acid receptor PYL2
Sapur.017G058800.1	15.42548126	-1.248674863	0.226003937	5.525014	3.29E-08	6.61E-08	grey	-0.364541587	2.68E-06		ATG61680.1		NA
Sapur.016G171300.1	0.031760987	-0.625682612	0.112458569	-5.52385	3.31E-08	6.64E-08	grey	-0.386742641	5.68E-07		ATG70560.3	NF-YB8	nuclear factor Y, subunit B8
Sapur.007G064400.1	1.888618781	-0.183992789	0.21455469	-5.52352	3.32E-08	6.66E-08	grey	-0.406502961	1.27E-07				
Sapur.003G132200.2	11.19769791	-0.694073555	0.13543888	-5.52344	3.32E-08	6.67E-08	grey	-0.386915351	1.57E-07		ATG32680.1		Homeodomain-like superfamily protein
Sapur.014G054300.1	43.61685625	-0.571864939	0.103531492	-5.52339	3.33E-08	6.67E-08	grey	-0.373369489	1.46E-06	GO:0009051	ATG08500.1	AtENOD;ILE;ENOD;L18	early nodulin-like protein 18
Sapur.001G008300.1	58.61198237	0.546209589	0.098909656	5.523341	3.35E-08	6.71E-08	grey	-0.39267651	2.68E-07	GO:0055085;GO:0016021;GO:0008324;GO:0006812	ATG58060.1		Cation efflux family protein
Sapur.016G160600.3	1.545025018	-1.232888891	0.223282427	-5.52305	3.36E-08	6.72E-08	grey	-0.289984875	0.000229533		ATG15030.2		
Sapur.15W0G0007000.1	379.3142942	-0.917236633	0.166133567	-5.5205	3.38E-08	6.76E-08	grey	-0.421471606	3.86E-08		ATG39700.1	ATEXP4;ATEXP4;ATHEXP A	expansin A4
Sapur.003G022700.1	1.090849152	-0.7109495	0.214418659	-5.51791	3.41E-08	6.87E-08	grey	-0.410047177	1.83E-08		ATG19720.1		Pentatricopeptide repeat (PPR-like) superfamily protein
Sapur.004G231900.1	9.731449601	-0.952308675	0.180385659	-5.51772	3.43E-08	6.88E-08	grey	-0.341527758	2.50E-05		ATG62310.1		hypothetical protein
Sapur.004G000100.1	11798.00737	0.234369882	0.04247771	5.517561	3.44E-08	6.89E-08	grey	-0.40307183	1.66E-07		ATG16640.1	TCTP	translationally controlled tumor-like protein
Sapur.014G091200.1	16.40333807	-0.67036576	0.121407587	-5.51755	3.44E-08	6.89E-08	grey	-0.12761982	2.81E-05	GO:0006355;GO:0003677	ATG33060.2	ANAC014;NAC014	NAC 014
Sapur.006G176400.1	15.28043969	-0.682852124	0.087672283	-5.51647	3.46E-08	6.92E-08	grey	-0.313202826	1.69E-06	GO:0005515	ATG22280.1	GTG1	general transcription factor group E6
Sapur.012G151000.1	41.36847871	0.863079115	0.156456963	5.5164	3.46E-08	6.93E-08	grey	-0.310232567	7.68E-05	GO:0055114;GO:0016491;GO:0008270	ATG61303.1		Oxidoreductase, zinc-binding dehydrogenase family protein
Sapur.004G056300.1	296.0326967	-0.252835753	0.046046863	-5.51606	3.47E-08	6.94E-08	grey	-0.372725592	1.69E-06		ATG25473.1	CPuORF12	conserved peptide upstream open reading frame 12
Sapur.017G112300.1	2.82461779	-0.943504895	0.171062019	-5.51554	3.48E-08	6.96E-08	grey	-0.409038178	1.02E-07		ATG14130.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.008G012300.1	631.9839996	0.360377384	0.065349223	5.514639	3.49E-08	7.00E-08	grey	-0.385117554	3.4E-07		ATG87310.2	AVH8;CEF1	family of unknown function (DUF828)
Sapur.017G056500.1	1.408983904	-0.618842285	0.126282848	-5.5138	3.51E-08	7.03E-08	grey	-0.412547027	7.92E-08	GO:0005886;GO:0005741	ATG21281.1	ATVDAC1;VDAC1	voltage-dependent anion channel 1
Sapur.003G177700.1	21.8596657	-0.669769496	0.12147258	-5.51392	3.51E-08	7.03E-08	grey	-0.004892888	0.950613115	GO:0003677;GO:0008289	ATG05230.1	HDG2	homeodomain-GLABROUS 2
Sapur.016G211400.1	6.513157547	-0.776088029	0.140540623	-5.5119	3.52E-08	7.05E-08	grey	-0.422268676	1.57E-08	GO:0005515	ATG54160.1		Ubiquitin-like superfamily protein
Sapur.005G054100.3	46.3936633	-0.42820505	0.076304045	-5.51223	3.54E-08	7.09E-08	grey	-0.397513133	2.53E-07		ATG08710.1		Regulator of chromosome condensation (RCC1) family protein
Sapur.006G160000.1	10.18834669	-0.714895158	0.142095742	-5.51189	3.55E-08	7.11E-08	grey	-0.4845228	5.28E-10		ATG20750.2		Protein of unknown function (DUF567)
Sapur.005G139100.1	126.0473604	0.526867752	0.095560059	5.511742	3.55E-08	7.11E-08	grey	-0.111282608	0.165277708	GO:0016788	ATG26430.1		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.016G182700.1	1.384606163	-0.264717742	0.12647152	-5.51144	3.56E-08	7.12E-08	grey	-0.387758527	2.52E-07	GO:0008234;GO:0006508	ATG49440.2		Papain family cysteine protease
Sapur.012G034000.1	71.58645243	-0.404517392	0.073338998	-5.51081	3.57E-08	7.15E-08	grey	-0.372305309	1.58E-06				
Sapur.002G195800.1	4.916212723	0.810315528	0.147072268	-5.50964	3.60E-08	7.20E-08	grey	-0.405472221	1.38E-07				transmembrane protein, putative
Sapur.001G186200.2	6.41026495	0.763807695	0.138518304	5.508353	3.62E-08	7.25E-08	grey	-0.357017235	4.45E-06		ATG48840.1	ATPTS;PANC;PTS	homolog of bacterial PANC
Sapur.014G054400.1	24.68398886	-0.417418764	0.075788889	-5.50823	3.63E-08	7.25E-08	grey	-0.384283875	6.74E-07		ATG68850.1	MAPKKK5	mitogen-activated protein kinase kinase kinase 5
Sapur.005G122300.1	20.55173869	-0.672881837	0.122167235	-5.50768	3.64E-08	7.28E-08	grey	-0.387645466	2.98E-07		ATG37560.1		Acetamidase/formamidase family
Sapur.15W0G0900100.1	1.670245538	-1.152254839	0.209317923	-5.50481	3.70E-08	7.39E-08	grey	-0.290836366	0.000219668		ATG10417.1		NA
Sapur.006G138300.1	222.9280754	-0.558131154	0.101405401	-5.50377	3.71E-08	7.44E-08	grey	-0.362906036	3.50E-06	GO:0005524;GO:0034551	ATG27480.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.003G102500.1	284.7622199	0.278248942	0.05055866	5.503487	3.72E-08	7.45E-08	grey	-0.391507113	3.97E-07		ATG51640.2	PYL8;ABCAR3	regulatory components of ABA receptor 3
Sapur.015G031700.1	14.72428711	-0.760231331	0.138017427	-5.50184	3.76E-08	7.52E-08	grey	-0.391060236	1.84E-07		ATG37610.1	SGR1;SAR	GRAS family transcription factor
Sapur.006G077800.2	2.470025671	-1.099617835	0.199885151	-5.5018	3.76E-08	7.52E-08	grey	-0.236937762	0.002810105	GO:0006355	ATG09230.1	PTAC13	plastid transcriptionally active 13
Sapur.015G169700.1	511.6645515	0.180756299	0.033046203	5.501538	3.76E-08	7.53E-08	grey	-0.388948874	4.80E-07	GO:0016787	ATG41551.1		Ankyrin-repeat/phosphatase-asm /DHHC zinc finger domain
Sapur.012G003700.1	26.98901671	0.661867362	0.120335871	5.500167	3.78E-08	7.59E-08	grey	-0.369820275	1.98E-06	GO:0006872;GO:0030001	ATG27580.1		Heavy metal transport/detoxification superfamily protein
Sapur.014G030400.1	26.13818595	0.994335897	0.180796823	5.499738	3.80E-08	7.61E-08	grey	-0.40682265	1.24E-07	GO:0005509			
Sapur.004G240400.1	32.67868381	0.645372028	0.117351483	5.499479	3.81E-08	7.62E-08	grey	-0.368717271	4.21E-07		ATG26290.1		hypothetical protein
Sapur.004G150000.2	11.20582603	-0.567067777	0.103117029	-5.4985	3.83E-08	7.66E-08	grey	-0.391374662	4.01E-07		ATG11590.1		
Sapur.005G188000.1	802.9910566	0.371282388	0.067527996	5.498202	3.84E-08	7.67E-08	grey	-0.391021168	4.06E-07	GO:0006355;GO:0005634;GO:0003677;GO:0009725	ATG19850.1	ARF5;IAA24;MP	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related
Sapur.017G025700.1	3.188482214	-0.882815312	0.160509019	-5.49753	3.85E-08	7.70E-08	grey	-0.416723229	5.67E-08	GO:0005515;GO:0043531	ATG27220.1		NB-ARC domain-containing disease resistance protein
Sapur.016G094900.1	1.424447994	-1.740442009	0.31658855	-5.49749	3.85E-08	7.70E-08	grey	-0.325243007	7.66E-07		ATG27410.1		NA
Sapur.017G053000.1	0.67317229	2.170089788	0.394792471	5.496786	3.87E-08	7.75E-08	grey	-0.364754212	2.64E-06		ATG30645.1		Plant protein of unknown function (DUF247)
Sapur.015W0G0900100.1	270.7183216	-0.526174178	0.09404273	-5.49592	3.88E-08	7.77E-08	grey	-0.426926461	2.04E-08		ATG27100.1		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.016G210100.2	31.570074	-0.553130375	0.100608397	-5.49294	3.95E-08	7.90E-08	grey	-0.131851754	0.166930984		ATG01750.1		Ankyrin-repeat family protein
Sapur.006G071100.1	161.3513856	-0.460835742	0.084078525	-5.48899	4.01E-08	8.03E-08	grey	-0.213317945	0.007305023		ATG37660.1		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.015G117000.1	139.6149702	-0.53946628	0.098277092	-5.48924	4.04E-08	8.07E-08	grey	-0.43423396	1.33E-08		ATG17210.1	ATHSL;HS1	heat stable protein 1
Sapur.018G058900.1	28.60767171	-0.419487975	0.076427778	-5.48868	4.05E-08	8.09E-08	grey	-0.413993434	7.06E-08				
Sapur.003G059100.1	64.65514432	-0.603986923	0.110051168	-5.48833	4.06E-08	8.11E-08	grey	-0.35661571	4.51E-06		ATG35290.1		hypothetical protein
Sapur.15W0G1210000.1	41.05765103	-0.933051956	0.170005542	-5.48825	4.06E-08	8.11E-08	grey	-0.386451663	5.76E-07				
Sapur.017G066500.1	20.68873207	0.816161113	0.152460599	-5.48741	4.08E-08	8.15E-08	grey	-0.369410668	1.50E-06	GO:0003824;GO:0006470;GO:0004722	ATG31660.1		Protein phosphatase 2C family protein
Sapur.019G011200.1	1.350878738	1.59202661	0.290180474	5.486333	4.10E-08	8.20E-08	grey	-0.357082282	4.42E-06	GO:0005524;GO:0007165;GO:0005515	ATG36930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.014G020300.1	221.6852316	0.618376185	0.075788752	5.485459	4.12E-08	8.24E-08	grey	-0.375394168	1.26E-06	GO:0006622;GO:0003824	ATG42120.1	AWU31;VEP1	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.008G204400.1	24.12734491	-0.465167721	0.084836992	-5.48308	4.18E-08	8.35E-08	grey	-0.405459984	1.88E-07		ATG54880.1		
Sapur.001G180600.1	24.44753255	-0.644838278	0.118306567	-5.48267	4.19E-08	8.37E-08	grey	-0.378444955	1.01E-06	GO:0004648;GO:0006672	ATG49760.1		Leucine-rich repeat protein kinase family protein
Sapur.016G120300.1	12.15363684	-0.772496898	0.140953384	-5.48051	4.24E-08	8.47E-08	grey	-0.390904706	4.15E-07	GO:0016151;GO:0006807	ATG21840.1	URE2	urease accessory protein UreF
Sapur.016G170700.5	30.25141781	0.490835755	0.092619085	5.479737	4.26E-08	8.50E-08	grey	-0.405428304	1.38E-07	GO:0016788;GO:0016020;GO:0008654	ATG29260.1	PGP1;PGP1;LPS51	phosphatidylglycerophosphate synthase 1
Sapur.001G260800.2	0.769751762	-0.803842416	0.420492284	-5.47869	4.28E-08	8.56E-08	grey	-0.237934411	1.42E-06	GO:0006412;GO:0003735	ATG19510.1	ATCCR1;CCR1;RRA	cinnamoyl-CoA reductase 1
Sapur.004G090400.1	1.551825107	1.365324929	0.230987198	5.478765	4.28E-08	8.55E-08	grey	-0.369517108	1.91E-06		ATG22340.3	CDS2	cytidinediphosphate diacylglycerol synthase 2
Sapur.017G059900.1	1.525242234	-0.558187138	0.114750005	-5.47863	4.28E-08	8.56E-08	grey	-0.375840861	1.26E-06	GO:0005114;GO:0009186	ATG20580.1	RNR2;RNR2A	phosphoribosylaminoimidazole carboxylase
Sapur.018G010300.1	6.427332041	-0.602866012	0.110011174	-5.4785	4.29E-08	8.56E-08	grey	-0.41525274	6.38E-08				hypothetical protein
Sapur.003G139300.1	3.866242423	-1.353170201	0.247005886	-5.4786	4.29E-08	8.56E-08	grey	-0.364991908	2.02E-06				
Sapur.001G117300.2	5.355850665	-0.877327824	0.160167525	-5.47756	4.31E-08	8.60E-08	grey	-0.360509713	4.28E-07	GO:0006612;GO:0003824	ATG32220.1		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.016G081800.3	0.600102956	-0.581218187	0.107774726	-5.47538	4.37E-08	8.72E-08	grey	-0.362164021	1.28E-08	GO:0007165;GO:0005515	ATG21510.1	ETR2	Signal transduction histidine kinase, hybrid type, ethylene sensor
Sapur.020G165500.1	3.384515763	0.895839361	0.166233582	-5.47662	4.34E-08	8.65E-08	grey	-0.378509986	1.02E-06	GO:0006508;GO:0004252	ATG50700.1		Subtilisin-like serine endopeptidase family protein
Sapur.006G045400.1	284.1904586	0.352828693	0.175069124	5.476819	4.35E-08	8.67E-08	grey	-0.33828588	4.7E-06		ATG32950.1		Putative glycosyl hydrolase of unknown function (DUF1680)
Sapur.015G023700.1	2.0841788	1.007536366	0.183988555	5.476098	4.35E-08	8.67E-08	grey	-0.400818746	1.96E-07	GO:0048544;GO:0006468;GO:0004672	ATG11340.1		S-locus lectin protein kinase family protein
Sapur.016G045900.1	4.707645642	0.713622216	0.130232223	5.475405	4.37E-08	8.71E-08	grey	-0.41035872	5.75E-08	GO:0005737;GO:0000045	ATG16520.2	ATG8F	Ubiquitin-like superfamily protein
Sapur.014G207700.1	21.4557727	-0.595292827	0.108720806	-5.47506	4.37E-08	8.71E-08	grey	-0.406210108	1.30E-07	GO:0045165;GO:0006355;GO:0003700	ATG44741.1		WINKY family transcription factor
Sapur.009G107000.1	1031.948587	0.317038893	0.057909683	5.47471	4.38E-08	8.76E-08	grey	-0.373452318	1.46E-06	GO:0046872;GO:0030001	ATG38580.1	ATFRP6;PFA;HPP26	farnesylated protein 6
Sapur.004G078200.1	68.00215556	-0.468667247	0.0638854	-5.47387	4.40E-08	8.78E-08	grey	-0.383909962	2.46E-06		ATG08120.1	MYB30	movement protein binding protein 2C
Sapur.7086000.1	0.910281813	-1.446424771	0.263988272	-5.47158	4.46E-08	8.89E-08	grey	-0.451782661	2.87E-09	GO:0005515	ATG34355.1	ATPSL;PS1	forkhead-associated (FHA) domain-containing protein
Sapur.015W0G1410000.1	9.216178612	-0.810068846	0.151875977	-5.4713	4.46E-08	8.91E-08	grey	-0.383241275	1.9E-07		ATG41670.1		
Sapur.006G113800.1	4.383070947	-0.818387308	0.152349881	-5.47125	4.47E-08	8.91E-08	grey	-0.363259967	2.93E-06		ATG34357.1		ARM repeat superfamily protein
Sapur.016G214000.1	767.7383867	-0.481488379	0.0265154	-5.4679	4.48E-08	8.94E-08	grey	-0.382542007	7.91E-07	GO:0006508;GO:0004252;GO:0005515	ATG27525.1	Deg1;DEGP1	DegP protease 1
Sapur.010G068400.7	0.516804682	-1.890229564	0.345775038	-5.46665	4.55E-08	9.14E-08	grey	-0.479441091	2.12E-10		ATG43745.1		Protein of unknown function (DUF2012)
Sapur.006G137800.1	352.100571	-0.528702293	0.098185023	-5.46624	4.60E-08	9.16E-08	grey	-0.419300242	8.34E-08	GO:0005114;GO:0004097;GO:0016491;GO:0008152			polyphenol oxidase
Sapur.013G054500.1	16.76394888	0.578016229	0.105756367	5.465951	4.60E-08	9.18E-08	grey	-0.38284596	1.01E-07		ATG18550.1	ATTCP1;BJBC1;TCP18	TCP family transcription factor
Sapur.018G061000.1	106.3977953	0.865285173	0.158336325	5.464914	4.63E-08	9.23E-08	grey	-0.42161525	3.82E-08	GO:0003677	ATG27480.1	HTA9	histone H2A protein 9
Sapur.15W0G0710000.1	0.727548999	-1.512402005	0.276764068	-5.4647	4.64E-08	9.24E-08	grey	-0.45681889	1.85E-09				
Sapur.003G043400.1	19.57262741	-0.389775764	0.071367582	-5.46319	4.68E-08	9.32E-08	grey	-0.067489323	0.455052265		ATG47640.3	PYE	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.015G205400.1	20.4985604	-0.525184194	0.096455104	-5.46118	4.68E-08	9.35E-08	grey	-0.403917788	1.81E-07	GO:0043531	ATG17680.1		disease resistance protein (TIR-NBS-LRR class), putative
Sapur.003G060000.1	28.77055375	-1.336059369	0.244783785	-5.46179	4.71E-08

Sapur.01G017900.1	3.28320504	1.09770095	3.20413619	5.37518B	7.65E-08	1.51E-07	grey	0.37111B526	1.71E-06	GO:0006355;GO:0003700	ATG13340.1	Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.01G0239400.1	229.3940867	-0.41025118	0.07633865	-5.17506	7.66E-08	1.51E-07	grey	-0.37285053	1.52E-06	GO:0043565;GO:0006355;GO:0003700	ATG51240.1	HYL;TED 5	Basic-leucine zipper (bZIP) transcription factor family protein
Sapur.01G0272000.2	12.15072884	-0.52676428	0.09428186	-5.17503	7.66E-08	1.51E-07	grey	-0.41097665	9.02E-08		ATG49760.1	SAP domain-containing protein	Det1 complexing ubiquitin ligase
Sapur.01G0410200.1	3.45729857	0.96143833	0.17884027	5.374232	7.68E-08	1.52E-07	grey	0.33964873	1.36E-05				hypothetical protein
Sapur.01G0280700.1	49.6072898	0.68992942	0.13637796	5.374153	7.68E-08	1.52E-07	grey	0.36542441	2.87E-06		ATG46630.1		hypothetical protein
Sapur.01G0151700.1	8.87307779	1.02350956	0.19060702	5.369737	7.89E-08	1.56E-07	grey	0.33187802	2.18E-05	GO:0016491	ATG27890.1	NQR	NADPH:quinone oxidoreductase
Sapur.01G0247200.1	0.75014953	2.94124948	0.54787799	5.36887	7.93E-08	1.57E-07	grey	0.42213851	3.66E-08		ATG42723.1	aminoacyl-tRNA ligase;ATP binding;nucleotide binding	retrotransposon gag protein
Sapur.01G0260700.1	18.72158	0.48740535	0.09079926	-5.36843	7.94E-08	1.57E-07	grey	-0.34829876	7.82E-06	GO:0008270;GO:0006355	ATG27110.2	FRS3	FAR1-related sequence 3
Sapur.01G0123900.1	0.881946	-2.06425868	0.38475585	-5.366624	8.02E-08	1.58E-07	grey	0.27128665	0.00257687				NA
Sapur.01G0280200.1	109.3756471	0.75349149	0.14025	5.3525	8.08E-08	1.60E-07	grey	-0.3978265	2.46E-07	GO:0048544;GO:0006468;GO:0005524;GO:0004672	ATG34300.1	lectin protein kinase family protein	Serine/Threonine-kinase
Sapur.01G0138000.1	289.8982711	-0.20965284	0.03907915	-5.36486	8.10E-08	1.60E-07	grey	-0.29266224	5.02E-08	GO:0048339;GO:0016020	ATG32040.1	Syntaxin;t-SNARE family protein	syntaxin family protein
Sapur.01G0136600.1	941.5161418	-0.02296949	0.04461164	-5.364	8.14E-08	1.61E-07	grey	-0.42738179	2.17E-08		ATG28835.1	Oligosaccharyltransferase complex subunit OSTC protein	oligosaccharyltransferase complex subunit OSTC protein
Sapur.01G0123100.1	18.47438165	-1.10911054	0.20679853	-5.36327	8.17E-08	1.61E-07	grey	-0.40247569	1.74E-07		ATG58848.1	Disease resistance protein (CC-NBS-LRR class) family	NA
Sapur.01G0262200.1	6.33432606	0.95020281	0.18128276	5.362027	8.20E-08	1.62E-07	grey	0.38064709	7.5E-07				NA
Sapur.01G0210000.1	68.91203184	0.77082955	0.14378982	-5.36062	8.23E-08	1.64E-07	grey	-0.32070557	4.22E-05	GO:0005515;GO:0006468;GO:0004672	ATG53440.1	Leucine-rich repeat transmembrane protein kinase	Leucine-rich repeat transmembrane protein kinase
Sapur.01G0180900.1	607.2708896	0.07268732	0.05047432	5.360297	8.26E-08	1.64E-07	grey	0.35271147	5.88E-06		ATG53455.1	AC82.ARATH;CDC25;CDC25	Rhodanese/cell cycle control phosphatase superfamily protein
Sapur.01G0275000.1	0.62512281	1.82745284	0.34093842	5.360064	8.32E-08	1.64E-07	grey	0.37025684	1.21E-06	GO:0005524;GO:0004386;GO:0006281;GO:0003678;GO:0000723	ATG28780.1	FIP1 helicase	NA
Sapur.01G0118300.1	176.9298213	0.27937162	0.07098679	3.35913	8.38E-08	1.65E-07	grey	0.39001461	4.44E-07	GO:0046872;GO:0030001	ATG32000.1	Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.01G0028500.1	65.28811044	0.75349067	0.06886226	5.356841	8.47E-08	1.66E-07	grey	-0.41069388	1.5E-07	GO:0016746;GO:0008152	ATG18850.2	LPA75	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative
Sapur.01G0177900.1	483.1624965	0.32997386	0.06032529	5.354264	8.59E-08	1.69E-07	grey	-0.35028106	6.92E-06		ATG19260.1		monogliceride lipase
Sapur.01G0102700.2	7.48968575	-0.75349149	0.14131304	-5.35426	8.59E-08	1.69E-07	grey	-0.38908914	4.7E-07	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATG19270.1	CYP707A4	cytochrome P450 family 707 ABA 8'-hydroxylase
Sapur.T177700.1	1.05416881	1.34976057	0.24568821	5.352395	8.64E-08	1.70E-07	grey	0.46897876	5.30E-10				NA
Sapur.01T0260300.1	0.75316663	-1.62307954	0.29933952	-5.35122	8.68E-08	1.71E-07	grey	-0.41116569	8.82E-08	GO:0004648;GO:0006672	ATG10530.1	Concanavalin A-like lectin protein kinase family protein	NA
Sapur.01G0239400.1	0.26772004	1.22979994	0.22075734	5.35126	8.69E-08	1.71E-07	grey	0.23085093	0.00302767	GO:0003677	ATG20970.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.01G0134200.2	3.95794564	0.85020887	0.16711408	5.35126	8.69E-08	1.71E-07	grey	-0.35615948	4.68E-06		ATG27440.1	Sec61G/Y1 Ribosomal protein (U1p) family protein	NA
Sapur.01G0265000.1	2622.211806	-0.14447928	0.02512743	-5.35122	8.74E-08	1.72E-07	grey	-0.41097703	8.97E-08	GO:0003013;GO:0030130;GO:0016192;GO:0006886;GO:0005198	ATG20760.1	EMB2777	clathrin light chain
Sapur.01G0290500.1	1.05640562	1.59760424	0.29861587	5.345362	8.83E-08	1.74E-07	grey	0.37931798	1.81E-06		ATG47730.1	Sec14p-like phosphatidylinositol transfer family protein	pelphosphoinositide-binding protein Sih1p
Sapur.01G0087300.1	221.7685012	0.25258442	0.04719224	5.34615	8.88E-08	1.74E-07	grey	-0.6345315	1.36E-08		ATG44610.2	Phosphoglycerate mutase family protein	NA
Sapur.01G0565000.1	49.89001525	-0.48522492	0.09073184	-5.34791	8.90E-08	1.75E-07	grey	-0.41384229	8.40E-07				NA
Sapur.01G0211200.1	5.90735297	0.70021359	0.17209143	5.34628	8.96E-08	1.76E-07	grey	0.41488044	6.57E-08	GO:0005515	ATG25470.1	ARIP2;RLP21	receptor like protein 21
Sapur.01G0205400.1	7.87241686	1.09049734	0.20390723	5.346053	8.99E-08	1.77E-07	grey	0.30987064	7.84E-05	GO:0005085;GO:0046872;GO:0030001;GO:0016020	ATG12750.1	ZIP1	zinc transporter 1 precursor
Sapur.01G0252800.1	42.15013867	0.41173133	0.08075	5.34525	8.99E-08	1.77E-07	grey	-0.39543831	2.36E-07		ATG27920.1	RNA helicase family protein	RNA helicase family protein
Sapur.01G0205500.2	1.36074033	3.31805149	0.24754356	5.344687	9.06E-08	1.78E-07	grey	-0.42338106	1.75E-07		ATG7169?.1	ATCKL;OK;CKL1	choline kinase 1
Sapur.01G0121700.1	18.96289906	-0.67224624	0.08833974	-5.34442	9.07E-08	1.78E-07	grey	-0.37201147	1.49E-06		ATG77700.1		Pathogenesis-related thaumatin superfamily protein
Sapur.01G0154100.2	1.54337643	1.40106817	0.21330818	-5.34321	9.13E-08	1.80E-07	grey	-0.40266693	1.67E-07		ATG22110.2		CCR-like protein, putative
Sapur.01G0260700.1	2.35476538	0.87084397	0.15274168	5.340971	9.15E-08	1.81E-07	grey	-0.3656057	1.32E-06	GO:0055114;GO:0016616;GO:0006694;GO:0003854	ATG6328.2	HSRR;MUR4;UXE1	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.01T0101300.1	64.9704015	0.65562203	0.12779333	5.340712	9.26E-08	1.82E-07	grey	-0.40872793	1.95E-07	GO:0043531	ATG14440.1	LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.01G0257300.1	1.05071986	1.56035853	0.29219127	5.340391	9.27E-08	1.82E-07	grey	0.40512642	1.42E-07				NA
Sapur.01G0053800.1	0.60338823	-0.98018377	0.17157097	-5.33917	9.34E-08	1.84E-07	grey	-0.44428093	5.6E-08		ATG15580.1	ABCG12;ATWBC12;CER5.G3	ABC-2 type transporter family protein	NA
Sapur.T175000.1	0.79454873	1.56695079	0.29353773	5.33819	9.39E-08	1.85E-07	grey	0.37245807	1.42E-06				NA
Sapur.01G0210300.1	21.38593139	0.53829315	0.10086648	5.33669	9.47E-08	1.86E-07	grey	0.33654247	3.01E-05		ATG25680.1	MOT1	molybdate transporter 1
Sapur.01G0142000.1	13.08251391	-0.49973845	0.09366456	-5.33524	9.54E-08	1.88E-07	grey	-0.38803873	5.13E-07				NA
Sapur.01G0238400.1	1.66022307	0.78884005	0.18117126	5.33488	9.56E-08	1.88E-07	grey	-0.56525769	1.34E-11	GO:0043531	ATG27220.1		NB-ARC domain-containing disease resistance protein
Sapur.01G0305700.1	294.9940893	-0.58388179	0.10936233	-5.33475	9.57E-08	1.88E-07	grey	-0.31784559	2.51E-05	GO:0006096;GO:0004332	ATG26530.1	Aldolase superfamily protein	fructose-bisphosphate aldolase
Sapur.01G0011700.1	1.08868984	1.57564783	0.29579668	5.33231	9.69E-08	1.90E-07	grey	0.35468846	1.24E-06		ATG60700.1	Plant protein 1208 of unknown function	NA
Sapur.01G0264800.1	849.522824	-0.27029283	0.05076174	-5.33307	9.66E-08	1.90E-07	grey	-0.38539842	6.22E-07	GO:0007165;GO:0000155;GO:0000160	ATG27320.1	AHK2;HK2	histidine kinase 2
Sapur.01G0156900.1	6.12953869	-0.62147188	0.11724846	-5.33127	9.75E-08	1.91E-07	grey	-0.40544052	1.38E-07				NA
Sapur.01G0245400.1	72.94031379	0.68369123	0.12826754	5.330356	9.80E-08	1.93E-07	grey	-0.42679754	2.49E-08	GO:0008017;GO:0007018;GO:0015232;GO:0007177;GO:0005871	ATG63645.1		P-loop nucleotide triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain
Sapur.01G0620700.1	4.08083463	-0.93141032	0.17476266	-5.32949	9.85E-08	1.94E-07	grey	-0.51479401	5.32E-12		ATG66600.4	Protein of unknown function; DUF547	ternary complex factor MIP1 leucine-zipper protein
Sapur.01G0611200.1	707.5653133	0.79130624	0.17326524	5.329223	9.94E-08	1.96E-07	grey	-0.40747216	1.8E-07	GO:0005525	ATG48278.1;ATG48278.2;F_RA871	RAB GTPase family 8A	small GTPase family RAB protein
Sapur.01G0119300.1	34.70567595	-0.45155585	0.08540710	-5.32919	9.97E-08	1.96E-07	grey	-0.39939594	2.20E-07	GO:0055114;GO:0016491;GO:0080152	ATG14170.1	ALDH6B2	aldehyde dehydrogenase 6B2
Sapur.01G0230100.1	6.36267327	0.64837738	0.12167586	5.327966	9.98E-08	1.96E-07	grey	0.41604765	2.42E-08		ATG29100.1		NA
Sapur.01G0247000.1	9.86066772	-0.77378586	0.14523587	-5.32784	9.94E-08	1.95E-07	grey	-0.35788429	4.21E-06				NA
Sapur.01G0218100.1	3.17664846	-0.85122695	0.15976712	-5.32667	1.00E-07	1.97E-07	grey	-0.61239411	0.48703101	GO:0003882	ATG22140.1	EBS	PHD finger family protein / bromo-adjacent homology (BAH) domain-containing protein
Sapur.01G0261100.2	1.83728164	-0.66538049	0.12497332	-5.32423	1.01E-07	1.99E-07	grey	-0.31640174	5.41E-05		ATG33630.1		3-beta-hydroxy-delta5-steroid dehydrogenase
Sapur.01G0280400.4	0.37681357	-0.54985286	0.10330235	-5.32366	1.02E-07	2.00E-07	grey	-0.38963608	4.57E-07	GO:0016567;GO:0006642	ATG32680.1	RING/U-box superfamily protein	zinc finger protein, putative
Sapur.01G0265100.1	4.46867589	-0.75932421	0.14263174	-5.32287	1.02E-07	2.01E-07	grey	-0.40731688	1.19E-07	GO:0015031;GO:0006464	ATG28830.1	Ubiquitin-conjugating enzyme/RWD-like protein	tumor susceptibility protein 101 protein
Sapur.01G0290300.2	10.7249362	0.50682421	0.09925966	-5.32211	1.03E-07	2.01E-07	grey	-0.09515728	2.03824969		ATG45170.1		outer envelope pore protein
Sapur.01G0151300.1	18.56055125	0.51452227	0.20962527	5.320543	1.03E-07	2.02E-07	grey	0.31440437	2.28E-05				NA
Sapur.01G0135700.1	0.96439873	-1.58180599	0.29738347	-5.31918	1.04E-07	2.05E-07	grey	-0.37381208	1.63E-06	GO:0046983	ATG02130.1	APTX	helix loop helix DNA-binding domain protein
Sapur.01G0225500.1	485.6166576	-0.29062379	0.04604148	-5.3179	1.05E-07	2.06E-07	grey	-0.48829138	1.13E-07	GO:0006338;GO:0016818;GO:0008270;GO:0003676;GO:0005524	ATG5130.1		DNA/RNA helicase protein
Sapur.01G0261600.1	5.17213187	-0.87283889	0.16423783	-5.31725	1.05E-07	2.07E-07	grey	-0.43025164	1.86E-08	GO:0016758;GO:0008152	ATG65550.1		UDP-Glycosyltransferase superfamily protein
Sapur.01G0155100.4	5.4587193	0.64932827	0.12313665	5.316777	1.06E-07	2.07E-07	grey	0.26222286	0.00075329	GO:0048472;GO:0005515	ATG56576.1		RING/U-box superfamily protein
Sapur.01G0251600.1	529.8457012	0.17209752	0.03254074	5.316333	1.06E-07	2.08E-07	grey	0.38087563	8.61E-07	GO:0005515	ATG54480.1	SKIP5;SKP5	SKP1/ASK-interacting protein 5
Sapur.01G0251100.1	245.4834413	0.37586149	0.06763699	5.316	1.06E-07	2.08E-07	grey	0.40829138	1.1E-07		ATG50750.2	PAF1	receptor like protein 9
Sapur.01T0029900.1	2.72722841	-0.43816835	0.27053448	-5.31495	1.07E-07	2.09E-07	grey	-0.41487419	6.76E-08	GO:0006468;GO:0004672	ATG21630.1	CERK1;LYSM RLK1	chitin elicitor receptor kinase 1
Sapur.01T0100500.1	14.90215462	1.51248238	0.29810832	5.312621	1.08E-07	2.12E-07	grey	0.39234882	1.78E-07		ATG29180.1		agenet domain-containing protein
Sapur.01G0130400.1	631.125388	0.45504142	0.08565741	5.311339	1.08E-07	2.12E-07	grey	0.46794421	6.43E-10	GO:0005515	ATG78070.1		Transducin/WD40 repeat-like superfamily protein
Sapur.T022100.1	0.64291836	1.57732754	0.29695781	5.310962	1.09E-07	2.14E-07	grey	0.37801279	1.05E-06		ATFIM1;FIM1	fimbrin 1	fimbrin 1
Sapur.01T0339500.1	6.16807655	-1.15180729	0.29263302	-5.31011	1.10E-07	2.15E-07	grey	0.39399654	3.40E-07	GO:0016866;GO:0008152	ATG16940.2		carbon-sulfur lyase, putative
Sapur.01G0247300.1	203.2396722	0.46284105	0.08348336	5.307553	1.11E-07	2.18E-07	grey	-0.39103173	4.12E-07	GO:0055515;GO:0006468;GO:0005524;GO:0004672	ATG14840.2		Leucine-rich repeat transmembrane protein kinase
Sapur.01G0616700.1	10.88904204	0.72760989	0.17304862	5.305336	1.12E-07	2.19E-07	grey	-0.36813127	2.10E-06	GO:0045454;GO:0015036;GO:0009055	ATG16600.1		Thioredoxin superfamily protein
Sapur.01G0429400.1	292.8367336	0.31795774	0.05992757	5.303472	1.14E-07	2.23E-07	grey	-0.35638341	4.62E-06	GO:0006508;GO:0004190	ATG18490.1		Eukaryotic aspartyl protease family protein
Sapur.01G0280400.4	7.94427247	0.72872742	0.13748183	5.3038	1.14E-07	2.23E-07	grey	-0.39866925	2.92E-07	GO:0004648;GO:0006672	ATG32675.2		Protein kinase superfamily protein
Sapur.01G0602700.1	164.42866	0.27165703	0.05123707	-5.30105	1.14E-07	2.23E-07	grey	-0.38134657	8.33E-07	GO:0005515;GO:0007275	ATG34520.1	ATTTG;LTTG;TTG;LUMR23	Transducin/WD40 repeat-like superfamily protein
Sapur.01G0204600.1	83.38834957	0.34329466	0.06620646	5.300284	1.15E-07	2.25E-07	grey	0.41482143	6.61E-08		ATG80160.1		Lactoylglutathione lyase / glyoxalase I family protein
Sapur.01T0070500.1	0.5213429	2.74763616	0.44317941	5.297291	1.18E-07	2.30E-07	grey	0.36785477	2.14E-06				NA
Sapur.01G0251700.1	0.66947357	2.31478384	0.43700851	5.296779	1.18E-07	2.31E-07	grey	0.39253982	3.68E-07	GO:0055114;GO:0020037;GO:0006979;GO:0004601	ATG22190.1		Peroxidase superfamily protein
Sapur.01T0054400.1	451.919471	0.25820321	0.04876648	5.295087	1.19E-07	2.33E-07	grey	0.37541108	2.06E-06		ATG16540.1		Per1-like family protein
Sapur.01G0107900.1	11.76189033	0.72310299	0.13645233	-5.29351	1.19E-07	2.35E-07	grey	-0.38914309	5.09E-07	GO:0005085	ATG0770?.OPT7	ATOPT7;OPT7	oligopeptide transporter 7
Sapur.01G0260600.1	302.9808021	-0.14987376	0.02737575	-5.29229	1.21E-07	2.37E-07	grey	-0.40285695	1.07E-07		ATG28130.1		N-acetylglucosamine(phosphatidylinositol)-de-N-acetylase family protein
Sapur.01G0113700.3	0.81998824	1.70060858	0.32009384	5.291086	1.22E-07	2.38E-07	grey	0.35901671	3.89E-06		ATG60840.1		hypothetical protein
Sapur.01G0151500.1	82.26591225	0.59488161	0.11240395	5.290242	1.22E-07	2.39E-07	grey	-0.16141747	0.04410274	GO:0016887;GO:0005524;GO:0005085;GO:0042626;GO:0016021;GO:0008810	ATG2560.1	PGP2	multidrug/pheromone exporter, MDR family, ABC transporter family protein
Sapur.01G0015500.1	230.4541105	0.67821924	0.12829814	-5.2887	1.23E-07	2.41E-07	grey	-0.38977462	4.51E-07	GO:0055515;GO:0045531	ATG2719?.1		NB-ARC domain-containing disease resistance protein
Sapur.01G0178300.1	3.24787831	0.88790624	0.16979064	5.288274	1.23E-07	2.41E-07	grey	0.32846816	2.78E-07	GO:0016157;GO:0005985	ATG3120.2	ATSPS4F	Sucrose phosphatase family protein
Sapur.01T0058300.1	561.8974886	-0.29518146	0.05581536	-5.28853	1.23E-07	2.42E-07	grey	-0.40207212	1.80E-07		ATG39260.1		binding;RNA binding
Sapur.01G0268400.1	0.87176268	-0.74796524	0.13050896	-5.28756	1.24E-07	2.43E-07	grey	-0.39265186	1.37E-07	GO:0046983	ATG24760.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.01G0193300.1	2401.701491	0.12843293	0.02429451	5.287222	1.24E-07	2.43E-07	grey	-0.37801253	1.06E-06	GO:0016887;GO:0005524	ATG19210.1	ATRU2;RU2	RNAse I inhibitor protein 2
Sapur.01G0152000.1	17.97953971	0.65406446	0.12419122	-5.28596	1.25E-07	2.45E-07	grey	-0.36727635	2.23E-06		ATG20980.1		Cupredoxin superfamily protein
Sapur.01G0224200.1	6.49568537	1.03984983	0.19674602	5.28521	1.26E-07	2.46E-07	grey	0.10369165	0.00110308	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATG9800.1	CYP80D1	cytochrome P450, family 80, subfamily D, polypeptide 1
Sapur.01G0908800.1	10.37614433	1.00075205	0.18938439	5.284125	1.26E-07	2.47E-07	grey	0.43457273	1.29E-08		ATG18677.2		hypothetical protein
Sapur.01G0020700.1	2.30502876	-0.48131298	0.20845684	-5.2828	1.27E-07	2.48E-07	grey	-0.37198358	5.8E-06	GO:0004324	ATG7930?.1	CLPX	ATP-dependent Clp protease ATP-binding subunit CLPX protein, putative
Sapur.01G0204600.1	352.7574765	0.22148251	0.04199597	5.27847	1.30E-07	2.55E-07	grey	0.36278281	2.82E-06	GO:0043214;GO:0030833;GO:0051629;GO:0005885	ATG60710.1	ARPC5;CRK	actin-related protein 2/3 complex subunit 5
Sapur.01G0173000.1	0.73693714	2.00019161	0.3968708	5.277186	1.31E-07	2.57E-07	grey	0.34510622	9.58E-06				NA
Sapur.01G0202000.1	7.80337664	0.58839961	0.11150731	5.276793	1.31E-07	2.57E-07	grey	0.27330128	1.47E-06		ATG47740.1		PPFOE thiol peptidase family protein
Sapur.01G0280300.1	3.76622973	1.52726428	0.22126789	5.275142	1.33E-07	2.60E-07	grey	0.42148068	6.11E-07	GO:0055114;GO:0016491;GO:0005507	ski18	SKI;SI; similar to	multicopper oxidase
Sapur.01T0239300.1	29.71505979	0.81617658	0.15473447	-5.27469	1.33E-07	2.60E-07	grey	-0.34376501	1.04E-05	GO:0006468;GO:0005524;GO:0004672	ATG67000.1		Protein kinase superfamily protein
Sapur.01T0256600.1	1.24518839	-0.42335163	0.10667658	-5.27423	1.33E-07	2.61E-07	grey	-0.38829938	1.27E-07	GO:0003677;GO:0006468;GO:0005524;GO:0004672	ATG66880.1	SNC4	suppressor of npr1-1 constitutive 4
Sapur.01G0214900.1	351.2459874	0.28763788	0.05454158	5.27421	1.33E-07	2.61E-07	grey	0.36746122	2.34E-06	GO:0005515	ATG80490.2	TPR1	TOPLESS-related 1
Sapur.01G0610100.1	50.40079295	-0.69577958	0.13193749	-5.27349	1.34E-07	2.62E-07	grey	-0.34504527	9.62E-06	GO:0048046;GO:0016762;GO:0006370;GO:0006818;GO:0003975;GO:0006553	ATG36870.1	XTH32	xyloglucan endotransglucosylase/hydrolase 32
Sapur.01G0416300.1	3.59076316	-0.81498087	0.15455767	-5.27328	1.34E-07	2.62E-07	grey	-0.36509748	3.11E-07	GO:0003677;GO:0004857;GO:0008801;GO:0071486;GO:0004199;GO:0009507	ATG28190.1	CSD2;CSD2D	superoxide dismutase [Cu-Zn] protein
Sapur.01G0181000.2	11.79698747	0.56801264	0.10772824	5.272051	1.34E-07	2.63E-07	grey	0.37664646	1.76E-06	GO:0016192;GO:0006904	ATVPS23;VPS23	Sec1/munc18-like (SM) family protein	vacuolar protein sorting-associated-like protein
Sapur.01G0214900.1	4.65652884	1.30099751	0.22778803	5.27264	1.34E-07	2.63E-07	grey	-0.34197843	1.17E-05	GO:0020750;GO:0006276	ATG21280.1		NA
Sapur.01G0115300.1	23.54814882	0.59410194	0.11260369	-5.27184	1.35E-07	2.66E-07	grey	-0.36641376	2.36E-06	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATG36130.1	CYP716A1	cytochrome P450, family 716, subfamily A, polypeptide 1
Sapur.01G0139200.1	155.7734671	0.68682489	0.09198131	5.270987	1.36E-07	2.66E-07	grey	0.33068301	2.34E-05		ATG5262.2	PGR5	proton gradient regulation protein
Sapur.01G0195600.1	0.41678282	2.36689738	0.41112638	-5.27015	1.36E-07	2.67E-07	grey	-0.68013429	2.00E-10	GO:0005515	ATG25780.1		Protein of unknown function (DUF677)
Sapur.01G0133000.1	187.9449022	0.23050132	0.04382169	-5.26969	1.37E-07	2.67E-07	grey	-0.40842678	2.01E-07	GO:0005515;GO:0006468;GO:0004672	ATG66139.1		Leucine-rich repeat transmembrane protein kinase
Sapur.01G2539600.6	0.81111881	1.58786523	0.30137941	5.268893	1.37E-07	2.68E-07	grey	-0.39095073	4.14E-07		ATG07940.1		dentin sialophosphoprotein-like protein, putative
Sapur.01G1197700.1	35.50723957	-0.56488281	0.10721653	-5.2686	1.37E-07	2.69E-07	grey	-0.41238993	8.15E-08		ATG55950.1		thioalkylesin receptor, putative
Sapur.01G0187000.1	20.5242748	-0.56484466	0.10730769	-5.26719	1.38E-07	2.71E-07	grey	-0.38124142	8.39E-07		ATG23110.1		transmembrane protein, putative
Sapur.01G0875000.2	16.2852981	0.48535855	0.09213704	5.266762	1.39E-07	2.71E-07	grey	0.41041983	9.36E-08		ATG15480.1		Protein of unknown function (DUF1218)
Sapur.01G0282300.1	41.27431328	0.62976259	0.08891165	5.266517	1.39E-07	2.72E-07	grey	0.38011669	9.06E-07		ATG23110.1		Protein of unknown function (DUF1218)
Sapur.01G1410100.1	269.0675931	-0.27617283	0.05174853	-5.2664	1.39E-07	2.72E-07	grey	0.00409507	0.95954552	GO:0019843;GO:0006412;GO:0005840;GO:0003735;GO:0016021;GO:0016020;GO:0022885	ATG34180.1	PGY2	Ribosomal protein L6 family
Sapur.01G0250100.1	2.23522564	-0.66134738	0.12507339	-5.26441	1.41E-07	2.75E-07	grey	0.41538072	9.01E-08				NA
Sapur.01G0469800.1	0.53864619	2.36879372	0.43108808	-5.26352	1.41E-07	2.76E-07	grey	-0.48049817	1.91E-10				NA
Sapur.01G0266000.2	2.31717471	0.26402691	0.05012449	5.262	1.41E-07	2.76E-07	grey	-0.2912804	0.00214623	GO:0046872;GO:0030001	ATG32650.1		Heavy metal transport/detoxification superfamily protein
Sapur.01G0112900.2	0.08882225	-0.41703128	0.26270289	-5.26275	1.42E-07	2.77E-07	grey	-0.38692933	5.56E-07	GO:0005515	ATG07300.1	BON2	Calcium-dependent phospholipid-binding Copine family protein
Sapur.01G0250300.1	1.93591833	-0.30727286	0.06000722	-5.26193	1.42E-07	2.78E-07	grey	-0.44052279	7.96E-08		ATG44220.1	ATHAP2A;HYA22A	HYA22-like protein
Sapur.01G2548100.1	6.58857532	1.51807863	0.28866466	5.261056	1.43E-07	2.80E-07	grey	-0.30492296	0.00103144	GO:0006355;GO:0003677	ATG18400.1	anac058;NAC058	NAC domain containing protein 58
Sapur.01G0138600.1	51.89401415	0.38627899	0.07342532	-5.26087	1.43E-07	2.80E-07	grey	-0.36239215	3.13E-06	GO:0006260;GO:0005524;GO:0003677	ATG09680.1	MCM8	minichromosome maintenance 8
Sapur.01G0245400.1	248.1458042	1.80661459	0.2483924	5.260246	1.44E-07	2.81E-07	grey	0.29164358	0.00312378	GO:0016829;GO:0004088	ATG14740.2	ATCA;CA2;CA1B;CA2	carbonic anhydrase 2
Sapur.01G0250900.2	1.00353855	1.75179285	0.33200442	5.259799	1.44E-07	2.82E-07	grey	0.03115569	0.68849297	GO:0016787	ATG34850.1	ATPAP2A;PAP26	purple acid phosphatase 26
Sapur.01G0481200.1	1.36460048	1.34976057	0.26391209	5.2591	1.44E-07	2.82E-07	grey	-0.40887139	1.8E-07	GO:0016491;GO:0051537	ATG61660.1	ATFER3;FER3;FER31	ferredoxin 3;ferredoxin 31 (ferredoxin-like protein 4)
Sapur.01G0927000.1	13.2585294	0.63607192	0.12096175	5.258732	1.45E-07	2.83E-07	grey	0.38589375	6.00E-07	GO:0048544	ATG27280.1		S-locus lectin protein kinase family protein
Sapur.01G0151200.1	137.4779796	0.25182329	0.04435413	5.257807	1.46E-07	2.85E-07	grey	0.35261697	1.77E-06		ATG3150.1	ATSUFE;CPSUFE;EMB1374	cysteine desulfurase family protein
Sapur.01G0185600.1	4.36055552	1.06142497	0.20190837	-5.25754	1.46E-07	2.85E-07	grey	-0.40207846	1.79E-07		ATG0150?.1	TAAC	thylakoid ATP/ADP carrier
Sapur.01G0357000.4	1.30886695	0.42207472	0.42128656	-5.25656	1.47E-07	2.87E-07	grey	-0.35126162	0.

Sapur.T042200.1	10.12543298	-0.81620854	0.157853166	-5.17089	2.33E-07	4.51E-07	grey	-0.363215893	2.38E-06		ATG54750.3	NA
Sapur.G016134100.1	0.78510294	1.72192289S	0.33300682S	5.170776	2.33E-07	4.51E-07	grey	0.33911813	1.40E-05	GO:0006355;GO:0003700	ATG53593.3	RAP2.12
Sapur.G012088600.2	2.02182047	1.16649135	0.22518739	5.170527	2.33E-07	4.51E-07	grey	-0.030285404	0.629195882	GO:0016020	ATG62120.1	
Sapur.G006018600.1	89.19973513	0.30182828	0.058384036	-5.16968	2.34E-07	4.54E-07	grey	-0.373413012	1.46E-06	GO:0055114;GO:0016491	ATG62530.1	
Sapur.G016134300.1	39.64194613	0.57239433	0.111658128	5.165624	2.36E-07	4.57E-07	grey	0.31938054	2.38E-05	GO:0008152;GO:0003824	ATG36888.2	ACS
Sapur.G012033600.1	1.17151716	1.15115849	0.30013386	5.168223	2.36E-07	4.57E-07	grey	-0.346729296	8.62E-06			
Sapur.G011490900.1	16.29812148	-0.38302901	0.074245643	-5.16691	2.38E-07	4.60E-07	grey	-0.37864529	1.01E-06	GO:0006468;GO:0006472;GO:0030246	ATG62120.1	
Sapur.G002884900.2	59.16849950	-0.31852148S	0.061503857	-5.16685	2.38E-07	4.60E-07	grey	-0.375807645	1.21E-06		ATG38890.2	
Sapur.G032158400.1	10.11427826	-1.26876585	0.245589869	-5.16662	2.38E-07	4.61E-07	grey	-0.297269735	0.000016295	GO:0004857;GO:0042545;GO:0030599;GO:0005618	ATG02810.1	
Sapur.G006173700.1	588.1707769	0.16341969	0.03168162	5.166442	2.38E-07	4.61E-07	grey	0.36433818	2.97E-06		ATG32400.1	RIB4
Sapur.G130276200.1	0.03097623	1.49447439	0.28923263	5.165409	2.40E-07	4.64E-07	grey	0.42857267	2.92E-06		ATG34880.1	
Sapur.G012085300.1	112.8134849	0.68258756S	0.13217871	5.16436	2.41E-07	4.66E-07	grey	0.407945453	1.18E-07	GO:0042398;GO:0004357	ATC51310.1	ATC51.CAD2.GDH1.GDH4.P
Sapur.G105037700.2	3.80704659	-0.89224004S	0.172775407	-5.16416	2.42E-07	4.67E-07	grey	-0.383951154	6.90E-07	GO:0005515	ATG27210.1	
Sapur.G141261100.5	4.09255229	-0.66521433	0.128828833	-5.16284	2.42E-07	4.67E-07	grey	-0.408844614	2.06E-07	GO:0005488	ATW001.WEE1	
Sapur.G115055800.1	1.13942129	-1.66819261	0.319164459	-5.16408	2.42E-07	4.67E-07	grey	-0.39078236	4.19E-07			
Sapur.G042890200.1	231.3282115	0.65188783	0.087389964	5.161344	2.45E-07	4.74E-07	grey	0.376565577	7.19E-06		ATG19190.1	
Sapur.I59W012530.1	10.60787847	-2.46257336	0.477221051	-5.16024	2.47E-07	4.77E-07	grey	-0.506245663	1.34E-11		ATG45470.1	
Sapur.G018954500.1	0.58141828	1.88764366S	0.36587835	5.159275	2.48E-07	4.79E-07	grey	0.34803869	7.95E-06			
Sapur.G002887800.1	164.1514583	-0.72814256	0.141162648	-5.15869	2.48E-07	4.79E-07	grey	-0.383364305	6.90E-07	GO:0005515;GO:0006468;GO:0004672	ATG53440.1	
Sapur.G002073200.2	13.11317126	0.767226842	0.148725987	5.15866	2.49E-07	4.81E-07	grey	0.3593123	3.76E-06		ATG32210.1	
Sapur.G011218001.1	3.17606006	-0.41148347	0.2133687	-5.15861	2.49E-07	4.81E-07	grey	-0.377017111	1.18E-06	GO:0055114;GO:0047134	ATG27660.1	
Sapur.G102884000.1	0.48306550S	-2.12015857	0.411256346	-5.15519	2.53E-07	4.89E-07	grey	-0.419823096	4.60E-08		ATG36985.1	DVL16;BOT4
Sapur.G013051700.1	18.58623984	-0.64738152S	0.126181093	-5.15318	2.55E-07	4.86E-07	grey	-0.375713644	1.34E-06		ATG62220.4	
Sapur.G051053500.1	1.59501806	1.98536925S	0.385115111	5.155002	2.54E-07	4.90E-07	grey	0.309925897	0.000128344	GO:0006468;GO:0004672	ATG24030.1	
Sapur.G012012300.1	111.2829726	0.35325248	0.068950573	5.151586	2.58E-07	4.96E-07	grey	0.359820872	3.93E-06		ATG7436.2	APL;WDF
Sapur.G002044300.1	108.8448728	0.35589189	0.068932507	5.151259	2.59E-07	5.00E-07	grey	0.335726437	1.72E-05		ATG57785.1	
Sapur.G061138700.2	2.43780911	-0.98325821	0.190909646	-5.15059	2.60E-07	5.02E-07	grey	-0.394462151	3.19E-07		ATG18900.1	
Sapur.G012344600.1	4.96021698	-0.67729488	0.170332212	-5.15079	2.60E-07	5.02E-07	grey	0.35365094	5.51E-06	GO:0003824	ATG62720.2	
Sapur.G041610000.2	1.2581783	-1.34207281	0.260622313	-5.14949	2.63E-07	5.06E-07	grey	-0.431070983	1.74E-06	GO:0005488;GO:0005634;GO:0000775	ATG04102.2	
Sapur.G120256600.1	0.15556763	0.66758829S	0.142946677	5.149439	2.63E-07	5.06E-07	grey	-0.374673874	1.34E-06	GO:0005515	ATG53552.2	
Sapur.G042600200.2	1.46299389	1.27746633	0.248069768	5.148921	2.62E-07	5.06E-07	grey	0.34463838	1.00E-05	GO:0006468;GO:0004672	ATG60720.1	ASKTHETA;ATSGK2;SK32
Sapur.G175240300.1	1.25143394	-0.64041347	0.084414725	-5.14888	2.62E-07	5.06E-07	grey	-0.387518856	5.03E-07	GO:0016758;GO:0008152	ATG22160.1	AtUGT83A1;UGT83A2
Sapur.G046131800.1	1.92482048	1.11641462	0.216863201	5.148066	2.63E-07	5.08E-07	grey	-0.38387351	2.06E-06			
Sapur.G012087800.1	10.145631	-1.28302648	0.248204638	-5.14726	2.64E-07	5.10E-07	grey	-0.435418223	1.20E-08	GO:0008897;GO:0003287	ATG11470.1	
Sapur.G132087700.1	0.56825512	2.10486373S	0.409011042	5.146227	2.66E-07	5.13E-07	grey	0.353802441	5.48E-06		ATG16460.1	
Sapur.G130428700.1	21.67293675	0.56487289	0.110016559	5.140659	2.73E-07	5.26E-07	grey	0.350262411	5.56E-06	GO:0055114;GO:0016491	ATG04870.2	PDE181;SPC1_ZDS
Sapur.G042692300.1	1.05669248	1.91397452	0.37245158	5.14643	2.68E-07	5.18E-07	grey	0.36253336	3.07E-06			
Sapur.G012812800.1	64.09747954	-0.50454443	0.098079407	-5.14425	2.69E-07	5.18E-07	grey	-0.353373825	3.79E-06		ATG04490.1	VTE5
Sapur.G050254900.1	34.28857319	-0.44946673	0.087398672	-5.14257	2.70E-07	5.20E-07	grey	-0.377591481	1.28E-06		ATG49100.1	
Sapur.G160271600.1	592.1289136	-0.88110349	0.132468484	-5.14176	2.72E-07	5.25E-07	grey	-0.39051565	4.31E-07	GO:0055114;GO:0016491;GO:0008270	ATG27970.1	ATCAD6;CAD6
Sapur.I19W005900.1	908.9327274	0.41434327	0.08439497	5.141474	2.73E-07	5.26E-07	grey	0.367838204	1.06E-06		ATG24620.1	
Sapur.G042500600.1	0.74316281	1.83000759	0.356108461	-5.14143	2.73E-07	5.26E-07	grey	-0.414842458	6.95E-08			
Sapur.G102656600.1	1.25827883	-1.34207281	0.260622313	-5.14949	2.63E-07	5.06E-07	grey	0.267177751	0.000152261		ATG19190.2	
Sapur.G052034000.4	3.74997408	-0.66319328	0.129870851	-5.13833	2.77E-07	5.35E-07	grey	0.078545831	0.328146407	GO:0016020;GO:0006970	ATG42540.1	ATG8J;GLR3.3
Sapur.G012080300.1	1.36466465	1.02078851	0.2170443	-5.13693	2.78E-07	5.36E-07	grey	-0.345328274	9.45E-06		ATG38455.1	
Sapur.G112067000.2	28.41113932	-0.86254493	0.168605519	-5.13791	2.78E-07	5.36E-07	grey	-0.283422426	5.86E-07	GO:0003676	ATG54580.1	
Sapur.G002039900.1	14.99284834	0.35251887	0.064282179	5.137533	2.78E-07	5.37E-07	grey	0.398362421	4.34E-07	GO:0005525	ATG16640.1	ARA-7;ARA7;ATRAB-F2B;AT1
Sapur.G030920000.1	233.5891282	-0.35401631	0.068418339	-5.13769	2.78E-07	5.37E-07	grey	0.368519458	6.02E-07		ATG17020.1	ATRMLK;ATKPD1;HET2;KPD
Sapur.G070689300.1	37.32667946	0.69303184	0.134894165	5.13746	2.78E-07	5.37E-07	grey	-0.404615276	1.49E-07	GO:0006629	PLA-I(beta)2	PLA-I(beta)2
Sapur.G105164200.1	0.81656688	1.48580879	0.290000577	5.135371	2.83E-07	5.46E-07	grey	-0.349208872	7.38E-06			
Sapur.I59W009700.1	46.49404947	1.05305483	0.224570233	5.134276	2.83E-07	5.46E-07	grey	0.353013427	6.61E-07	GO:0005515	ATG23280.1	
Sapur.G061390000.1	59.11529365	0.85283837	0.164080519	5.134127	2.83E-07	5.46E-07	grey	0.275797947	0.000127	GO:0008270;GO:0004089	ATG16861.1	ABCL;ELO2
Sapur.G046102800.1	7.35791159	-0.58216252	0.113395568	-5.13412	2.83E-07	5.46E-07	grey	-0.337507726	1.54E-05	GO:0005488;GO:0005618;GO:0005975;GO:0004553	ATG47140.2	carbonic anhydrase 2
Sapur.G013176000.3	22.42175550	-0.62847549	0.077472748	-5.13408	2.84E-07	5.47E-07	grey	-0.381671841	5.65E-07	GO:0006412;GO:0005840;GO:0003735	ATG21580.1	TCH4;RTH22
Sapur.G017121400.1	68.30271869	-0.80793145	0.17489694	-5.13406	2.84E-07	5.47E-07	grey	-0.415814805	6.10E-08	GO:0006872;GO:0030001	ATG25280.1	
Sapur.G175260100.1	8.31263837	-0.52742219	0.10602574	-5.13334	2.85E-07	5.48E-07	grey	-0.374763807	1.31E-06		ATG28655.1	
Sapur.G010279200.1	771.2705516	-0.42416947	0.082406769	-5.13269	2.86E-07	5.50E-07	grey	-0.439027631	8.82E-09		ATG23690.1	
Sapur.G120201300.1	17.20660225	0.51445441	0.100233802	5.131561	2.87E-07	5.53E-07	grey	0.352326319	6.86E-06	GO:0005515	ATG47890.1	ARIA;PT_RL;PT
Sapur.I105W001.1	0.80064455	1.40618329	0.290528224	5.130718	2.88E-07	5.56E-07	grey	0.368519458	2.04E-06		ATG17020.1	ATRMLK;ATKPD1;HET2;KPD
Sapur.G162011400.1	240.5289595	0.63729198	0.124234951	5.130052	2.90E-07	5.58E-07	grey	0.349857329	7.07E-06	GO:0016758;GO:0008152	UGT71C4	UGT71C4
Sapur.G060213300.1	57.60557139	0.80800507	0.159665	5.129665	2.90E-07	5.59E-07	grey	0.344746603	9.80E-06	GO:0016758;GO:0008152	ATG22400.1	UGT-like;AtUGT85A1;UGT85A1
Sapur.G081302000.1	16.15323544	0.68864564	0.132661746	5.129245	2.91E-07	5.60E-07	grey	0.385887899	6.02E-07		ATG14570.1	
Sapur.G013107700.1	0.60394076	-1.68009381	0.327788726	-5.12829	2.92E-07	5.61E-07	grey	-0.34953171	2.71E-06	GO:0003237	ATG28320.1	LEC2
Sapur.G170081900.2	2.25521296	0.98241737	0.191622611	5.126833	2.95E-07	5.67E-07	grey	0.323087032	4.19E-05	GO:0008270	ATG15790.2	
Sapur.G086182200.1	1.11413175	0.82284264	0.161463997	5.126369	2.95E-07	5.68E-07	grey	0.367194919	2.25E-06	GO:0008270	ATG21275.1	
Sapur.G051199000.1	352.5748846	-0.38776522	0.076425254	-5.12661	2.96E-07	5.69E-07	grey	-0.373891095	1.02E-06	GO:0004648;GO:0004672	ATG35230.1	BSK1
Sapur.G016107700.1	14.24003029	0.95704562	0.186761458	5.124443	2.96E-07	5.70E-07	grey	-0.352340344	7.56E-07			
Sapur.G032648400.1	4.55613768	-0.81931477	0.159893309	-5.12411	2.96E-07	5.71E-07	grey	-0.344075943	1.02E-05	GO:0080048	ATG36850.1	VTC2
Sapur.I59W006900.1	10.82739208	0.73568681	0.145500496	5.123613	3.00E-07	5.77E-07	grey	0.36196429	3.19E-06	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATG45730.1	
Sapur.G062200600.1	104.0853544	-0.55239984	0.108974727	-5.12292	3.01E-07	5.79E-07	grey	-0.360936088	4.14E-07		ATG22630.1	
Sapur.G130258000.1	0.40097973	1.91150991	0.373167675	5.121963	3.02E-07	5.82E-07	grey	0.362837581	3.01E-06		ATG30550.1	
Sapur.G046200300.2	2.12428867	1.14125395	0.2228129	-5.12183	3.02E-07	5.82E-07	grey	-0.380052118	9.18E-07	GO:0005515	ATC00FL1;COP1;DET340;EMB	ATC00FL1;COP1;DET340;EMB
Sapur.T145500.1	6.56593767	0.64007329	0.126977406	5.121503	3.03E-07	5.83E-07	grey	0.383891043	6.93E-07		ATG56120.1	
Sapur.I19W004800.2	1.44570261	-1.15395535	0.225325515	-5.12106	3.04E-07	5.84E-07	grey	-0.374593682	1.31E-06		ATG56120.1	DCPS
Sapur.G012415500.1	4.80818257	0.80175277	0.15657081	-5.12059	3.05E-07	5.86E-07	grey	-0.356565382	4.54E-06			
Sapur.G056207800.1	783.7883008	0.37251803	0.073095648	5.120042	3.05E-07	5.87E-07	grey	0.346436318	8.81E-06		ATG34230.1	
Sapur.T152000.1	0.42995975	1.59859348	0.312132481	5.119674	3.06E-07	5.88E-07	grey	0.402237205	1.75E-07		ATG15110.1	CYP97B3
Sapur.G012329700.1	20.76318216	-0.30905425	0.060457732	-5.11937	3.07E-07	5.89E-07	grey	-0.308318813	8.55E-05		ATG47390.1	
Sapur.G056205800.2	3.52520216	-0.98270588S	0.174388263	-5.11929	3.07E-07	5.90E-07	grey	-0.331575702	0.184690867	GO:0003723	ATG19196.1	PUM02;PUM2
Sapur.G120201000.1	31.64453563	-0.55673289	0.108763256	-5.11867	3.08E-07	5.91E-07	grey	-0.373399666	1.46E-06	GO:0005975;GO:0004553	ATG24318.1	
Sapur.G052073000.1	12.24367787	-0.67233076	0.092257566	-5.11867	3.08E-07	5.91E-07	grey	-0.372627553	1.54E-06		ATG28520.1	
Sapur.G105203000.2	10.8070392	-0.47220555	0.092288093	-5.11829	3.08E-07	5.93E-07	grey	-0.383391111	7.19E-07	GO:0005385;GO:0016021;GO:0008324;GO:0006812	ATG51630.1	
Sapur.G015361000.1	0.52231666	-1.17380139	0.229612424	-5.11816	3.08E-07	5.93E-07	grey	-0.364968897	2.61E-06	GO:0016020;GO:0016586;GO:0005198;GO:0003824	ATG28290.1	AMT2;AMT2;1;ATAMT2
Sapur.G040284600.1	16.48996349	-1.77625681	0.34708158	-5.11769	3.09E-07	5.94E-07	grey	-0.319686557	4.48E-05		ATG41000.1	
Sapur.G012088300.1	22.56611442	-0.49681325	0.09708784	-5.11717	3.10E-07	5.96E-07	grey	-0.37138668	1.46E-06	GO:0000123	ATG16100.2	
Sapur.G061182200.1	625.2116237	0.36760806	0.07183889	5.117117	3.10E-07	5.96E-07	grey	0.325817164	3.13E-05	GO:0035434;GO:0016021;GO:0005375	ATG20650.1	COPT5
Sapur.G175124700.3	0.85226277	-0.53255669	0.103577273	-5.11652	3.11E-07	5.98E-07	grey	-0.345645851	3.38E-06		ATG45600.1	
Sapur.G096077000.1	6.36264845	0.66127942	0.129278509	5.116225	3.12E-07	5.99E-07	grey	0.345428899	9.50E-06	GO:0016758;GO:0008152	ATG15490.1	UGT73B4
Sapur.G030790600.1	0.70024508	1.66886093	0.326208056	5.11543	3.13E-07	6.01E-07	grey	0.373165611	1.70E-06	GO:0018024	ATG45248.5	Nucleolar histone methyltransferase-related protein
Sapur.G010447001.1	0.90799384	-0.60877485	0.119019856	-5.1149	3.14E-07	6.02E-07	grey	-0.393816659	3.31E-07		ATG10101.1	CPS273-I
Sapur.G066080700.1	3.63022739	-0.68972886	0.13482281	-5.11354	3.14E-07	6.07E-07	grey	-0.409421656	1.01E-07	GO:0005515	ATG74720.1	QKY
Sapur.G180204200.1	2246.213952	0.17456356	0.034145733	5.112216	3.18E-07	6.11E-07	grey	0.342431346	1.16E-05		ATG22361.1	
Sapur.G120054400.1	8.75527739	0.67565691	0.132238091	5.111296	3.20E-07	6.14E-07	grey	0.387534755	1.32E-07	GO:0005515	ATG71400.1	ARIUP12;RLP12
Sapur.G050222300.1	297.8187104	-0.22388932	0.04517597	-5.1069	3.22E-07	6.18E-07	grey	-0.395881029	1.87E-07	GO:0008234;GO:0006508	ATG09810.1	NRC79
Sapur.G170059800.1	21.16252296	1.56426828	0.302678597	5.108548	3.23E-07	6.23E-07	grey	0.432494411	1.54E-08		ATG38380.2	
Sapur.G066247700.1	1.02787884	1.46375648	0.28650776	5.10792	3.24E-07	6.25E-07	grey	-0.374384864	1.36E-06		ATG21646.1	
Sapur.G102652500.1	102.5790814	0.19359471	0.03790635	5.107151	3.27E-07	6.28E-07	grey	0.356895073	4.46E-06		ATG76340.1	GONST3
Sapur.G162210600.1	3.10444324	0.92283646	0.180608857	5.107128	3.27E-07	6.28E-07	grey	0.335450206	7.56E-05	GO:0008138;GO:0006470	ATG05530.1	LSF1
Sapur.G041310800.1	0.60478204	1.04004802	0.204143205	5.106609	3.28E-07	6.29E-07	grey	0.353228687	4.99E-06			
Sapur.G071239600.1	4.21007095	-1.00681892	0.216707342	-5.10654	3.28E-07	6.30E-07	grey	-0.36119158	3.36E-06			
Sapur.G092842600.1	41.4016756	-0.84416762	0.165384491	-5.10489	3.31E-07	6.35E-07	grey	-0.434302445	1.02E-08	GO:0005524	ATG50930.1	BCS1
Sapur.G092410400.1	911.5388909	0.39520092	0.077438608	5.104716	3.31E-07	6.36E-07	grey	0.451760558	2.87E-09			
Sapur.G052038800.1	5.67729181	-0.60489753	0.11849821	-5.10455	3.32E-07	6.36E-07	grey	-0.369791177	2.10E-07			
Sapur.G120093000.1	5.02654886	-0.93549176S	0.183203232	-5.10383	3.33E-07	6.38E-07	grey	-0.3957032	2.91E-07	GO:0019773;GO:0005511;GO:0004175	ATG16470.1	PAB1
Sapur.G105139800.1	233.4714969	0.62108645	0.045444042	5.101169	3.44E-07	6.61E-07	grey	0.378076457	1.01E-06	GO:0016020;GO:0005198	ATG31600.1	
Sapur.G041297700.1	1501.370181	0.52899703	0.103678877	5.102274	3.36E-07	6.46E-07	grey	0.352340846	2.56E-06		ATG34950.1	
Sapur.G012058000.1	16.54443237	-0.65157571	0.127731184	-5.10147	3.37E-07	6.46E-07	grey	-0.366840411	2.20E-06	GO:0006355;GO:0003677	ATG47553.1	
Sapur.G180242900.1	917.178248	0.22363666	0.043918869	5.099486	3.41E-07	6.53E-07	grey	0.346491748	8.78E-06		ATG33110.2	
Sapur.G070119300.1	172.3722629	0.40488647S	0.079415076	5.098509	3.42E-07	6.56E-07	grey	0.378319168	1.31E-06	GO:0005515	ATG42310.2	
Sapur.G170081800.3	1.88871537	-1.12746151	0.221152777	-5.09264	3.47E-07	6.67E-07	grey	-0.082418534	0.304769015	GO:0006468;GO:0005524;GO:0004672	BIR1	BAK1-interacting receptor-like kinase 1
Sapur.G020690200.1	0.69231464	-1.72415957	0.338248736	-5.09731	3.45E-07	6.60E-07	grey	-0.412617213	7.87E-08		ATG38200.2	VEL1
Sapur.G120100600.1	14.30799353	-0.64316466	0.125882869	-5.09727	3.45E-07	6.60E-07	grey	-0.352601842	1.86E-06	GO:0017704;GO:0016868;GO:0005975	ATG20180.1	ATPGMP;PGM;PGM1;STF1
Sapur.G016101800.1	0.72840917	1.75985765	0.341396968	5.096694	3.46E-07	6.62E-07	grey	0.327501478	2.91E-05		ATG42420.1	
Sapur.G120100900.1	9.71565223	-0.87341556	0.171375606	-5.09655	3.46E-07	6.62E-07	grey	-0.372653211	1.60E-06			
Sapur.G036012300.7	9.57417656	0.56075252	0.110031006	5.096314	3.46E-07	6.64E-07	grey	0.293678187	0.000189919		ATG41790.1	
Sapur.G170240300.1	1.67278789	1.02128023	0.200463661	5.096126	3.50E-07	6.71E-07	grey	0.35662288	4.55E-06	GO:0042545;GO:0030598;GO:0005618	ATG24130.1	
Sapur.G161830600.1	112.7255466	-0.24294190	0.047713227	-5.09171	3.51E-07	6.80E-07	grey	-0.392712725	3.63E-07		ATG34320.1	
Sapur.G120100500.1	130.1113488	-0.86609134	0.17026257	-5.09162	3.51E-07	6.80E-07	grey	-0.387362605	5.32E-07		ATG30050.1	
Sapur.G136119800.1	72.65861628	-0.28770067S	0.056518425	-5.09039	3.57E-07	6.84E-07	grey	-0.367167697	2.60E-07		ATG20710.1	
Sapur.G102079200.2	0.52885572	-1.84075784	0.361632323	-5.09009	3.58E-07	6.85E-07	grey	-0.451725769	2.97E-09		ATG28940.1	
Sapur.G062887000.1	730.5776577	0.17228826	0.033881029	5.086615	3.58E-07	6.87E-07	grey	-0.364872621	4.22E-07		ATG44720.1	
Sapur.G106181000.1	22.68552021	0.47121893	0.092588641	5.089327	3.58E-07	6.88E-07	grey	0.384170381	6.80E-07	GO:0016192;GO:0006904	ATVPS32;VPS32	
Sapur.G050250500.1	131.7316944	0.34852341	0.069159177	5.088669	3.61E-07	6.90E-07	grey	0.381867883	8.02E-07	GO:0007165;GO:0005515;GO:0043531	ATG17680.1	
Sapur.T061900.1	3.59471561	1.05157738	0.217189125	5.088458	3.61E-07	6.91E-07	grey	0.429291111	4.25E-08		ATG70100.1	ATCRM1;ATKPD1;HET2;KPD
Sapur.G120100100.1	31.54171127	-0.45230184	0.088858451	-5.08378	3.62E-07	6.93E-07	grey	-0.363494106	7.46E-07		ATG29960.1	CYP97C;CYP2
Sapur.G086015300.1	29.32292127	-0.57720516	0.113470593	-5.08739	3.63E-07	6.95E-07	grey	-0.355588789	4.87E-06		ATG18630.1	
Sapur.G120100200.1	2.25883304	-0.97819192	0.190737562	-5.08629	3.65E-07	6.99E-07	grey	-0.42210201	1.79E-07		ATG19100.1	LTP3
Sapur.G012016700.1	51.93079503	1.00881921	0.216642479	5.085602	3.66E-07	7.01E-07	grey	0.427637272	2.32E-08		ATG25180.1	ARR12;RR12
Sapur.G162417000.3	4.88862543	0.82507803S	0.162426365	-5.08525	3.67E-07	7.03E-07	grey	0.079254822	0.32502713	GO:0006414;GO:0005622;GO:0003746	ATG11120.1	
Sapur.G170120500.1	2.96882724	-1.30600848S	0.257431938	-5.08489	3.68E-07	7.04E-07	grey	-0.336325729	1.66E-05		ATG32720.1	
Sapur.G020690700.8	8.20821107	0.51947624	0.102167117	5.084574	3.68E-07	7.05E-07	grey	0.088287229	0.317546002	GO:0043169;GO:0005975;GO:0003824	ATG76130.1	AMY2;ATAMY2
Sapur.G050263200.1	10.46236908	-0.60087974	0.12411623	-5.0802	3.71E-07	7.10E-07	grey	-0.335038344	1.74E-05	GO:0004857		
Sapur.G061139900.1	437.1382744	0.29234581	0.057409226	5.080135	3.71E-07	7.10E-07	grey	-0.373264818	1.64E-06	GO:0007165	ATG57630.1	CIPK21;SnRK3.4
Sapur.G051774000.3	28.3654229	0.51228083	0.08080517	5.08781	3.72E-07	7.12E-07	grey	0.1938105	0.307984	GO:0016020;GO:0016471;GO:0015992	ATG30100.1	AVAN43;VMA32
Sapur.T080400.2	25.93071771	0.31496043	0.06168836	5.08181	3.74E-07	7.15E-07	grey	0.273623273	1.10E-06	GO:0007119;GO:0006891	ATG31780.1	
Sapur.G120100400.1	1.36775487	-1.16318208	0.226470889	-5.08151	3.80E-07	7.27E-07	grey	0.399326458	2.21E-07	GO:0003247	ATG42170.1	
Sapur.G012011200.2	2.65600908	0.86470307	0.17029947	-5.07771	3.82E-07	7.31E-07	grey	-0.44924588	3.60E-09		ATG46450.1	
Sapur.G130288300.1	33.42087830	-0.50269665	0.098629895	-5.07691	3.84E-07	7.34E-07	grey	0.350718754	2.04E-06		ATG54840.1	
Sapur.G162215600.7	3.62505255S	-2.79944712S	0.157510425	-5.07552	3.86E-07	7.39E-07	grey	-0.334218384	1.96E-05	GO:0008168	ATG14430.1	
Sapur.G030271200.1	746.6410522	-0.17155394	0.03411901	-5.07516	3.87E-07	7.40E-07	grey	-0.304579808	3.16E-07	GO:0005515;GO:0000160;GO:0007165;GO:0000155	ATG60340.1	AHK3;LJG1N;LETR;ETR1
Sapur.G180670600.1	2.16878243	0.82356563	0.162105567	5.074475	3.89E-07	7.45E-07	grey	0.368765043	2.01E-06	GO:0016020	ATG30200.3	VEL1
Sapur.G016252600.1	173.0391223	0.95397115	0.187926321	5.074467	3.89E-07	7.45E-07	grey	0.449873655	4.30E-09	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATG27510.1	
Sapur.G030260600.1	286.1153834	-0.43484899	0.085736269	-5.07428	3.89E-07	7.46E-07	grey	0.335182342	1.98E-05		ATT1M23-1;TIM23-1	
Sapur.G016134200.1	113.1415634	-0.33728191	0.066478827	-5.07389	3.90E-07	7.45E-07	grey	-0.381775526	8.07E-07		ATG16920.1	PFU2;UBC23
Sapur.G130217700.1	336.4795358	-0.65423483	0.089938855	-5.07284	3.91E-07	7.49E-07	grey	-0.393092174	1.78E-07		ATG15810.2	RAU6.13
Sapur.G162715600.1	16.52918546	-1.14150429	0.225062217	-5.07065	3.94E-07	7.53E-07	grey	0.361734395	3.24E-06	GO:0004674;GO:0048544;GO:0006468;GO:0004672	ATG27290.1	
Sapur.G120100300.1	2.08873044	-0.67182788	0.132661769	-5.07045	3.94E-07	7.54E-07	grey	-0.376393006	1.58E-06		ATG27235.1	
Sapur.G021664600.1	13.55668865	-0.41209374	0.081211857	-5.07084	3.94E-07	7.57E-07	grey	0.416232677	1.86E-08		ATG10630.1	ARIA1F;ATARF1A;F
Sapur.G002859100.1	41.74705217	-0.46882489	0.092336409	-5.06938	3.96E-07	7.59E-07	grey	-0.380791918	8.03E-07	GO:0005515	ATG36540.1	
Sapur.G103636100.3	28.28124623	-0.52746024	0.104078726	-5.06865	4.01E-07	7.65E-07	grey	0.357390417	4.35E-06		ATG40870.1	PDE181;SPC1_ZDS
Sapur.G102030100.1	18.2832643	0.87650355S	0.172552233	5.068048	4.02E-07	7.68E-07	grey	0.331440882	6.52E-05			
Sapur.G052075800.1	2.10202115	-0.81140046

Sapur.01G0209400.1	372.6679821	-2.226386395	0.045239843	-5.00524	5.58E-07	1.06E-06	grey	-0.382397608	7.72E-07	ATSG19900.1	PRL1-interacting factor, putative
Sapur.01G0203600.1	34.02032121	-0.279201988	0.055786425	-5.00502	5.59E-07	1.06E-06	grey	-0.399863769	2.12E-07	ATSG36980.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01G0204300.1	7.073934433	-0.622000000	0.124038836	-5.00456	5.60E-07	1.06E-06	grey	-0.365615275	2.49E-06	ATSG36520.1	ATPPR5,EMB2463 Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.004G172200.1	1125.860906	0.211348406	0.042235161	5.004087	5.61E-07	1.06E-06	grey	0.353028801	5.76E-06	GO:0004468,GO:0004672	RER Malectin/receptor-like protein kinase family protein
Sapur.005G0195400.1	470.1238449	-0.430808861	0.086113949	-5.00394	5.62E-07	1.07E-06	grey	-0.377271658	1.11E-06	GO:0004629,GO:0006508,GO:0004190	APA1,ATAPA1 aspartic protease A1
Sapur.007G118400.1	2.137623436	-1.268813999	0.253583784	-5.00357	5.63E-07	1.07E-06	grey	-0.366555486	2.34E-06	ATSG40470.1	Plant protein of unknown function (DUF247)
Sapur.005G1431000.2	6.760372231	-0.535722582	0.107008398	-5.00355	5.63E-07	1.07E-06	grey	0.277302913	0.000446214	GO:0005515	ATSG27290.1 Glutathione S-transferase family protein
Sapur.013G135700.1	24.72045054	-0.407836999	0.080508269	-5.00262	5.66E-07	1.07E-06	grey	0.382304183	7.77E-07	FLA21	ATSG36920.1 FASCICLIN-like arabinogalactan protein 21 precursor
Sapur.008G0300000.1	202.4294661	0.223388029	0.044656498	5.002363	5.68E-07	1.07E-06	grey	0.347758877	8.10E-06	GO:0045454	ATPDI1-4,TPDI11-3,PDI-like 1-3 PDI-like 1-3 protein disulfide isomerase, putative
Sapur.005G0232600.1	0.584283621	1.758256155	0.351564479	5.00139	5.68E-07	1.08E-06	grey	0.35182703	6.23E-06		hypothetical protein
Sapur.009G0604000.1	205.1424625	0.163048362	0.032507493	5.001868	5.68E-07	1.08E-06	grey	0.352387087	6.01E-06		ATP30 protein
Sapur.004G0268800.1	29.86169027	0.617377393	0.103438883	5.968291	5.68E-07	1.08E-06	grey	-0.31413108	6.16E-05	ATSG37080.1 RIP3	RDP interactive partner 3 interactor of constitutive active ROPs protein, putative
Sapur.004G1245000.1	10.42143715	3.312642229	0.662406441	5.000884	5.71E-07	1.08E-06	grey	0.301656396	0.000129956	GO:0009733	ATSG38840.1 SAUR-like auxin-responsive protein family
Sapur.004G0216200.1	1.088452499	1.748863248	0.349671215	5.00067	5.71E-07	1.08E-06	grey	0.32720442	4.41E-06		ATSG40140.1 Plant protein of unknown function (DUF247)
Sapur.012G0050600.1	13.1439258	0.523661499	0.104722233	5.00051	5.72E-07	1.08E-06	grey	0.378207211	1.04E-06	GO:0005515	ATSG31080.1 ABR,ZIP1,RLP15 receptor-like protein 35
Sapur.006G0801300.2	43.52834925	0.558018313	0.101623212	5.490608	5.76E-07	1.09E-06	grey	0.352809661	5.94E-06		ATSG37060.3 NF-YB8 nuclear transcription factor Y protein
Sapur.008G0381100.1	195.5587874	0.31657483	0.063372864	4.995432	5.87E-07	1.11E-06	grey	0.348883093	7.52E-06	GO:0005515	ATSG75270.1 DHAR2 dehydroascorbate reductase 2 glutathione S-transferase DHAR2
Sapur.009G1307800.1	99.79759994	-0.439269384	0.087935027	-4.99539	5.87E-07	1.11E-06	grey	-0.360154523	3.60E-06		NA sorting neuro
Sapur.004G1938800.1	7.808692278	-0.656388312	0.131435614	-4.99243	5.90E-07	1.11E-06	grey	-0.348846024	7.95E-06	GO:0005085,GO:0016020,GO:0015297,GO:0015238,GO:0008855	ATSG38330.1 MATE efflux family protein MATE efflux family protein
Sapur.001G0854500.1	1.685855431	-0.016818839	0.003742064	-4.99072	6.02E-07	1.14E-06	grey	-0.397042203	2.82E-07	GO:0006310	ATSG25905.1 Polynucleotidyl transferase, ribonuclease H-like superfamily protein holliday junction resolvase, putative
Sapur.008G0949600.1	10.34019371	0.625618364	0.122792565	4.990518	6.02E-07	1.14E-06	grey	0.34093832	1.25E-05		ATSG35840.1 Protein of unknown function (DUF620) kinase, putative
Sapur.004G1016000.1	133.6822999	0.287758929	0.057663351	4.990153	6.03E-07	1.14E-06	grey	0.333873504	1.93E-05		ATSG18400.1 NA
Sapur.005G0232300.1	8.300904874	0.639457483	0.128148469	4.99012	6.03E-07	1.14E-06	grey	-0.410424746	9.36E-08		NA NA
Sapur.007G0313400.1	2.233743522	1.125831372	0.225631238	4.98966	6.05E-07	1.15E-06	grey	0.347393994	8.30E-06	ATSG36230.3	Protein of unknown function (DUF726) transmembrane and coiled-coil protein, putative
Sapur.006G1957000.1	297.6264955	-0.455258181	0.092032629	-4.97963	6.09E-07	1.15E-06	grey	-0.374523988	9.52E-07	ATSG28370.1	Phosphoglycerate dehydrogenase and lipid transport superfamily protein polyketide cyclase/dehydrase and lipid transporter
Sapur.012G0870000.1	44.93856294	0.321035621	0.06450066	-4.97726	6.45E-07	1.22E-06	grey	-0.418934832	4.75E-08	GO:0005085,GO:0004185	ATSG15000.1 Glycosyl hydrolase family protein with chitinase insertion domain glycosyl hydrolase family 18 protein
Sapur.004G0247900.1	40.68855547	0.244228233	0.0847434	4.97457	6.46E-07	1.22E-06	grey	0.34540921	1.04E-05		ATSG40510.1 Protein of unknown function (DUF246) nuclear protein E3-3, putative
Sapur.004G0203500.1	66.70691202	0.491467297	0.098761546	4.976302	6.48E-07	1.23E-06	grey	0.329659949	2.48E-05		ATSG40630.1 Wound-responsive family protein wound induced-like protein, putative
Sapur.006G2214000.1	15.84556609	0.316417984	0.064138799	4.977669	6.47E-07	1.23E-06	grey	0.3647745	1.71E-06		ATSG04310.1 Plant protein of unknown function acetyltransferase family protein
Sapur.T005400.1	427.6542787	-0.355700834	0.071494152	-4.97524	6.52E-07	1.24E-06	grey	-0.395804959	2.86E-07		ATSG54690.1 G-HGAX,GAMMA-HGAX,HGA gamma histone variant H2AX
Sapur.004G1623300.1	16.12388877	0.364868496	0.074094382	4.97456	6.52E-07	1.24E-06	grey	0.332632148	2.98E-05		ATSG35850.2 NDI1 RPM1-interacting protein 4 (RIN4) family protein
Sapur.010G0191400.1	153.3135895	-0.650092762	0.130865325	-4.97403	6.56E-07	1.24E-06	grey	-0.362792253	3.02E-06		ATSG27330.1 ATKCR1,KCR1,YBR159 beta-ketoacyl reductase 1 beta-ketoacyl-(acyl-carrier) reductase
Sapur.013G0730300.1	63.95819095	0.367581342	0.074000349	4.969261	6.73E-07	1.27E-06	grey	0.309673017	8.01E-05		ATSG37160.1 alpha/beta-hydrolases superfamily protein acinodoin-binding heat-shock protein
Sapur.010G0180900.1	105.5995729	0.836859975	0.169863016	4.924421	8.15E-07	1.54E-06	grey	0.310082668	7.75E-05	GO:0016829,GO:0010333,GO:0008152,GO:0000287	ATSG16740.1 ATTPS03,TPS03 terpene synthase 03 alpha-farnesene synthase
Sapur.005G0930600.2	9.020854103	0.678772315	0.136522315	4.971877	6.63E-07	1.25E-06	grey	0.284542762	0.003304143		ATSG51130.1 transmembrane protein, putative
Sapur.008G0808000.1	2.15066182	2.305617462	0.463917129	4.970963	6.65E-07	1.25E-06	grey	0.331324653	0.180451526	GO:0003676	ATSG38535.1 DJ11G,Gp-patch domain-containing protein nucleic acid-binding protein
Sapur.005G1549000.1	32.66573011	0.526470623	0.105600302	4.971268	6.65E-07	1.25E-06	grey	0.329845671	2.46E-05		ATSG06890.1 Protein of unknown function (DUF511)
Sapur.T004900.1	57.73004615	0.521880254	0.107925688	4.97126	6.65E-07	1.25E-06	grey	-0.28017164	0.000379512		ATSG36751.1 ankyrin repeat protein NA
Sapur.010G0227700.1	195.8846546	0.250717564	0.050433773	4.971224	6.65E-07	1.26E-06	grey	0.342295984	1.14E-05	GO:0005515,GO:0000160	ATSG40580.1 EIN4 Signal transduction histidine kinase, hybrid-type, ethylene sensor
Sapur.008G1364000.4	8.775576684	0.486964769	0.097881839	4.971216	6.65E-07	1.26E-06	grey	0.078548531	0.328164807		ATSG41340.1 CKL1,CKL11 casein kinase I-like protein
Sapur.008G0200800.1	508.1481467	0.213122087	0.042873392	4.9705	6.68E-07	1.26E-06	grey	0.385513832	6.17E-07		ATSG22060.1 GRAS family transcription factor PAT1
Sapur.006G0375600.1	4.002057958	0.879783321	0.177004326	4.97044	6.68E-07	1.26E-06	grey	0.331269642	1.25E-05	GO:0006887,GO:0005515	ATEXO70H2,EXO70H2 exocyst subunit exo70 family protein H2
Sapur.01B0005500.1	43.86752899	0.46324479	0.093607128	4.970185	6.68E-07	1.26E-06	grey	0.364817574	2.62E-06	GO:0006281,GO:0004519	ATSG31150.1 endonuclease V family protein NA
Sapur.004G1938300.1	17.8059738	0.526078357	0.106058893	4.968743	6.74E-07	1.27E-06	grey	0.382738019	7.53E-07		ATSG66880.1 SNRK2-3,SNRK2.3,SRK2I SNRK2-related protein kinase 2.3 NA
Sapur.010G1361800.1	2.971997607	-0.368180584	0.291848813	-4.9677	6.78E-07	1.28E-06	grey	-0.384356805	6.71E-07	GO:0046983	ATSG37150.1 basic helix-loop-helix (bHLH) DNA-binding superfamily protein NA
Sapur.009G0240600.1	0.5374582	2.345361765	0.472126884	4.967653	6.78E-07	1.28E-06	grey	0.391178278	4.07E-07		ATSG07530.1 ATGRAS2,GRAS2,SCL14 SCARECROW-like 14 GRAS family transcription factor
Sapur.01G1118001.1	1.457909092	0.648134142	0.128401392	4.960409	6.88E-07	1.28E-06	grey	0.324832329	1.32E-05	GO:0005508,GO:0004252	ATSG10510.1 Subtilase family protein subtilisin-like protease, putative
Sapur.004G0591600.1	1.500566693	1.774853368	0.345105411	4.966875	6.80E-07	1.28E-06	grey	0.379661564	9.19E-07	GO:0016788	ATSG40960.1 GDSL lipase 1 GDSL lipase 1
Sapur.005G1232600.1	14.870784	1.438431512	0.289668456	4.965756	6.84E-07	1.29E-06	grey	0.409231331	1.03E-07	GO:0071805,GO:0016020,GO:0015079	ATSG41090.1 KUP11 K+ uptake permease 11 NA
Sapur.002G0111000.3	8.506188677	-0.750931008	0.151246397	-4.964951	6.87E-07	1.30E-06	grey	0.251723931	0.00147144	GO:0005515,GO:0016021	ATSG16980.2 Major facilitator superfamily protein Nipocampus abundant transcript 1 protein
Sapur.004G1660800.1	0.603730026	2.182072253	0.442016763	4.96429	7.11E-07	1.34E-06	grey	-0.68854009	8.52E-11		NA transmembrane protein
Sapur.T004900.1	5.194223602	0.629881294	0.127007427	4.957851	7.13E-07	1.35E-06	grey	0.382740072	7.53E-07		NA
Sapur.005G1338900.1	406.3309476	0.249657866	0.050360878	4.957658	7.13E-07	1.35E-06	grey	-0.379448038	1.52E-07	GO:0009055	ATSG15350.1 AtENODL17,ENODL17 early nodulin-like protein 17 blue copper-like protein
Sapur.010G1341000.1	152.9128441	-0.266287418	0.053715201	-4.95739	7.14E-07	1.35E-06	grey	-0.33922244	3.40E-07	GO:0016020	ATSG54120.1 LEMD (ligand-effect modulator 3) family protein / CDC50 family protein LEMD (ligand-effect modulator 3) family protein
Sapur.012G0500600.1	3.380388813	0.872017275	0.176104091	4.955122	7.23E-07	1.36E-06	grey	0.352805062	6.42E-06	GO:0008168	ATSG28350.2 S-adenosyl-L-methionine-dependent methyltransferases superfamily protein S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.004G0271300.1	85.06677794	0.386091835	0.060568921	4.953352	7.28E-07	1.37E-06	grey	0.357827829	4.02E-06	GO:0012125,GO:0016048,GO:0010215	ATSG22210.1 COBRA like protein precursor COBRA-like protein precursor
Sapur.01G0209300.1	76.80743878	-0.382334756	0.077227563	-4.95334	7.29E-07	1.38E-06	grey	-0.256805611	0.001200841	GO:0010011,GO:0006338	ATSG43500.2 ARP9,ATARP9 actin-related protein 9 actin-related protein
Sapur.006G2939000.1	8.807075814	-0.398988477	0.081868381	-4.9522	7.30E-07	1.38E-06	grey	-0.389497448	4.61E-07		ATSG31720.1 basic helix-loop-helix (bHLH) DNA-binding superfamily protein NA
Sapur.013G0860600.1	1415.062037	0.137156855	0.027609353	4.952771	7.32E-07	1.38E-06	grey	0.368842251	2.92E-06	GO:0005091	ATSG07120.1 SNX2b sorting nexin 2b NA
Sapur.004G0234200.1	10.00001242	0.914984827	0.184764683	4.952672	7.32E-07	1.38E-06	grey	0.388528655	4.60E-07	GO:0005515,GO:0043531	ATSG36930.2 Disease resistance protein (TIR-NBS-LRR class) family NA
Sapur.01G0694000.1	1.550053867	1.295916471	0.261675812	4.95245	7.33E-07	1.38E-06	grey	0.343870773	1.17E-05	GO:0005515,GO:0016491,GO:0005507	ATSG06230.1 LAC7 laccase 7 laccase
Sapur.004G0268300.1	2.170239287	1.074198387	0.216921238	4.952409	7.33E-07	1.38E-06	grey	0.303237205	0.000113236		ATSG55150.1 Protein of unknown function (DUF674) NA
Sapur.009G0221200.1	103.6981261	-0.512166786	0.103446824	-4.95101	7.38E-07	1.39E-06	grey	-0.367750851	2.16E-06		ATSG28780.1 Pathogenesis-related thaumatin superfamily protein thaumatin-like protein
Sapur.01G0392200.1	290.3735325	0.231564234	0.046775625	4.950958	7.38E-07	1.39E-06	grey	0.34144706	1.21E-05		ATSG29840.1 Yippee family putative zinc-binding protein yippee zinc-binding DNA-binding/NtcL8, centromere assembly protein
Sapur.009G1353000.1	264.6062038	-0.341398383	0.069344242	-4.95064	7.40E-07	1.40E-06	grey	-0.42018958	4.29E-08	GO:0051726	ATSG75150.1 Gnd2/cyclin-D-interacting protein NA
Sapur.004G1604000.1	4.699191581	-0.684611917	0.138294153	-4.9504	7.41E-07	1.40E-06	grey	-0.342605335	1.12E-05		NA NA
Sapur.004G0681000.1	55.56257515	0.373071724	0.075137598	-4.94682	7.53E-07	1.42E-06	grey	-0.378281306	9.04E-07		ATSG58490.1 Phosphatidic acid phosphatase (PAP2) family protein sphingosine-1-phosphate phosphatase
Sapur.003G1132600.2	1.870865926	1.379913423	0.279121268	4.943777	7.68E-07	1.44E-06	grey	0.111612675	0.101876174	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	ATSG07530.1 PGP11 P-glycoprotein 11 multidrug/pheromone exporter, MDR family, ABC transporter family protein
Sapur.006G0946600.1	0.995663273	1.373801105	0.277937005	4.943218	7.68E-07	1.44E-06	grey	-0.349002015	1.76E-07		ATSG47210.1 HYD2,HYD2 hydroxysteroid dehydrogenase 2 short-chain dehydrogenase family protein
Sapur.01G0305500.1	108.3684376	0.518055868	0.104824993	-4.9421	7.73E-07	1.46E-06	grey	-0.355576323	4.88E-06		ATSG52870.1 IQ calmodulin-binding motif family protein calmodulin-binding family protein, putative
Sapur.004G0227400.1	130.5155479	0.316651072	0.064080251	4.941108	7.77E-07	1.46E-06	grey	-0.323473171	2.37E-05	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATSG14690.1 CYP72A15 cytochrome P450 family 72, subfamily A, polypeptide 15 cytochrome P450 family monooxygenase
Sapur.006G1127700.2	0.950641797	1.433157452	0.290056395	-4.94102	7.77E-07	1.46E-06	grey	-0.363412985	2.89E-06	GO:0016157,GO:0005985	ATSG43190.1 ATSUS4,SUS4 sucrose synthase 4 sucrose synthase
Sapur.005G1930500.4	3.09185165	0.753575152	0.153575829	-4.94028	7.80E-07	1.47E-06	grey	-0.010796685	0.814804527		ATSG40470.1 bZIP transcription factor family protein bzip and reproductive organ-expressed protein
Sapur.013G0930001.1	3.882082611	1.480769209	0.299816639	4.93885	7.86E-07	1.48E-06	grey	0.353818841	5.47E-06	GO:0006429	ATSG14930.2 SAG101 senescence-associated gene 101 NA
Sapur.01B0252900.1	73.39239922	-0.495026298	0.100237731	-4.93852	7.87E-07	1.48E-06	grey	-0.357856496	4.20E-06		ATSG35490.1 NA NA
Sapur.01G0208800.1	228.2609901	-0.461682054	0.094380879	-4.93751	7.90E-07	1.49E-06	grey	-0.366515466	2.35E-06	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATSG56330.1 CYP94D2 cytochrome P450, family 94, subfamily D, polypeptide 2 cytochrome P450 family protein
Sapur.007G0784000.4	0.993650952	1.440306752	0.291797384	-4.93629	7.94E-07	1.50E-06	grey	-0.249960722	0.001502679		ATSG39630.1 NA hypothetical protein
Sapur.005G0250200.1	0.656726263	1.304344494	0.264676264	-4.93625	7.94E-07	1.50E-06	grey	0.412260911	8.10E-08		NA hypothetical protein
Sapur.01G1316000.1	2.365409914	1.394577989	0.282599975	4.934844	8.02E-07	1.51E-06	grey	0.315841213	6.36E-05		NA NA
Sapur.017G0854500.1	4.783469104	2.121671523	0.429156654	-4.93361	8.07E-07	1.52E-06	grey	-0.373310205	1.60E-06	GO:0045017,GO:0004144	ATSG31930.1 O-acyltransferase (WSD1-like) family protein O-acyltransferase WSD1
Sapur.003G0297000.1	17.04686565	0.429819333	0.087120707	4.933607	8.07E-07	1.52E-06	grey	0.363461728	2.86E-06	GO:0005515,GO:0030117,GO:0016192,GO:0006886,GO:0005198	ATSG23460.1 Coatomer, beta'1 subunit coatomer beta subunit, putative
Sapur.008G0300100.1	0.705807903	1.462216	0.296281272	4.931119	8.18E-07	1.54E-06	grey	0.353183762	5.65E-06		NA NA
Sapur.005G0855000.1	16.13976014	1.122451827	0.227648877	-4.93063	8.20E-07	1.54E-06	grey	-0.404678271	1.47E-07	GO:0005515	ATSG58190.2 ABR,PP5,RLP9 receptor-like protein 9 LRR amino-terminal domain protein
Sapur.009G0415400.4	14.64895684	0.754267984	0.153175629	-4.92925	8.36E-07	1.57E-06	grey	-0.392374775	2.75E-07	GO:0005515	ATSG52530.1 SLX1 SLX1-like protein SLX1-like protein
Sapur.01G0683300.1	87.72132196	-0.254607979	0.049145901	-4.92808	8.38E-07	1.56E-06	grey	-0.382617003	7.02E-07		ATSG50990.1 Tetratricopeptide repeat (TPR)-like superfamily protein PPR containing protein
Sapur.01G0125500.1	7.887994926	-0.578489183	0.117400767	-4.92747	8.38E-07	1.57E-06	grey	-0.38894873	4.80E-07		ATSG39010.1 NA NA
Sapur.01T0284400.1	119.6564114	0.312387053	0.063398805	4.92728	8.34E-07	1.57E-06	grey	-0.277773605	0.000427804	GO:0046923,GO:0016021,GO:0006621	ATSG50340.1 ERD2B endoplasmic reticulum retention defective 2B ER lumen protein retaining receptor
Sapur.003G0818800.1	453.9998618	0.259857581	0.052792636	4.925206	8.43E-07	1.59E-06	grey	0.341796211	1.18E-05	GO:0008270,GO:0003677	ATSG12440.2 A20/AN1-like zinc finger family protein zinc finger A20 and AN1 domain stress-associated protein
Sapur.007G0250500.1	43.11000389	0.258802535	0.052514385	4.92441	8.46E-07	1.60E-06	grey	-0.384059195	5.04E-07		ATSG40560.1 Pentatricopeptide repeat (PPR) superfamily protein PPR containing protein
Sapur.004G1004000.1	2.613670126	-0.830710853	0.168705791	-4.92402	8.48E-07	1.60E-06	grey	-0.381278181	8.09E-07		ATSG08490.1 Tetratricopeptide repeat (TPR)-like superfamily protein cyclin domain/PPR containing protein
Sapur.007G0854300.1	5.658841473	0.752667304	0.153294576	-4.92302	8.50E-07	1.60E-06	grey	-0.380504394	5.68E-07		ATSG44940.1 Integrase-type DNA-binding superfamily protein AP2/EREBP domain transcription factor
Sapur.004G0364000.1	105.7018181	0.668582207	0.131703187	4.92103	8.61E-07	1.62E-06	grey	0.385997823	5.95E-07	GO:0006629	ATSG44830.1 DAD1 alpha/beta-Hydrolases superfamily protein phospholipase
Sapur.004G1337000.1	3.375738897	0.736227909	0.146622633	4.9202	8.62E-07	1.62E-06	grey	-0.373142479	1.10E-06		ATSG27490.2 Tyr/Ser-Gln dipeptide transporter family protein GTPase activator protein, putative
Sapur.015G2663000.1	44.4712152	-0.535298949	0.108805974	-4.91976	8.67E-07	1.63E-06	grey	-0.364261099	2.74E-06	GO:0005789	ATSG54130.1 ATMAMR,MAMR membrane-associated mannitol-induced vesicle-associated protein 4-1
Sapur.01G1481000.1	3.11224655	0.871661472	0.177195121	4.919162	8.69E-07	1.63E-06	grey	0.335477038	1.75E-05	GO:0045454	ATSG17520.1 ATPDI5,ATPDI11-1,PDI5,PDI PDI-like 1-1 protein disulfide isomerase
Sapur.010G1347001.1	40.36667382	-0.462775757	0.0931742	-4.91915	8.68E-07	1.64E-06	grey	-0.319401589	0.00017421		ATSG59570.1 NEDD1 Transducin/WD40 repeat-like superfamily protein NA
Sapur.003G1921000.1	8.004991467	0.725621718	0.147510767	4.91911	8.68E-07	1.64E-06	grey	0.347634188	8.16E-06		NA transmembrane protein, putative
Sapur.009G0945000.1	2.599132664	0.667387267	0.137626267	4.91817	8.74E-07	1.65E-06	grey	-0.385790752	6.08E-07		ATSG08030.1 Protein of unknown function, DUF642 transmembrane protein, putative
Sapur.017G0544000.1	133.9899595	-0.543570234	0.110536318	-4.91757	8.76E-07	1.65E-06	grey	-0.432765399	1.26E-08		ATSG27030.1 NA transmembrane protein, putative
Sapur.01G0164500.1	225.7893884	-0.365764326	0.054151599	-4.91757	8.76E-07	1.65E-06	grey	-0.360073499	2.93E-06		ATSG01370.1 Protein of unknown function (DUF3245) RNA-binding protein, putative
Sapur.003G1338000.1	13.13132434	0.545271494	0.110898708	-4.91684	8.80E-07	1.65E-06	grey	-0.372608603	1.20E-06		ATSG01430.1 Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family harpin-induced protein
Sapur.004G0268200.1	396.7767344	0.268159008	0.054266579	4.941108	7.77E-07	1.46E-06	grey	0.353183762	5.65E-06	GO:0003676	ATSG44720.1 RNA-binding (RRM/RBD/RNP motifs) family protein heterogeneous nuclear ribonucleoprotein G RNA recognition motif protein
Sapur.01G0918000.2	12.10242047	0.954779894	0.194234249	4.915863	8.84E-07	1.66E-06	grey	0.196578772	0.010639828	GO:0008046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	ATSG10550.1 XET,ATH33 xyloglucan:xyloglucosyl transferase 33 xyloglucan endotransglycosylase hydrolase
Sapur.003G0501500.1	0.892022869	1.582165882	0.325318187	4.915493	8.84E-07	1.66E-06	grey	0.342664017	1.12E-05	GO:0008146	ATSG07010.1 ATST2A,ST2A sulfotransferase 2A flavonol 4'-sulfotransferase, putative
Sapur.013G0117000.1	2.562571772	1.026046	0.208790438	4.914239	8.91E-07	1.68E-06	grey	0.273102489	1.60E-06		ATSG32340.1 PRA1.B4 prenylated RAB acceptor 1.B4 PRA1 family protein
Sapur.01G1339200.1	505.5468981	0.291252534	0.059282396	4.912885	8.97E-07	1.69E-06	grey	0.329184048	2.56E-05		ATSG38160.1 NA NA
Sapur.011G0250001.1	173.1617427	0.347978587	0.274206647	4.912688	8.98E-07	1.69E-06	grey	-0.468910118	2.01E-08		NA NA
Sapur.15S2057800.1	5.669927817	-0.951245821	0.19365487	-4.91207	9.01E-07	1.69E-06	grey	-0.371977708	1.62E-06		ATSG43551.1 ATPSL,PSL1 forkhead-associated (FHA) domain-containing protein NA
Sapur.15H0267600.1	29.62762373	0.611449189	0.129513769	4.911449	9.04E-07	1.70E-06	grey	-0.359348336	4.76E-06		ATSG29120.1 ATP binding microtubule motor family protein NA
Sapur.01G0042000.1	29.89327306	0.785243884	0.158802227	4.911081	9.06E-07	1.70E-06	grey	0.381362375	5.89E-07		ATSG11950.1 Putative lysine decarboxylase family protein lysine decarboxylase, putative
Sapur.004G0268400.1	807.7240182	0.247585888	0.050281775	4.91107	9.06E-07	1.70E-06	grey	-0.382612721	7.02E-07		ATSG41410.2 ATSAR1,KIC,PIR,PIR121,PIR1 transcription factor family protein 1210-specific p53 sensitive protein
Sapur.004G1184000.1	761.5774884	0.223172481	0.045462971	4.90888	9.16E-07	1.72E-06	grey	-0.356892614	4.47E-06	GO:0055114,GO:0009165,GO:0006465,GO:0004146,GO:0008231,GO:0004799	ATSG16370.1 THY-1 thymidylate synthase 1 dihydrofolate reductase-thymidylate synthase
Sapur.003G0281500.1	331.1725153	0.267009164	0.054178862	4.908575	9.17E-07	1.72E-06	grey	0.345612274	1.66E-05	GO:0005515	ATSG31700.2 DNA/RNA-like superfamily protein NA
Sapur.01B0265300.1	16.91230885	0.711447943	0.144939999	4.908568	9.17E-07	1.72E-06	grey	0.371168843	8.88E-07		ATSG25930.1 Protein kinase family protein with leucine-rich repeat domain protein kinase family protein
Sapur.T008100.1	0.032370895	1.502027883	0.30600319	-4.90804	9.18E-07	1.73E-06	grey	-0.37595687	1.22E-06	GO:0016021,GO:0016020,GO:0022857	ATSG18200.1 nodulin MtN21 /EamA-like transporter family protein auxin-induced protein SAG64
Sapur.003G2945000.1	1154.598991	-0.188521753	0.038408933	-4.9083	9.19E-07	1.73E-06	grey	-0.418152027	4.91E-08		ATSG75140.1 NA plant/P18D16-17 protein
Sapur.01G1419000.1	3.352124889	-0.801487708	0.163341126	-4.90764	9.22E-07	1.73E-06	grey	-0.363202725	2.88E-06	GO:0008270,GO:0005515	ATSG72220.1 RING/U-box superfamily protein NA
Sapur.005G1313000.1	10.0884664	0.610310312	0.124326654	4.907586	9.22E-07	1.73E-06	grey	0.324981131	1.81E-05		ATSG28710.1 Nucleotide-diphosphate-sugar transferase family protein nucleotide-diphosphate-sugar transferase
Sapur.005G0410500.1	282.6015222	0.234508241	0.047807642	-4.90713	9.24E-07	1.74E-06	grey	-0.36485722	2.63E-06		ATSG28830.1 calcium-binding EF hand family protein calcium-binding EF hand protein
Sapur.005G0751000.1	1.054	0.788846661	0.160639897	-4.9069	9.34E-07	1.75E-06	grey	-0.318844117	4.98E-07		ATSG75140.1 NA NA
Sapur.01G1419000.1	3.352124889	-0.801487708	0.163341126	-4.90764	9.22E-07	1.73E-06	grey	-0.363202725	2.88E-06	GO:0008270,GO:0005515	ATSG72220.1 RING/U-box superfamily protein NA
Sapur.005G1313000.1	10.0884664	0.610310312	0.124326654	4.907586	9.22E-07	1.73E-06	grey	0.324981131	1.81E-05		ATSG28710.1 Nucleotide-diphosphate-sugar transferase family protein nucleotide-diphosphate-sugar transferase
Sapur.005G0410500.1	282.6015222	0.234508241	0.047807642	-4.90713	9.24E-07	1.74E-06	grey	-0.36485722	2.63E-06		ATSG28830.1 calcium-binding EF hand family protein calcium-binding EF hand protein
Sapur.005G0751000.1	1.054	0.788846661	0.160639897	-4.9069	9.34E-07	1.75E-06	grey	-0.318844117	4.98E-07		ATSG75140.1 NA NA
Sapur.003G2686000.3	10.23304153	0.535617184	0.109217139	4.90415	9.38E-07	1.76E-06	grey	0.353576256	5.56E-06	GO:0005085,GO:0016021	ATSG16470.1 ATSLC4ETL1,ETL1,SLC4-ETL1 sucrose transporter 4 sucrose transporter 4
Sapur.003G0318000.1	226.4889913	0.345501012	0.07005629	4.903407	9.42E-07	1.77E-06	grey	-0.344596281	1.02E-05	GO:0004281	ATSG35230.1 RHOMBOID-like protein 13 rhomboid family protein

Sapur.004G124400.1	78.6449847	6.086557281	0.141832207	4.84063	1.29E-06	2.41E-06	grey	0.32041872	4.26E-05	GO:0009733	AT5G18020.1	SAUR-like auxin-responsive protein family	NA
Sapur.017G077600.1	16.11864606	-1.154802047	0.238568873	-4.84012	1.30E-06	2.42E-06	grey	-0.35912349	3.86E-06	GO:0006887;GO:0000145	AT5G29400.1	exocyst subunit exo70 family protein E1	NA
Sapur.T007100.1	18.77397905	-0.516447473	0.106702819	-4.84005	1.30E-06	2.42E-06	grey	-0.37078268	1.75E-06	GO:0005975;GO:0004553	AT5G47040.2	O-Glycosyl hydrolases family 17 protein	NA
Sapur.014G047100.1	12.48393199	-0.674104402	0.139293483	-4.83945	1.30E-06	2.42E-06	grey	-0.35389191	4.78E-06				transmembrane protein, putative
Sapur.005G167700.1	513.385257	0.190817368	0.039403384	4.83829	1.31E-06	2.44E-06	grey	0.33882683	2.61E-05		AT5G15160.1		transmembrane protein, putative
Sapur.009G021200.5	0.56871263	-1.689641774	0.349199195	-4.83862	1.31E-06	2.44E-06	grey	-2.38990647	4.47E-07	GO:0006468;GO:0004672	AT2G28930.1	PPK18;PK18	protein kinase 18
Sapur.006L139500.2	9.301047791	0.782373724	0.161709089	4.83816	1.31E-06	2.44E-06	grey	0.42663829	4.12E-08		AT3G31660.2	Protein of unknown function (DUF3527)	DUF3527 domain protein
Sapur.017G081000.1	18.8627777	-0.553728224	0.114478425	-4.83687	1.32E-06	2.46E-06	grey	-0.33223151	2.18E-05		AT5G18390.2	Protein kinase superfamily protein	NA
Sapur.018G010000.1	847.1640706	0.15431135	0.031907008	4.836284	1.32E-06	2.46E-06	grey	0.34471592	9.81E-06		AT5G11500.1		coiled-coil protein
Sapur.003G024000.1	266.8898689	-0.197251297	0.040763211	-4.83639	1.32E-06	2.47E-06	grey	-0.38569865	5.92E-07		AT1G17615.1		transmembrane protein, putative
Sapur.017G080800.1	0.420026445	-2.161145015	0.446908829	-4.83585	1.33E-06	2.48E-06	grey	-0.47321956	3.88E-10		AT5G43505.1	LCR30	low-molecular-weight cysteine-rich 30
Sapur.007G127400.1	1.450479466	-0.882759271	0.181452125	-4.83524	1.33E-06	2.48E-06	grey	-0.37881243	9.95E-07		AT2G31230.1	GRAM domain protein / ABA-responsive protein-related	GRAM domain protein
Sapur.003G023300.1	35.88635856	-0.303683208	0.06261975	-4.83367	1.34E-06	2.50E-06	grey	-0.36754019	2.25E-05	GO:0005525	AT5G79640.1	GTP-binding protein, HflX	GTP-binding protein HflX
Sapur.004G027900.1	4.527412651	-0.356383008	0.073600197	-4.83356	1.34E-06	2.50E-06	grey	-0.40640804	1.28E-07				NA
Sapur.002G024800.1	957.6227056	0.20209808	0.041809582	4.833361	1.34E-06	2.50E-06	grey	0.34586407	9.13E-06	GO:0004518	AT5G19680.2	Wound-responsive family protein	wound responsive protein
Sapur.006L139000.1	221.3149947	0.350401274	0.072461194	4.833158	1.34E-06	2.50E-06	grey	0.3865441	1.72E-05	GO:0003677;GO:0005515	AT5G39440.1	pathogenesis-related homeodomain protein A	HD domain class transcription factor, putative
Sapur.017G120300.1	2.482616367	-1.256264371	0.259927184	-4.83314	1.34E-06	2.50E-06	grey	-0.31992141	4.42E-05		AT5G27581.1	Copper transport protein family	hypothetical protein
Sapur.002G079300.1	150.0409421	0.248360741	0.051388714	4.832982	1.35E-06	2.51E-06	grey	0.32027470	8.33E-06	GO:0005114;GO:0016616;GO:0006994;GO:0003854	AT4G00110.1	GAE3	UDP-D-glucuronate 4-epimerase 3
Sapur.002G050300.1	1.524827936	-0.667774495	0.138208283	-4.83253	1.35E-06	2.51E-06	grey	-0.36431032	7.22E-06		AT5G08130.1		epidermal patterning factor-like protein, putative
Sapur.003G077100.3	13.82293137	-0.479525753	0.099246671	-4.83175	1.35E-06	2.52E-06	grey	-0.37399805	1.61E-06		AT5G22550.1	Phosphatidic acid phosphatase (PAP2) family protein	PAP2 superfamily protein
Sapur.008G029800.1	9.161921483	0.73284577	0.152000361	4.82242	1.40E-06	2.60E-06	grey	-0.38649106	5.76E-07		AT5G66051.1	Expressed protein	hypothetical protein
Sapur.002G135100.1	261.1731909	0.163907543	0.03394562	4.828533	1.38E-06	2.56E-06	grey	0.34207092	1.66E-05		AT3G02290.1		hypothetical protein
Sapur.005G049600.1	7.290656161	1.022341382	0.211683438	4.827987	1.38E-06	2.56E-06	grey	0.36018278	3.51E-06				hypothetical protein
Sapur.016G231200.1	3.397889991	-0.731686393	0.151564098	-4.82757	1.38E-06	2.57E-06	grey	-0.08987523	2.162988706		AT5G05080.2	ATUBC22;UBC22	ubiquitin-conjugating enzyme 22
Sapur.004G230200.3	11.45844996	-0.553638897	0.115471188	-4.82635	1.39E-06	2.58E-06	grey	-0.35207606	8.88806995	GO:0006412;GO:0005840;GO:0005622;GO:0003735	AT4G17020.1	Ribosomal protein L18e family protein	60S ribosomal protein L36
Sapur.010G122700.1	0.85027597	-1.412408846	0.292666525	-4.82573	1.39E-06	2.59E-06	grey	-0.34864807	9.13E-06	GO:0004518	AT3G49480.2	QLI;QLI6;MDD2;LKI2	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.017G074300.1	38.19430012	0.421366895	0.087325565	4.825083	1.40E-06	2.60E-06	grey	0.32691296	2.92E-05		AT5G26280.1		hypothetical protein
Sapur.018G028800.2	28.16613362	-0.389888023	0.080818592	-4.82404	1.40E-06	2.60E-06	grey	-0.34397051	1.03E-05		AT4G25570.1	TIFYB	TIFY domain protein B
Sapur.002G194900.1	0.920534959	-1.404069368	0.291070018	-4.82387	1.40E-06	2.62E-06	grey	0.35717857	4.39E-06				NA
Sapur.004G168100.1	1.099650437	-0.623886681	0.130247473	-4.82327	1.40E-06	2.62E-06	grey	-0.34430174	7.96E-06	GO:0005085;GO:0016020;GO:0006810;GO:0005215;GO:0006863;GO:0005345	AT5G10960.1	ATJ2;LJ2G1	AZA-guanine resistant1
Sapur.015WG041200.1	4.053663091	-0.672502662	0.139440342	-4.82287	1.42E-06	2.62E-06	grey	-0.1051274	0.000102007		AT5G18215.1	Protein of unknown function, DUF599	transmembrane protein, putative
Sapur.017G177000.1	9.755352907	-0.365202262	0.075261146	-4.82258	1.42E-06	2.62E-06	grey	-0.36271633	1.03E-06	GO:0005515;GO:0006468;GO:0005524;GO:0004672	AT5G47570.1	Leucine-rich repeat protein kinase family protein	receptor-kinase, putative
Sapur.015G005500.1	0.467832947	-1.689302335	0.392156438	-4.82168	1.42E-06	2.66E-06	grey	-0.36667802	2.33E-06				NA
Sapur.004G117300.1	0.294673116	-1.804082257	0.374232256	-4.82027	1.43E-06	2.66E-06	grey	-0.51317889	3.86E-12				NA
Sapur.016G131200.1	94.91934633	-0.325782368	0.067582943	-4.82048	1.43E-06	2.66E-06	grey	-0.34957419	7.20E-06		AT5G59150.1		transmembrane protein, putative
Sapur.003G060300.1	105.7143983	-0.257891625	0.04870349	-4.81867	1.44E-06	2.67E-06	grey	-0.36677662	3.46E-06	GO:0008233;GO:0005198;GO:0005634	AT5G19370.1	AESP;ESP;RSW4	aspasse
Sapur.016G160500.1	7451.509669	0.250899622	0.052006216	4.819615	1.44E-06	2.67E-06	grey	-0.33353939	1.97E-05	GO:0016788	AT4G16370.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.016G282800.2	7.608861658	0.591795543	0.122825544	-4.81818	1.45E-06	2.69E-06	grey	-0.2624622	0.009062358	GO:0005114;GO:0016491;GO:0006807;GO:0016638;GO:000653	AT5G04140.2	FD-GOGAT;GLS1;GLU1;GLU1	glutamate synthase 1
Sapur.005G054600.1	0.501854244	-0.778861064	0.167969653	-4.81766	1.45E-06	2.69E-06	grey	-0.35813476	2.04E-06	GO:0009231;GO:0009355;GO:0008652	AT1G74670.1	CYP-cyclophilin type II	2h;2CA-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II
Sapur.013G147000.1	16.78456938	-0.563015778	0.121635558	-4.81745	1.45E-06	2.70E-06	grey	-0.34282669	1.01E-05		AT4G03650.1	EMB2777	Sec61G/U1-dimerization/protein (Uptp) family protein
Sapur.006G055200.1	86.65415819	-0.402329465	0.085523808	-4.81693	1.46E-06	2.71E-06	grey	0.3435157	1.06E-05	GO:0016021;GO:0006810;GO:0005337	AT5G02630.1	Nucleoside transporter family protein	equilibrative nucleoside transporter
Sapur.004G093400.2	1.689960112	0.007356615	0.209275627	-4.814732	1.47E-06	2.76E-06	grey	-0.36454289	2.34E-06	GO:0050080;GO:0006633	AT4G04320.1	malonyl-CoA decarboxylase family protein	malonyl-CoA decarboxylase
Sapur.007G048300.1	60.51164671	-0.275628404	0.057526146	-4.8178	1.48E-06	2.77E-06	grey	-0.3560329	2.72E-06		AT4G27445.1		calcium ion-binding protein, putative
Sapur.016G097900.1	175.2519978	-0.793873809	0.164979186	-4.81196	1.49E-06	2.78E-06	grey	-0.30026931	0.000132982	GO:0016747	AT5G02130.1	HXXXD-type acyl-transferase family protein	BAHD acyltransferase
Sapur.003G031900.1	1659.736621	-0.87975449	0.183263168	-4.81161	1.49E-06	2.79E-06	grey	-0.37368068	1.43E-06	GO:0003924;GO:0007017;GO:0005874	AT5G05010.1	TUB5	tubulin beta 5 (TUB5)
Sapur.009G060700.1	94.64154314	-0.32146218	0.066820854	-4.81081	1.50E-06	2.79E-06	grey	-0.39328832	3.48E-07	GO:0016758;GO:0008152	AT3G30140.2	UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase, putative
Sapur.003G023600.1	2918.40263	0.157889353	0.035110185	4.810185	1.50E-06	2.79E-06	grey	-0.32789072	2.76E-05	GO:0009378;GO:0006333;GO:0006281	AAA-type ATPase family protein	AAA-type ATPase family protein	26 proteasome regulatory cyclophes, ATPase RPT4
Sapur.009G117900.1	402.8659255	0.372955404	0.077536598	4.810419	1.51E-06	2.80E-06	grey	-0.37519984	1.12E-06		AT5G45550.1	Mob1/phocein family protein	Mps one binder kinase activator-like protein 1A
Sapur.015WG121600.1	165.6246282	-0.564141763	0.117285308	-4.8102	1.51E-06	2.80E-06	grey	-0.35779163	4.21E-06		AT5G47140.1	NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase reductase
Sapur.006G176800.2	1.450759904	-0.743241395	0.154516481	-4.81012	1.51E-06	2.80E-06	grey	-0.36231835	2.07E-06		AT2G15145.1		DUF4378 domain protein
Sapur.T089100.1	2.727260275	1.070453627	0.223455613	4.808326	1.52E-06	2.81E-06	grey	0.35879299	3.94E-06	GO:0005881;GO:0000398;GO:0000387	AT5G54385.1	ARM repeat superfamily protein	NA
Sapur.T144100.1	1.067510287	1.345193027	0.279766647	4.808324	1.52E-06	2.81E-06	grey	0.34802764	7.94E-06				NA
Sapur.016G138700.1	1105.45767	0.430874011	0.089631928	4.807733	1.53E-06	2.82E-06	grey	0.31963916	4.49E-05	GO:0003676	AT5G07350.1	RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein G RNA recognition motif protein
Sapur.006G088000.1	494.7791314	-0.268489269	0.057236161	-4.80748	1.53E-06	2.84E-06	grey	-0.35452207	5.35E-06	GO:0006810;GO:0005669	AT1G10570.1	TAF12;TAFH18	TBP-associated factor TFIID subunit 12
Sapur.013G183800.1	32.12859751	-0.781614079	0.162472056	-4.80707	1.53E-06	2.84E-06	grey	-0.27419329	1.38E-06	GO:0009733	AT4G09530.1	SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.004G203300.1	0.704148552	-1.576355584	0.328522464	-4.80414	1.55E-06	2.85E-06	grey	-0.32362589	3.89E-05	GO:0004383	AT5G44080.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	BHLH transcription factor
Sapur.T109900.1	0.356183012	1.65015056	0.343505056	4.80393	1.55E-06	2.86E-06	grey	0.43527568	1.22E-08		AT3G26380.1	Melibiase family protein	NA
Sapur.016G123400.2	6.612781095	-0.399852483	0.083258492	-4.80358	1.55E-06	2.86E-06	grey	-0.34399527	2.11E-06	GO:0008168;GO:0006479	AT2G39510.1	arginine methyltransferase 11	arginine N-methyltransferase
Sapur.016G062900.1	4.613631994	-0.864889957	0.19203784	-4.80351	1.55E-06	2.86E-06	grey	-0.31996159	4.40E-05	GO:0008270;GO:0005515	AT2G35910.1	RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.006G164500.1	647.5172781	-0.177132911	0.036885454	-4.80276	1.56E-06	2.90E-06	grey	-0.38140413	8.29E-07		AT5G11760.1		EEIG1/EHBP1 protein amino-terminal domain protein
Sapur.014G104100.1	972.6767813	-0.241140145	0.05022147	-4.80147	1.57E-06	2.91E-06	grey	-0.32902347	4.82E-05	GO:0008650	AT5G07710.1	Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress protein, putative
Sapur.004G017700.1	103.8418294	0.247706305	0.051591776	4.801271	1.58E-06	2.92E-06	grey	0.33750866	1.54E-05		AT5G38500.1	Protein of unknown function (DUF581)	plant/P20M13-60 protein
Sapur.003G051200.1	49.6168824	-0.658895368	0.1361842	-4.79925	1.58E-06	2.93E-06	grey	-0.3581188	2.93E-06		AT3G44460.1	LRR and NB-ARC domains	NA
Sapur.005G051600.1	5.170494067	0.790393949	0.164738781	4.797882	1.60E-06	2.98E-06	grey	0.32746073	2.89E-05				NA
Sapur.006G139500.1	19.02888849	-0.458145227	0.087238229	-4.7972	1.60E-06	2.98E-06	grey	-0.36602646	2.58E-06	GO:0005114;GO:0016491	AT1G77730.1	ATCBR;CBR;CBR1	NADH cytochrome b5 reductase 1
Sapur.015WG067000.1	577.0714331	0.158545693	0.033039441	4.796646	1.61E-06	2.99E-06	grey	0.32131126	2.89E-05	GO:0051536;GO:0016226;GO:0005506	AT1G01110.1	SufE/NIFU family protein	iron-sulfur cluster assembly protein
Sapur.018G008600.1	30.90239697	-0.170683844	0.035762781	-4.79669	1.61E-06	2.99E-06	grey	-0.42809804	2.25E-08	GO:0005515	AT5G42360.1	transducin family protein / WD-40 repeat family protein	transducin family protein
Sapur.007G042100.1	39.61513256	0.476245971	0.099305369	4.795773	1.62E-06	2.99E-06	grey	0.29775761	0.000152259	GO:0006468;GO:0005524;GO:0004672	AT5G07080.1	MAPKKK19	MAP kinase kinase kinase 19
Sapur.008G167700.1	5.658501361	-0.540446891	0.112710676	-4.79499	1.63E-06	2.99E-06	grey	-0.38755941	5.31E-07		AT5G58970.4	HAPSC_NF-YC9	nuclear transcription factor Y subunit C-9
Sapur.011G185800.1	17.09617747	-0.681671191	0.142143	-4.79376	1.64E-06	3.01E-06	grey	-0.36631499	2.38E-06		AT3G22481.1	Cytochrome b561/ferric reductase transmembrane family protein	NA
Sapur.016G279900.1	328.6966556	1.092163932	0.22785974	4.793141	1.64E-06	3.04E-06	grey	0.35380345	5.62E-06	GO:0016829;GO:0010333;GO:0008152;GO:0000287	AT3G19660.2	ATTPS21;TPS21	terpene synthase 21
Sapur.005G073300.1	11.05282792	-0.672524167	0.09615168	-4.79311	1.64E-06	3.04E-06	grey	-0.29570819	0.000169947		AT2G31461.1	CLPP2;NCLPP7	nuclear-encoded CLP protease P7 protease P7
Sapur.006G089800.1	53.19157556	0.523661265	0.109275509	4.791779	1.65E-06	3.05E-06	grey	0.35560523	4.87E-06	GO:0055085;GO:0016021	AT3G18830.1	ATPTS;ATPMTS;PMTS	polyol/monosaccharide transporter 5
Sapur.016G155600.1	0.915455884	0.787907318	0.164249915	4.79177	1.65E-06	3.05E-06	grey	-0.39161004	1.64E-07		AT1G14200.1	alpha/beta-hydrolase family protein	epoxide hydrolase, putative
Sapur.009G111600.2	5.76476312	-0.586069698	0.12254995	-4.78964	1.67E-06	3.10E-06	grey	0.30715677	0.000122964	GO:0005089	AT4G38430.1	ATROPGEF1;ROPGEF1	Rop guanyl-nucleotide exchange factor 1
Sapur.016G239800.1	3.425852763	-0.811684663	0.176378918	-4.78905	1.68E-06	3.11E-06	grey	-0.38499345	6.40E-07				NA
Sapur.002G009400.2	25.67226599	0.531971323	0.111088661	4.788839	1.68E-06	3.11E-06	grey	-0.29321558	7.15145398	GO:0008236;GO:0005508;GO:0070008;GO:0004252	AT5G76140.1	Prolyl oligopeptidase family protein	prolyl oligopeptidase
Sapur.006G182600.1	2.820587894	-0.877957518	0.18335594	-4.78842	1.68E-06	3.11E-06	grey	-0.34986317	7.07E-06	GO:0003824;GO:0006470;GO:0004722	AT5G16560.1	Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.005G197000.1	18.25868862	-0.554524486	0.075992233	-4.78783	1.68E-06	3.12E-06	grey	-0.32169156	0.012120205	GO:0005840	AT4G22140.1	PHD Finger / bromo-adjacent homology (BAH) domain-containing protein	PHD Finger transcription factor, putative
Sapur.013G092500.1	1.203366769	2.025368	0.421112259	4.786828	1.68E-06	3.12E-06	grey	0.33167935	2.50E-05	GO:0005524;GO:0006468;GO:0005515;GO:0004672	AT5G19130.1	S-locus lectin protein kinase family protein	LM receptor-like Serine/Threonine-kinase
Sapur.009G112900.1	0.848323947	-1.523207	0.317964621	-4.78479	1.75E-06	3.26E-06	grey	-0.34787686	2.00E-06		AT4G26930.1	NF01	Ribosomal protein L21
Sapur.T140600.1	5.652228251	0.593792189	0.124100364	4.784474	1.71E-06	3.18E-06	grey	0.35260174	6.13E-06		AT5G24870.1	Helicase/SANT-associated, DNA binding protein	NA
Sapur.015WG046100.1	0.623308763	-1.87613038	0.392176123	4.783888	1.71E-06	3.18E-06	grey	0.31933233	4.57E-05				NA
Sapur.013G037400.1	711.2862828	0.18271202	0.038194246	4.783758	1.72E-06	3.19E-06	grey	0.32780587	2.77E-05		AT3G04780.1	Protein of unknown function (DUF3000)	RTH domain plant protein
Sapur.T015300.1	21.27823864	0.586605749	0.122658842	-4.78279	1.73E-06	3.20E-06	grey	-0.32279168	2.06E-05				NA
Sapur.004G124000.1	172.8946679	0.49141874	0.102753672	4.782493	1.73E-06	3.21E-06	grey	0.32274825	3.75E-05	GO:0009733	AT5G18020.1	SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.005G097300.1	11.03164692	-0.654868944	0.136878918	-4.78438	1.73E-06	3.21E-06	grey	-0.33892062	2.46E-05	GO:0005524;GO:0003824	AT1G04020.1	4-phosphopantothenoylcysteine adenylyltransferase	phosphopantothenoylcysteine adenylyltransferase
Sapur.014G125600.1	360.7843698	-0.291191757	0.06088975	-4.78157	1.74E-06	3.22E-06	grey	-0.37588703	1.12E-06	GO:0016020;GO:0006810;GO:0005215	AT5G18290.2	SIP1;2;SIP1B	Aquaporin-like superfamily protein
Sapur.016G238300.2	139.7914991	0.397705056	0.083206334	4.779745	1.76E-06	3.25E-06	grey	-0.35238329	0.515466599	GO:0005114;GO:0016491;GO:0008270	AT5G15060.1	Grx0/1-like zinc-binding alcohol dehydrogenase family protein	zinc-binding dehydrogenase, putative
Sapur.001G030300.1	1.946626111	-1.382326584	0.289211674	-4.77669	1.76E-06	3.26E-06	grey	-0.32574072	5.68E-06		AT1G22100.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/LTP family protein
Sapur.T008700.1	0.31727459	1.659613763	0.347429866	4.776831	1.78E-06	3.30E-06	grey	0.42870506	2.12E-08		AT5G51530.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3
Sapur.T149100.1	0.64600347	-1.585793597	0.41572988	-4.77662	1.78E-06	3.30E-06	grey	-0.36788376	3.66E-07		AT3G60180.1		Plant protein of unknown function (DUF247)
Sapur.001G087700.1	42.8848058	0.413540045	0.086576431	4.776424	1.78E-06	3.30E-06	grey	0.34598582	9.06E-06		AT3G46550.1	Major facilitator superfamily protein	NA
Sapur.015WG019800.1	0.036423262	-1.90320651	0.207746927	-4.77511	1.80E-06	3.33E-06	grey	-0.32268874	1.57E-05	GO:0048544;GO:0006468;GO:0005524;GO:0004672	AT3G04080.1	Protein kinase superfamily protein	NA
Sapur.009G030700.1	275.8352441	0.430351625	0.090135479	4.774498	1.80E-06	3.33E-06	grey	-0.33736360	6.74879363	GO:0008184;GO:0005975	AT5G46370.1	ATPHG2;PHG2	alpha-glucan phosphorylase, H
Sapur.003G084900.1	6.207326793	-0.780284801	0.173457129	-4.77375	1.82E-06	3.36E-06	grey	-0.36775115	2.15E-06		AT4G14560.1	Gibberellin-regulated family protein	gibberellin-regulated protein
Sapur.015WG091400.4	7.401378908	-0.916691192	0.192088098	-4.7712	1.83E-06	3.39E-06	grey	-0.23602572	1.69E-05	GO:0007264;GO:0005525	AT4G40040.1	ARACB;ATRACB;ATROP10;RI	RHO-related protein from plants 10	small GTPase
Sapur.003G026600.2	1.19687385	-0.555808891	0.123427638	-4.77112	1.83E-06	3.39E-06	grey	-0.34654576	7.38E-06		AT3G18310.1		hypothetical protein
Sapur.013G168000.2	8.02383946	-0.440626854	0.092353789	-4.77108	1.83E-06	3.39E-06	grey	-0.29258241	3.67E-07	GO:0008270	AT5G05570.1	ATRBK1;HRT1;RBK1;ROC1	RING-box protein
Sapur.018G117300.1	1.387577138	1.560593631	0.328658377	4.770907	1.83E-06	3.39E-06	grey	0.28988737	0.000229619	GO:0003247;GO:0006468;GO:0005524;GO:0004672	AT4G16120.1	WAK1	wall associated kinase-like 1
Sapur.015WG113100.1	180.618294	0.173179498	0.036201967	-4.7705	1.84E-06	3.40E-06	grey	-0.39064974	5.21E-07		AT5G04910.1		hypothetical protein
Sapur.009G130400.1	82.97513808	0.703626357	0.147499005	4.77038	1.84E-06	3.40E-06	grey	0.33746384	1.51E-05	GO:0005515	AT5G02790.1	GSTL3	glutathione S-transferase family protein
Sapur.002G139300.1	293.3331212	0.298406884	0.062572631	4.769671	1.85E-06	3.41E-06	grey	0.34180608	1.12E-05		AT3G58520.1	JB	Chaperone DnaJ-domain superfamily protein
Sapur.010G013900.2	1.318451154	0.383607665	0.227158777	-4.76856	1.86E-06	3.42E-06	grey	-0.36960923	1.89E-06		AT5G12930.1	Transducin/WD40 repeat-like superfamily protein	transducin/WD40 domain protein
Sapur.014G130300.1	202.3041825	0.331365854	0.069488573	4.767199	1.87E-06	3.44E-06	grey	0.30980707	1.16E-05	GO:0005515	AT2G44840.1	Leucine-rich repeat (LRR) family protein	receptor-like kinase
Sapur.016G159600.3	22.10922569	-0.429141224	0.090018768	-4.76694	1.87E-06	3.46E-06	grey	-0.35497243	5.07E-06		AT5G12240.1		hypothetical protein
Sapur.015WG068600.1	2.066664831	-1.178255491	0.247185218	-4.76669	1.87E-06	3.46E-06	grey	-0.34717196	7.46E-06				NA
Sapur.006G147900.1	311.6434748	-0.170343353	0.03573836	-4.7664	1.88E-06	3.46E-06	grey	-0.37315583	1.48E-06	GO:0005515;GO:0003723	AT5G57870.2	eIFiso4G1	MIF4G domain-containing protein / MA3 domain-containing protein
Sapur.012G380800.2	25.92069697	0.403061561	0.084568913	4.766185	1.88E-06	3.47E-06	grey	0.16971692	0.033587333	GO:0005515	AT3G12225.2	WW domain-containing protein	WW domain protein, putative
Sapur.017G054200.1	2.045691614	-1.142342221	0.239684293	-4.76082	1.88E-06	3.48E-06	grey	-0.38255138	7.61E-07		AT5G07010.1	GRAS family transcription factor	GRAS family transcription factor
Sapur.018G005800.1	54.06517052	0.333373493	0.069976821	-4.76405	1.90E-06	3.51E-06	grey	-0.35367294	3.76E-06		AT5G06320.2	Translation elongation factor EF1A/initiation factor IF2/gamma family protein	translation elongation factor EF-1alpha
Sapur.015WG010000.1	1.135580207	-0.610663109	0.128066204	-4.76384	1.91E-06	3.51E-06	grey	-0.36154205	2.57E-06		AT5G15150.1	DNA heat shock N-terminal domain family protein	Dnaj family protein
Sapur.007G076900.1	8.316709176	0.584260091	0.122675051	4.762664	1.91E-06	3.52E-06	grey	0.31803018	1.86E-05		AT4G14540.1	NF-YB3	nuclear transcription factor Y subunit B-3
Sapur.016G261500.1	22.94039995	0.482647702	0.101358555	4.76179	1.92E-06	3.54E-06	grey	-0.35401705	5.20E-06	GO:0015743	AT5G08440.1	Aluminum activated malate transporter family protein	aluminum activated malate transporter
Sapur.018G091900.1	0.514850609	1.763564497	0.370745277	4.761417	1.92E-06	3.54E-06	grey	0.39463249	3.14E-07	GO:0005515	AT5G74190.1	ARIA;FLS;RLP15	receptor like protein 15
Sapur.008G278300.1	1.883842403	0.924896651	0.19369227	4.76032	1.93E-06	3.57E-06	grey	0.39064974	5.21E-07		AT5G04410.1	Ubiquitin-like superfamily protein	autophagy-related protein 8h
Sapur.016G269100.1	2024.943678	0.210752969	0.044272988	4.760305	1.93E-06	3.57E-06	grey	0.31484319	5.02E-05		AT5G64750.1	ATDSS1;;DSS1;I1	deletion of SUV3 suppressor 10
Sapur.016G304300.1	95.73368688	0.293883557	0.06263517	4.690671	1.94E-06	3.58E-06	grey	0.34218008	1.11E-05		AT3G52820.1	O-acyltransferase (WSD1-like) family protein	O-acyltransferase (WSD1-like) family protein
Sapur.016G061800.1	1618.095776	-0.23318522	0.048993394	-4.75562	1.94E-06	3.59E-06	grey	-0.37758814	1.09E-06		AT5G06390.1	FLA17	FASCICLIN-like arabinogalactan protein 17 precursor
Sapur.006G241900.1	116.996831	0.252401709	0.053028112	4.75944	1.94E-06	3.59E-06	grey	0.32284638	3.63E-05		AT5G19370.1	ASAT1;ATASAT1;ATSAT1	acyl-CoA sterol acyl transferase 1
Sapur.010G194200.1	2.326614179	0.603315641	0.193188217	4.757947	1.96E-06	3.63E-06	grey	0.31828057	4.68E-05		AT5G47740.1	Protein of unknown function (DUF2849)	DUF2849 family protein
Sapur.003G146400.1	4.382898048	1.075735966	0.226095711	4.757879	1.96E-06	3.63E-06	grey	0.26536609	0.000982443	GO:0042546;GO:0016020;GO:0008107	AT3G02320.1	ATFT1;ATFUT1;FT1;MUR2	fucosyltransferase 1
Sapur.016G244000.1	54.1939607	0.611284128	0.129482519	4.757783	1.96E-06	3.63E-06	grey	-0.3575128	4.29E-06		AT3G61680.1	NA	NA
Sapur.006G069000.6	2.393926061	0.895598489	0.188243994	4.757647	1.96E-06	3.62E-06	grey	0.07730491	0.136120979	GO:0005515	AT4G34910.1	ATPRMD4;PRMD4	pre-mRNA-processing protein 40A
Sapur.T018500.1	1.053373447	0.734758885	0.154461807	4.756754	1.97E-06	3.64E-06	grey	0.35189816	4.80E-06	GO:0008374;GO:0016410;GO:0004144	AT4G00480.1	membrane bound O-acyltransferase (MBOAT) family protein	dioxylglycerol O-acyltransferase
Sapur.004G269300.1	72.08516826	-0.417630835	0.087601387	-4.75564	1.97E-06	3.64E-06	grey	-0.40497519	1.43E-07		AT4G09360.1	Plant protein of unknown function (DUF863)

Sapur.006G034900.1	311.0838605	0.25701007	0.05117887	4.67462	2.94E-06	5.39E-06	grey	0.352331168	6.03E-06	GO:0055114 GO:0051287 GO:0046168 GO:0016616 GO:0005975 GO:0004367 GO:0050833	ATG04154B.2	GPDHC1	G-phosphoglycerate dehydrogenase family protein	glycerol-3-phosphate dehydrogenase [NAD+]1, cytosolic proteinh2C putative		
Sapur.009G096600.1	3.018887871	0.187445308	0.200566599	4.673915	2.94E-06	5.41E-06	grey	0.322985826	3.69E-05		ATG06350.1	SHI	Lateral root primordium (LRP) protein related	lateral root primordium-like protein, putative		
Sapur.017G037900.1	128.5677916	0.280219516	0.059598405	4.673566	2.94E-06	5.42E-06	grey	0.327880809	0.01295	GO:0005515 GO:0006468 GO:0005524 GO:0004672	ATG08480.1	RKL1	receptor-like kinase 1	inactive receptor kinase, putative		
Sapur.010G020300.1	69.9186462	0.588295681	0.125893643	4.67296	2.97E-06	5.46E-06	grey	-0.347457967	8.24E-06		ATG18670.1		Ankyrin repeat family protein	inversin, putative		
Sapur.003G363000.1	3.103960314	0.764100398	0.163032834	4.67327	2.96E-06	5.45E-06	grey	-0.36522355	2.56E-06	GO:0006355 GO:0003700	ATG25180.1		Integrase-type DNA-binding superfamily protein	ethylene-responsive transcription factor ERF003		
Sapur.006G020500.1	173.0688106	0.519198287	0.11113986	4.671576	2.99E-06	5.47E-06	grey	0.315275987	5.77E-05	GO:0006508 GO:0004197	ATG04200.1	AtMC9,MC9	metacaspase 9	ICE-like protease (caspase) p20 domain protein		
Sapur.002G189600.1	21.40039084	0.389486262	0.083377739	4.67135	2.99E-06	5.48E-06	grey	-0.316473877	5.28E-05	GO:0006412 GO:0005840 GO:0005622 GO:0003735	ATG62990.1		Ribosomal protein S30 family protein	40S ribosomal protein S30		
Sapur.7125800.1	0.548758526	4.46576131	0.954507461	4.67309	3.00E-06	5.49E-06	grey	-0.343315543	1.08E-05	GO:0006412 GO:0005840 GO:0005622 GO:0003735	ATG60800.1		Nucleic acid-binding, OB-fold-like protein	Nucleic acid-binding, OB-fold-like protein		
Sapur.016G116800.1	2231.957439	-0.37325465	0.080345826	-4.67049	3.00E-06	5.50E-06	grey	-0.366168756	2.40E-06	GO:0055114 GO:0016491 GO:0005507	ATG25105.1		Plant L-ascorbate oxidase	L-ascorbate oxidase		
Sapur.005G140300.1	12.48129544	-2.06919224	0.443183657	-4.67069	3.00E-06	5.51E-06	grey	-0.325318231	4.13E-05	GO:0055114 GO:0016020 GO:0005524	ATG46700.1	ATCRK1,CRK3	CDPK-related kinase 3	CDPK-related kinase		
Sapur.016G156100.1	1.230717655	1.550801517	0.332005582	4.660802	3.04E-06	5.57E-06	grey	0.29461265	0.000184407	GO:0055114 GO:0020037 GO:0016705 GO:0005506	ATG12740.1	CYP742	cytochrome P450, family 87, subfamily A, polypeptide 2	NA		
Sapur.003G179100.1	14.58128848	0.876560204	0.190261865	4.661446	3.10E-06	5.67E-06	grey	0.3547062	1.51E-06					transmembrane protein, putative		
Sapur.016G282300.1	251.3552814	0.166406905	0.035681491	4.663676	3.11E-06	5.68E-06	grey	0.338692198	1.43E-05	GO:0055114 GO:0016671 GO:0005783 GO:0003756	ATG72280.1	AERO1,ERO1	endoplasmic reticulum oxidoreductas 1	endoplasmic oxidoreductin protein		
Sapur.003G181100.2	7.518842276	0.152087867	0.03259887	4.6628	3.13E-06	5.71E-06	grey	0.32605419	0.00		ATG07520.1		Phosphoinositide phosphatase family protein	transmembrane protein, putative		
Sapur.018G227900.1	0.470924038	1.67152088	0.358517557	4.66234	3.13E-06	5.72E-06	grey	0.380952921	8.56E-07	GO:0055114 GO:0016491	ATG33550.1	ATGA2OX1,GA3OX1,GA4	gibberellin 2-oxidase 1	gibberellin 3-beta hydroxylase		
Sapur.006G260600.1	60.35929659	0.614321206	0.091015876	4.66234	3.13E-06	5.72E-06	grey	0.325152542	3.78E-05	GO:0004574 GO:0048544 GO:0006458 GO:0004672	ATG11328.1		S-lectin lectin protein kinase family protein	S-lectin lectin protein kinase family		
Sapur.006G236500.1	50.34667221	-0.607538028	0.130384225	-4.66117	3.14E-06	5.75E-06	grey	-0.343914535	1.03E-05		ATG14460.1		LRR and NB-ARC domains-containing disease resistance protein	NA		
Sapur.004G001900.1	2.07838006	1.080996531	0.231922972	4.661051	3.15E-06	5.76E-06	grey	0.352003057	6.56E-06		ATG35810.1		Ankyrin repeat family protein	transmembrane protein, putative		
Sapur.7156380.1	0.353643475	1.756358021	0.335479302	4.657149	3.17E-06	5.78E-06	grey	0.380302471	9.75E-07		ATG15110.1	CYP97B3	cytochrome P97, subfamily B, polypeptide 3	NA		
Sapur.005G146400.1	6.340215525	0.613940395	0.131730789	4.660569	3.15E-06	5.77E-06	grey	0.365943317	2.44E-06		ATG31450.1	SCL1	SCARECROW-like 1	GRAS family transcription factor		
Sapur.009G055900.1	218.9613895	0.25427524	0.054611176	4.65577	3.16E-06	5.79E-06	grey	0.31268684	6.68E-05		ATG29910.1			reactive oxygen species modulator 1		
Sapur.7163500.1	1.304814962	-1.46375452	0.314919254	-4.65943	3.17E-06	5.80E-06	grey	-0.352034652	6.15E-06					NA		
Sapur.016G268200.2	1.502043331	1.175357768	0.252273427	4.656058	3.18E-06	5.81E-06	grey	0.210004186	0.019757668		ATG03120.1			hypothetical protein		
Sapur.003G179900.1	7.63614568	0.587859156	0.126237236	4.65678	3.21E-06	5.87E-06	grey	-0.336495377	1.64E-05		ATG05065.1	CLE20	CLAVATA/ESR-RELATED 20	hypothetical protein		
Sapur.003G133900.8	5.328832284	0.555759681	0.119339502	4.656643	3.21E-06	5.88E-06	grey	0.352670234	6.34E-06	GO:0042578 GO:0016090 GO:0003993	ATG02024.1		Phosphoinositide phosphatase family protein	phosphoinositide phosphatase		
Sapur.016G093300.4	25.10743478	0.296280935	0.063610078	4.654144	3.25E-06	5.95E-06	grey	0.377208836	1.12E-05		ATG08370.1	ARG1	Chaperone DnaJ-domain superfamily protein	chaperone protein DnaJ		
Sapur.003G339100.1	387.4749808	0.184289486	0.039609563	4.652651	3.28E-06	5.99E-06	grey	0.346842057	8.53E-06	GO:0006887 GO:0000145	ATE0D7D01,END7D03		exocyst subunit exo70 family protein f3	exocyst subunit exo70-D1		
Sapur.005G073300.1	123.9673873	0.556144079	0.119514493	4.651661	3.29E-06	6.01E-06	grey	0.307321154	0.0465		ATG16925.1		Vacuolar transport factor 2 (VPT2) family protein	F-box protein SKIP8		
Sapur.016G291600.1	0.820663368	-1.530369986	0.329108287	-4.65008	3.32E-06	6.06E-06	grey	-0.353045454	5.94E-06	GO:0055114 GO:0016491 GO:0005507	ATG60020.1	ATLAC17,LAC17	laccase 17	laccase		
Sapur.7047100.1	1.371378661	0.618800208	0.1767281	4.64996	3.32E-06	6.07E-06	grey	-0.313874393	6.25E-05					NA		
Sapur.016G198700.1	1.850762645	-1.058759894	0.227591891	-4.64956	3.33E-06	6.08E-06	grey	-0.365008873	2.60E-06		ATG02030.1		transferases, transferring acyl groups other than amino-acyl group;acyltransferases	NA		
Sapur.006G131000.1	3.364216604	0.457867869	0.166493443	4.64918	3.34E-06	6.09E-06	grey	-0.316970944	3.46E-05	GO:0030127 GO:0008270 GO:0006888 GO:0006886	ATG41670.1		Sec23/Sec24 protein transport family protein	protein transporter Sec23		
Sapur.004G015300.1	1.404455884	1.199723984	0.258077484	4.648732	3.34E-06	6.10E-06	grey	0.322716329	3.75E-05	GO:0006468 GO:0004672	ATG05200.1	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	cysteine-rich receptor-like kinase		
Sapur.016G218000.3	18.76831224	0.417468796	0.089859219	4.64809	3.35E-06	6.12E-06	grey	0.328164428	2.76E-05	GO:0005515	ATG25160.1		F-box family protein	F-box protein		
Sapur.003G161600.1	5.629425633	0.781674183	0.168257954	4.645689	3.39E-06	6.19E-06	grey	0.310778826	7.45E-05		ATG47190.1	ATMYB2,MYB2	myb domain protein 2	Myb-like transcription factor Myb protein		
Sapur.014G105100.4	4.852866028	0.472227611	0.101632838	4.645042	3.39E-06	6.20E-06	grey	-0.433127149	1.47E-08		ATG24585.1		2-oxoglutarate(2OG) and Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate(2OG) and Fe(II)-dependent		
Sapur.010G036700.1	0.746571226	-1.763444414	0.384016398	-4.64419	3.41E-06	6.24E-06	grey	-0.364862707	2.62E-06		ATG50160.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative		
Sapur.013G296400.1	102.9873562	0.321828854	0.069299422	4.644	3.42E-06	6.26E-06	grey	-0.340308067	1.32E-05	GO:0005515	ATG10000.2		Thioredoxin family protein	glutathione S-transferase, amino-terminal domain protein		
Sapur.013G095000.1	1047.712898	0.152748884	0.033174654	4.64032	3.43E-06	6.25E-06	grey	-0.335624749	1.78E-05	GO:0009116 GO:0003824	ATG26190.1		Phosphoserine aminotransferase family protein	bark storage protein, putative		
Sapur.006G115400.1	48.09054955	0.315611215	0.067692931	-4.64251	3.44E-06	6.29E-06	grey	-0.318345488	5.28E-05		ATG08930.1	ACT7	actin 7	actin		
Sapur.006G093500.1	96.6508777	0.554545482	0.119124684	4.641475	3.45E-06	6.31E-06	grey	0.329291253	3.51E-05		ATG42120.1	SCR,SCR1	GRAS family transcription factor	GRAS family transcription factor		
Sapur.013G105200.1	215.7556607	0.218185303	0.047014448	4.640814	3.47E-06	6.34E-06	grey	0.345161265	9.34E-06	GO:0006468 GO:0004672	ATG16670.1		Protein kinase superfamily protein	tyrosine kinase domain protein		
Sapur.001G178600.1	1.138608457	0.732279139	0.158061239	4.63967	3.48E-06	6.37E-06	grey	0.337838399	1.51E-05	GO:0016787	ATG18840.2	EDF2,RAP2.8,RAV2,TEM2	radiation sensitive E2 (RTE2) family protein	B1-DNA-binding domain protein		
Sapur.007G057700.1	30.52918701	-0.468703962	0.101570545	-4.63942	3.48E-06	6.38E-06	grey	-0.424605497	3.03E-08	GO:0016998 GO:0006032 GO:0004568	ATG21500.1	ATHCHI8,B-CHI,CHI-B,JHCHI	basic chitinase	chitinase		
Sapur.7046100.1	110.6793605	0.290061616	0.062760627	4.63849	3.49E-06	6.39E-06	grey	-0.338890654	1.10E-05	GO:0016758 GO:0008152 GO:0003824 GO:0005975	ATG07020.2		UDP-Glycosyltransferase superfamily protein	UDP-glucose:sterol glucosyltransferase		
Sapur.008G113100.1	14.28803388	0.518831842	0.111834425	-4.63929	3.50E-06	6.38E-06	grey	-0.360797272	3.45E-06	GO:0008017 GO:0009910 GO:0000226	ATG03910.1	ATMAPRE-6,MAPRE-6	Microtubule associated protein (MAPRE/AGE1) family protein	microtubule-associated protein, putative		
Sapur.013G089400.1	154.8481616	0.250417411	0.053960759	4.63815	3.52E-06	6.42E-06	grey	-0.361798407	2.50E-06		ATG46900.1	ATMEK12,MEK12	methyl esterase 12	polyneuridine-aldehyde esterase		
Sapur.004G147200.3	14.91521803	0.387160203	0.08348817	4.637304	3.53E-06	6.44E-06	grey	-0.378807559	0.024235426	GO:0005515	ATG03740.1	ATBPM4,BPM4	BTB-POZ and MATH domain 4	BTB-POZ and MATH domain protein		
Sapur.009G091200.2	48.52635565	0.314966384	0.067934183	4.636342	3.55E-06	6.47E-06	grey	0.369704275	1.89E-06	GO:0005515 GO:0007165	ATG34660.1	AGB1,ATGB1,JLB1K	G/TP binding protein beta 1	guanine nucleotide-binding protein subunit beta		
Sapur.019G144800.4	0.6060898	-4.448366261	0.912435863	-4.63572	3.56E-06	6.48E-06	grey	-0.362036486	0.436340005	GO:0005515	ATG36810.2		SWI/SNF/NAP superfamily protein	SWI/SNF/NAP domain protein		
Sapur.019G021500.1	66.134744	0.527461142	0.115945547	4.635289	3.56E-06	6.50E-06	grey	0.348984123	1.24E-05	GO:0007165 GO:0005515 GO:0043531	ATG36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA		
Sapur.016G141800.1	11.98718208	0.523393025	0.112960605	4.63488	3.57E-06	6.51E-06	grey	-0.353884604	4.78E-06					hypothetical protein		
Sapur.008G091600.1	178.0270979	0.263504829	0.056860277	-4.63425	3.58E-06	6.54E-06	grey	-0.40227208	1.77E-07		ATG04990.1	ATSUN1,SUN1	SAD1/UNC-84 domain protein 1	Sad1/unc-like protein		
Sapur.001G187100.1	173.4154737	0.227502884	0.050833168	4.633223	3.60E-06	6.57E-06	grey	0.33341603	2.01E-05		ATG17120.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein		
Sapur.011G077800.1	341.940981	0.197022323	0.042541768	4.633148	3.60E-06	6.57E-06	grey	0.330315519	2.43E-05		ATG17160.1		pfkB-like carbohydrate kinase family protein	PfkB-type carbohydrate kinase family protein		
Sapur.016G241000.2	1.059913868	0.222352397	0.1326543	4.632105	3.61E-06	6.58E-06	grey	-0.363833139	2.85E-06		ATG34663.1			plant/TIR/CC-21 protein, putative		
Sapur.001G102400.1	162.6768897	0.332994681	0.071876945	4.632844	3.61E-06	6.58E-06	grey	0.309070793	8.20E-05	GO:0005885 GO:0016021	ATG47420.1	ATPS1,PS3	phosphate starvation-induced gene 3	glycerol-3-phosphate transporter		
Sapur.012G082600.1	362.6853011	0.280739105	0.060509719	-4.63368	3.61E-06	6.58E-06	grey	-0.303861371	0.000109918	GO:0017009	ATG51020.1	CRL	crumpled leaf	crumpled LEAF protein		
Sapur.016G208800.1	0.528701153	-0.276192437	0.374047175	-4.63209	3.62E-06	6.60E-06	grey	-0.363954578	2.79E-06		ATG27440.1			NA		
Sapur.019G089900.1	293.9499994	0.796491847	0.171987352	4.631107	3.64E-06	6.63E-06	grey	0.277388869	0.000425863	GO:0008061 GO:0016998 GO:0006032 GO:0004568	ATG54420.1	ATCHITIV,ATEP3,CHIV,EP3	homolog of carrot EP3-3 chitinase	class IV chitinase		
Sapur.011G082000.1	854.4481416	0.242077411	0.05996628	4.63087	3.64E-06	6.64E-06	grey	-0.383807781	1.68E-07	GO:0004854	ATG45190.1	AHL2,ATAHL2	AT-hook motif containing protein	F1F3/E2C5-biophosphate nucleotidase		
Sapur.15W0G0030300.1	375.7792614	0.495806190	0.107392109	4.630517	3.65E-06	6.65E-06	grey	0.276599478	0.024235426	GO:0005515	ATG23460.1	LSU2	response to low sulfur 2	hypothetical protein		
Sapur.016G150600.1	438.3104064	0.619376336	0.09050887	4.63046	3.65E-06	6.66E-06	grey	0.279924276	0.033388064	GO:0005515 GO:0050665 GO:0016491	ATG34790.1	ED1,ER,NRE123	FAD-binding Berberine family protein	reticuline oxidase, putative		
Sapur.7086500.1	365.2639899	0.207839543	0.044927648	-4.62609	3.73E-06	6.79E-06	grey	-0.349654874	7.21E-06		ATG23890.1			NA		
Sapur.005G111000.1	70.56182825	0.425854164	0.092034864	-4.62532	3.74E-06	6.80E-06	grey	-0.352867276	5.61E-06		ATG28720.2		Homeodomain-like superfamily protein	Myb-like DNA-binding domain protein		
Sapur.012G058000.1	2.102016723	-1.285642409	0.279488901	-4.62546	3.74E-06	6.81E-06	grey	-0.315749666	5.62E-05		ATG29180.1			hypothetical protein		
Sapur.003G011300.1	58.78994131	0.150881928	0.110239346	4.625316	3.76E-06	6.85E-06	grey	-0.305269666	0.000103548		ATG76030.1			syringolide-induced protein 14-1-1, putative		
Sapur.013G100900.1	6.458578896	-0.567466654	0.122607553	-4.62476	3.75E-06	6.84E-06	grey	-0.354375471	5.28E-06	GO:0016020 GO:0008810 GO:0005215	ATG22540.1		Major facilitator superfamily protein	NA		
Sapur.006G085400.1	0.808831007	-1.406488961	0.306159038	-4.62412	3.76E-06	6.86E-06	grey	-0.324206622	1.88E-05		ATG02650.2		Tautomerase/MIF superfamily protein	macrophage migration inhibitory factor family protein		
Sapur.004G283200.2	0.805367753	1.477179266	0.318552297	4.623143	3.76E-06	6.86E-06	grey	0.343192135	1.08E-05		ATG31191.1			hypothetical protein		
Sapur.016G177000.1	23.4745887	-0.650370802	0.140609072	-4.62368	3.79E-06	6.90E-06	grey	-0.339808141	1.31E-05		ATG06060.1		NADP(H-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase family protein		
Sapur.005Z078400.2	1.068139302	0.567184634	0.123163627	4.623346	3.79E-06	6.91E-06	grey	-0.352696818	6.12E-06		ATG26610.1			hypothetical protein		
Sapur.007G041900.1	417.0217561	0.259388855	0.056125296	-4.6216	3.81E-06	6.94E-06	grey	-0.4351891	1.42E-08		ATG7041900	RALR,34	raf-like 34	rapid alkalinization factor		
Sapur.016G254700.1	0.458873544	1.646889491	0.356359586	4.621132	3.81E-06	6.95E-06	grey	-0.419732164	4.46E-08		ATG27321.1		Regulator of IgsA activity in the MVIB pathway protein	NA		
Sapur.009G099400.1	1073.151249	0.176181032	0.038215459	-4.62067	3.83E-06	6.97E-06	grey	-0.392149698	3.69E-07		ATG21250.1		NADP(H-linked oxidoreductase superfamily protein	NADP-dependent D-sorbitol-6-phosphate dehydrogenase		
Sapur.003G111200.5	19.05811884	0.372822179	0.080809443	-4.61988	3.84E-06	6.99E-06	grey	-0.353307658	4.98E-06	GO:0005515	ATG2060B.3	ATCSN7,COP15,CSN7,FUSS	Signalosome (PCI) domain containing protein	COP9 complex subunit 7a		
Sapur.004G113100.1	142.5328312	0.197851026	0.042829144	4.619542	3.85E-06	7.01E-06	grey	0.418327769	5.10E-08	GO:0005515	ATG18860.1		transducin family protein / WD-40 repeat family protein	NA		
Sapur.7106500.1	1.89361693	1.060883377	0.231418892	4.619299	3.85E-06	7.01E-06	grey	0.337799217	1.51E-05		ATG42530.1			NA		
Sapur.004G050900.1	21.14120459	-0.512705738	0.110535651	-4.61914	3.85E-06	7.02E-06	grey	-0.331519774	2.22E-05	GO:0006468 GO:0004672	ATG24010.1		Protein kinase superfamily protein	receptor-like kinase, putative		
Sapur.009G121600.3	6.361663483	0.520770465	0.112745549	-4.61907	3.85E-06	7.02E-06	grey	-0.33845547	1.01E-05	GO:0012792 GO:0005634 GO:0005515 GO:0008280 GO:0007064 GO:0006628	ATG27170.2	SMC3,TTN7	Structural maintenance of chromosomes (SMC) family protein	structural maintenance of chromosomes protein		
Sapur.004G283900.1	2.906074899	0.859575935	0.185178219	4.618806	3.86E-06	7.04E-06	grey	0.353117766	5.78E-06		ATG27141.1			hypothetical protein		
Sapur.003G145900.2	1.892518884	0.939462081	0.203433162	-4.61804	3.87E-06	7.05E-06	grey	-0.375890904	1.21E-06		ATG12390.1		Nascent polypeptide-associated complex (NAC), alpha subunit family protein	nascent polypeptide associated complex protein alpha		
Sapur.005G030900.1	4.609869313	1.645461661	0.356132569	4.617815	3.88E-06	7.07E-06	grey	0.367364177	2.04E-06					NA		
Sapur.004G097300.1	415.98944	0.121766377	0.026385586	4.614882	3.93E-06	7.16E-06	grey	0.341288117	1.22E-05	GO:0008270 GO:0005975 GO:0004476 GO:0009298	ATG07070.1	DINS,PMI2	Mannose-6-phosphate isomerase, type I	mannose-6-phosphate isomerase		
Sapur.016G160600.1	1313.746802	0.305829764	0.077119865	4.610983	3.94E-06	7.18E-06	grey	0.291239219	0.002232337		ATG27160.1		Sec14p-like phosphatidylinositol transfer family protein	divergent CRAL/TRIO domain protein		
Sapur.012G029600.4	0.542984676	-1.663303761	0.360481505	-4.61384	3.95E-06	7.20E-06	grey	-0.232327624	0.003279383					monoamine-oxidase A repressor R1 zf-AEMK-R1: zinc-finger protein	NA	
Sapur.013G265500.1	0.851712925	-1.567254014	0.342154154	-4.61349	3.96E-06	7.21E-06	grey	-0.331123988	6.12E-05		ATG19930.1	ATCHS,CHS,TT4	Chalcone and stilbene synthase family protein	chalcone synthase family protein		
Sapur.15W0G2140900.1	3.287954981	-0.1057452	0.220246149	-4.61185	3.99E-06	7.27E-06	grey	-0.338152022	1.48E-05		ATG45470.1		Protein of unknown function (DUF594)	transmembrane protein, putative		
Sapur.017G208900.1	1305.798351	0.230025257	0.05000891	-4.61165	3.99E-06	7.27E-06	grey	-0.373224331	1.72E-06		ATG64270.1		splicing factor, putative	splicing factor 3B subunit 1		
Sapur.15W0G4410280.1	14.51754549	-0.650570066	0.141160363	-4.6095	4.04E-06	7.35E-06	grey	-0.310256558	1.76E-05	GO:0006355 GO:0005634 GO:0003700 GO:0004881,GO:0003677	AGL42,AGL42	AGAMOUS-like 42	MADS box transcription factor	MADS box transcription factor		
Sapur.009G117700.1	6.313657293	0.902026611	0.195731877	4.608481	4.06E-06	7.38E-06	grey	0.318211164	4.85E-05					NA		
Sapur.015G000500.1	5.930059446	0.579011305	0.125680415	4.607746	4.07E-06	7.41E-06	grey	0.354381046	2.75E-06					hypothetical protein		
Sapur.016G102000.1	95.19623461	0.458326576	0.099512991	4.607706	4.07E-06	7.41E-06	grey	0.384053832	6.85E-07		ATG01060.1		myb-like HTH transcriptional regulator family protein	Myb-like DNA-binding domain protein		
Sapur.015G129600.1	64.92867	0.656829752	0.09068831	4.607211	4.08E-06	7.42E-06	grey	0.283413117	0.000172119	GO:0008270 GO:0005515	ATG26800.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein		
Sapur.015G149100.4	3.699149888	-0.663322003	0.143562319	-4.60689	4.09E-06	7.44E-06	grey	-0.311347806	1.61E05801	GO:0006355 GO:0005634 GO:0003602 GO:0003677	HMGB1,NFD1	HMGB1,NFD1	high mobility group B1	high mobility group B protein		
Sapur.006G227400.2	1.765988863	1.005042166	0.218277187	4.604271	4.09E-06	7.44E-06	grey	0.331642402	0.694006694		ATG22440.1		Plant Tudor-like RNA-binding protein	agenet domain protein		
Sapur.009G028000.1	16.25558593	-0.480678827	0.10435071	-4.60638	4.10E-06	7.46E-06	grey	-0.349907089	7.02E-06		ATG41200.1			hypothetical protein		
Sapur.013G082500.1	116.8655559	-0.353127226	0.076822723	-4.60207564	4.65E-7	4.61E-06	grey	-0.358806563	1.37E-06		ATG44820.2			DUF4402 domain protein		
Sapur.003G172200.1	113.1993511	-0.518530882	0.112591378	-4.60549	4.12E-06	7.48E-06	grey	-0.343435314	1.01E-05					NA		
Sapur.004G245800.1	100.7881973	-0.863460882	0.187538372	-4.60467	4.13E-06	7.51E-06	grey	-0.347397966	8.28E-06	GO:0005515 GO:0006468 GO:0005524 GO:0004672	ATG46330.1	FLS2	Leucine-rich receptor-like protein kinase family protein	NA		
Sapur.016G291100.1	12.02450034	-0.572171336	0.124077938	-4.60405	4.14E-06	7.53E-06	grey	-0.347479751	8.24E-06		ATG46520.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA		
Sapur.017G129000.1	8.817994223	1.124895921	0.244306358	4.603924	4.17E-06	7.58E-06	grey	0.29497714	0.000176612	GO:0006872 GO:0030001	ATG01490.1		Heavy metal transport/detoxification superfamily protein	metal ion-binding protein, putative		
Sapur.15W0G1220280.3	6.651175208	-0.506184477	0.10998137	-4.60243	4.18E-06	7.59E-06	grey	-0.322268988	3.78E-05	GO:0008168 GO:0006139	ATG69680.1	EMB1691	Methyltransferase PMT-470 family protein	methyltransferase 8 family protein		
Sapur.012G082000.2	32.89145229	0.300638828	0.065337091	4.602054	4.18E-06	7.61E-06	grey	0.345293383	9.17E-06	GO:0003674	ATG30480.1	DRT111	D111/G-patch domain-containing protein	DNA-damage-repair/toleration protein DRT111, putative		
Sapur.015G117700.2	0.720140001	-0.7368721	0.163617806	-4.6188	4.19E-06	7.63E-06	grey	0.00511192	0.943167317	GO:0007165 GO:0005515 GO:0005515,GO:0003924,GO:0019398,GO:0009584	ATG18790.1	HF1,OOP1,PHYB	phytochrome B	phytochrome B protein		
Sapur.011G117800.1	63.475879	1.218117046	0.264730214	4.601353	4.20E-06	7.64E-06	grey	-0.265408847	0.000781287	GO:0055114 GO:0050660 GO:0016491	ATG44390.1		FAD-binding Berberine family protein	reticuline oxidase		
Sapur.015G075000.1	15.24806633	0.279055575	0.060642953	4.601	4.20E-06	7.64E-06	grey	-0.364008861	0.000762289		ATG46645.1			FAD-binding protein		
Sapur.019G222100.1	80.8727939	0.563675071	0.125233932	4.600564	4.21E-06	7.66E-06	grey	0.324545499	3.37E-05		ATG41180.1		VQ motif-containing protein	NA		
Sapur.012G280500.1	149.4484052	-0.436042809	0.094815281	-4.59888	4.25E-06	7.72E-06	grey	-0.348638285	7.65E-06	GO:0016020	ATG50740.1		Transmembrane proteins 14C	NA		
Sapur.012G097600.2	0.493995884	2.070581852	0.452145431	4.598854	4.25E-06	7.72E-06	grey	0.303556136	6.88E-06	GO:0055114 GO:0016491 GO:0010181	ATG09260.1	ATOPR2,OPR2	12-oxophytodienoate reductase 2	hetwuol dehydrogenase 3 hydrolase domain protein		
Sapur.008G077700.1	11.12813353	0.904697938	0.131491442	4.598762	4.25E-06	7.72E-06	grey	-0.392060705	3.81E-07	GO:0003881 GO:0003677 GO:0006355 GO:0005634 GO:0003700	ATG68120.1	AGL7,AP1	K-box region and MADS-box transcription factor family protein	MADS box transcription factor APETALA 1		
Sapur.016G184800.1	12.63367904	0.273837794	0.059718975	4.597966	4.25E-06	7.73E-06	grey	0.363159144	2.36E-06		ATG61980.1			DUF247 domain protein		
Sapur.010G102000.1	749.8781759	0.137751441	0.029692227	4.598144	4.26E-06	7.75E-06	grey	0.321840204	6.11E-05		ATG60560.1		NADP(H-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase family protein		
Sapur.016G208300.1	13.83139908	0.529203833	0.115178879	4.59664	4.26E-06	7.76E-06	grey	0.32348204	3.60E-05		ATG41250.1		Histone2 deacetylase complex (HAD) superfamily protein	hetwuol dehydrogenase 3 hydrolase domain protein		
Sapur.006G090600.1	8.860742444	0.687485817	0.14961519	4.595027	4.33E-06	7.86E-06	grey	0.341102313	1.22E-05	GO:0016021 GO:0006952	ATM4,OsML4,ML04		Seven transmembrane MLO family protein	NA		
Sapur.004G246200.1	160.7543104	0.267188154	0.058206643	4.593765	4.35E-06	7.91E-06	grey	-0.109016582	0.739874599	GO:0005515 GO:0005839 GO:0004298	ATG46960.1	PBA1	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	proteasome subunit beta type protein		
Sapur.005G062500.3	1.801384799	-0.000188139	0.217762248	-4.59273	4.37E-06	7.96E-06	grey	-0.204978253	0.019016755	GO:0005515	ATG22125.1	CSI1	binding	cellulose synthase-interactive protein		
Sapur.006G370300.1	8.578130094	0.427423571	0.093128449	4.592	4.37E-06	7.96E-06	grey	-0.306404607	9.26E-05	GO:0005515	ATG11540.1

Sapur.01G0206300.1	3.79321624	-6.62306852	0.137712743	-5.1713	6.27E-06	1.13E-05	grey	-0.31202873	5.60E-05				NA
Sapur.01G0122600.1	310.1587897	6.14413646	0.031912238	4.517049	6.27E-06	1.13E-05	grey	0.35085218	6.63E-06	GO:0046983	ATSG05805.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	bHLH transcription factor, putative
Sapur.01G0595100.1	251.3133613	6.36539487	0.08082149	4.51626	6.28E-06	1.13E-05	grey	-0.33270678	3.38E-05	GO:0043531	ATSG14470.1	NB-ARC domain-containing disease resistance protein	NA
Sapur.01G0943200.1	4.892788668	8.99001838	0.239252767	4.51539	6.32E-06	1.14E-05	grey	0.32503806	4.27E-05	GO:0007165;GO:0005515;GO:0043531	ATSG36930.2	Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.01G0241200.1	14.83317837	2.38323883	0.08620468	4.51534	6.36E-06	1.14E-05	grey	-0.33521258	2.66E-05		ATSG62030.1	diphthamide synthase DPH2 family protein	diphthamide biosynthesis protein
Sapur.01G0963000.1	207.3825743	-0.46070381	0.097533627	-4.51506	6.33E-06	1.14E-05	grey	-0.35969646	3.71E-06		ATSG54532.1	Auxin-responsive GH3 family protein	indole-3-acetic acid-amido synthetase GH3.6 protein
Sapur.01G0111500.1	11.45498344	8.65087343	1.945308593	4.514893	6.33E-06	1.14E-05	grey	0.28896476	0.000242174		ATSG54740.1	seed storage albumin 5	protease inhibitor/seed storage/LTP family protein
Sapur.00G0505800.2	5.697924451	0.570585151	0.126376241	4.514867	6.34E-06	1.14E-05	grey	-0.28306596	0.000237875	GO:0006872	ATSG19420.1	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain	regulator of chromosome condensation-like protein with FYVE zinc finger protein
Sapur.00T0041400.2	4.327263303	-0.675633463	0.14967692	-4.51395	6.36E-06	1.15E-05	grey	-0.32744133?	2.84E-05	GO:0005515;GO:0071949	ATSG67030.1	ABA1,ATABA1,ATZIP,IBS1,I	zeaxanthin epoxidase (ZEP) (ABA1)
Sapur.01G0267900.1	28.23737565	0.56053149	0.124267743	4.513692	6.37E-06	1.15E-05	grey	-0.32068735	-2.42E-05	GO:0004674;GO:0048546;GO:0006468;GO:0004672	AHG13R3	receptor kinase 3	NA
Sapur.00T0105500.3	12.07044952	-0.43618548	0.096644287	-4.51331	6.38E-06	1.15E-05	grey	-0.07691125	0.338353202		ATSG12680.1	PEPKR2	phosphoenolpyruvate carboxylase-related kinase 2
Sapur.01G0122900.1	47.74688402	1.16161041	0.261584093	4.513248	6.38E-06	1.15E-05	grey	-0.32717616	2.88E-05	GO:0043531	ATSG14460.1	LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.01T0085500.1	3.38507072	0.945864451	0.209586611	4.513	6.39E-06	1.15E-05	grey	-0.32060935	4.25E-05	GO:0007165;GO:0005515	ATSG36930.1	Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.01G0207900.1	3.75043094	0.818027223	0.181227159	4.51223	6.40E-06	1.15E-05	grey	-0.32166631	3.19E-05		ATSG16660.1	Pollen Ole e 1 allergen and extensin family protein	pollen protein Ole E 1-like protein
Sapur.01G0608000.1	19.84708887	1.90495562	2.449183413	4.51151	6.44E-06	1.16E-05	grey	-0.36220349	2.04E-06	GO:0048544;GO:0006468;GO:0004672	ATSG11340.1	S-locus lectin protein kinase family protein	Serine/Threonine-kinase
Sapur.01G0285700.1	368.9618134	0.124969752	0.027507163	4.510709	6.46E-06	1.16E-05	grey	-0.31715672	2.20E-05		ATSG14323.2	Protein of unknown function (DUF3644)	DUF3644 family protein
Sapur.T150400.1	9.1663871	-5.52687125	1.116808392	-4.51056	6.47E-06	1.16E-05	grey	-0.32153019	3.18E-05		ATSG28370.1		NA
Sapur.00G0299800.1	158.6968658	-0.38548946	0.085480155	-4.5097	6.49E-06	1.17E-05	grey	-0.33206639	2.00E-05	GO:0043565;GO:0006355;GO:0005634;GO:0003700	ATSG07320.1	AT-HSFA3,HSFA3	heat shock transcription factor A3
Sapur.01G0145100.1	345.7386267	0.567227171	0.140960994	4.508755	6.52E-06	1.17E-05	grey	0.31447829	2.20E-05		ATSG21620.1	ERD (early-responsive to dehydration stress) family protein	ERD family protein
Sapur.01G0887000.1	9.506781513	-0.601322909	0.13339519	-4.50783	6.55E-06	1.18E-05	grey	-0.33791472	1.92E-05	GO:0008138;GO:0006470	ATSG23720.1	PHS1	dual specificity protein phosphatase family protein
Sapur.T130300.1	34.8026689	1.28224626	0.075537613	4.503682	6.56E-06	1.18E-05	grey	-0.32776564	1.64E-05				NA
Sapur.01G0259200.1	818.689661	0.201600674	0.044739076	-4.50614	6.60E-06	1.19E-05	grey	-0.36462585	2.70E-06		ATSG46670.1	Domain of unknown function (DUF23)	plant/KS(2)-12 protein
Sapur.01W0023300.1	10.82747542	2.62584128	0.138931589	4.501747	6.61E-06	1.19E-05	grey	-0.35027193	4.56E-06		ATSG17920.1	Outer cell wall GPI-anchored protein 3	outer arm dynein light chain 1, putative
Sapur.00G0303300.1	1.352875345	6.672237033	0.371240242	4.504434	6.66E-06	1.20E-05	grey	-0.23194096	0.003467236				NA
Sapur.01G0139100.1	0.460823219	-3.81862527	0.848239168	-4.50318	6.68E-06	1.20E-05	grey	-0.36875675	5.19E-07		ATSG14030.1	KNU	CZH2 and CZHC zinc fingers superfamily protein
Sapur.01G0890300.1	3.815771037	-0.76021241	0.169388038	-4.50284	6.71E-06	1.21E-05	grey	-0.32355418	3.57E-05	GO:0016747	ATSG26040.1	HXXXD-type acyl-transferase family protein	alcohol acyltransferase
Sapur.01G0282800.1	0.940606863	1.447078417	0.321471221	4.502669	6.73E-06	1.21E-05	grey	-0.33947824	1.37E-05	GO:0005515	ATSG17180.1	ATGST1;ZS,GSTU25	glutathione S-transferase T4/z 25
Sapur.01G0614005.1	2.234487372	-0.66183182	0.150171308	-4.50265	6.75E-06	1.21E-05	grey	-0.27418148	1.38E-06		ATSG25240.1		hypothetical protein
Sapur.01G0930600.1	194.7176762	0.251767862	0.055919887	4.502292	6.73E-06	1.21E-05	grey	0.34893816	7.51E-06				NA
Sapur.01G0247000.1	260.5418556	0.221188259	0.071680622	4.500752	6.77E-06	1.22E-05	grey	0.31943443	4.54E-05	GO:0008270;GO:0005622	ATSG27310.1	B-box type zinc finger family protein	hypothetical protein
Sapur.01G0125900.1	2.5804231	1.074201234	0.238743775	4.49939	6.81E-06	1.23E-05	grey	0.18061471	7.95E-05		ATSG03670.1	ankyrin repeat family protein	NA
Sapur.00G0122400.1	11.48815845	0.450062554	0.09348123	-4.49911	6.82E-06	1.23E-05	grey	-0.31705968	7.48E-05				hypothetical protein
Sapur.01G0115600.1	174.3483736	0.275052952	0.06824850A	4.498646	6.84E-06	1.23E-05	grey	0.31397951	6.35E-05		ATSG42620.1	MAAO_OR0.9;PPS	RNA-like superfamily protein
Sapur.01G0238100.1	832.6271279	0.283169268	0.062907212	4.498325	6.85E-06	1.23E-05	grey	0.34877978	4.92E-05		ATSG08725.1	ARABIDOPSIS ARGP19	arabinogalactan protein 19
Sapur.00G0969000.3	21.9802902	0.322421182	0.07167949	4.49797	6.88E-06	1.23E-05	grey	0.37163495	1.65E-05	GO:0006468;GO:0005524;GO:0004672	ATSG53030.1	SRPR4	ser/arg-rich protein kinase 4
Sapur.00G0179300.1	986.7556039	0.127454258	0.028349518	4.49793	6.88E-06	1.23E-05	grey	0.38394553	2.36E-07	GO:0005525	ATSG31680.1	ARABIDILE/RABA5d	RAB GTPase homolog A5D
Sapur.01G0899700.1	21.94091801	-0.618723374	0.137613182	-4.49611	6.92E-06	1.24E-05	grey	-0.34371388	1.05E-05				NA
Sapur.01B0204900.1	458.4145994	0.181385428	0.040349365	4.495752	6.93E-06	1.25E-05	grey	0.29206915	0.000196398	GO:0003677	ATSG27481.1	HTA9	histone H2A protein 9
Sapur.01G0268700.1	11.66412969	0.577408614	0.128437127	4.495652	6.94E-06	1.25E-05	grey	-0.36476292	0.000104051		ATSG71360.1		membrane CHL-like protein
Sapur.01G0240400.1	26.1135143	-0.76991408	0.171295836	-4.49465	6.97E-06	1.25E-05	grey	-0.31460559	6.00E-05				transmembrane protein, putative
Sapur.00G0128900.1	23.98332909	-0.721126015	0.160445849	-4.49443	6.98E-06	1.25E-05	grey	-0.25467879	0.012087669		ATSG22910.1	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	NA
Sapur.01G0141600.1	243.4222229	-0.173205535	0.038538357	-4.49437	6.98E-06	1.25E-05	grey	-0.36158524	2.57E-06		ATSG10980.1	PLACE family protein	NA
Sapur.01B0277900.1	861.4128659	0.200208884	0.044578693	-4.49328	7.02E-06	1.26E-05	grey	-0.35498208	1.32E-06	GO:0016021	ATSG08552.2	hepatoblast transmembrane protein2	hemolysin-III-like protein
Sapur.01G0309600.1	41.94892419	0.361156677	0.080874243	-4.49222	7.05E-06	1.27E-05	grey	-0.35855613	4.48E-06		ATSG22190.1		cytochrome protein b6, putative
Sapur.00G0204900.1	2.58826684	-0.74588576	0.16607588	-4.49184	7.06E-06	1.27E-05	grey	-0.32511134	3.26E-05				NA
Sapur.01G0271200.5	1.088685896	1.20974273	0.269334737	4.491262	7.08E-06	1.27E-05	grey	-0.35779316	4.23E-06	GO:0003824;GO:0006470;GO:0004722	ATSG31481.1	Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.00G0281200.1	54.1834299	0.338820193	0.074288177	-4.49062	7.13E-06	1.28E-05	grey	0.0795561	0.325631577	GO:0042398;GO:0004357	ATSG19180.1	glutamate-cysteine ligase	glutamate-cysteine ligase
Sapur.02G0928800.1	138.9108483	-0.353625159	0.077642722	-4.48932	7.15E-06	1.28E-05	grey	-0.31746699	1.38E-05		SCL-3,SCL3	scarecrow-like 3	GRAS family transcription factor
Sapur.00G0717000.1	4.0195259	0.927010024	0.206539081	4.488303	7.18E-06	1.29E-05	grey	0.37071827	1.76E-06		ATSG7678.1	FHY1,FRY1,PAT3	far-red elongated hypocotyl 1
Sapur.01B0240600.1	95.85743973	0.266451199	0.07266302	4.488253	7.18E-06	1.29E-05	grey	0.42195877	3.71E-08				hypothetical protein
Sapur.00G0144000.1	6342.936416	0.886460118	0.197565055	4.486917	7.23E-06	1.30E-05	grey	0.32370898	3.54E-05	GO:0008652;GO:0008270;GO:0003873;GO:0009086	ATCMS,ATMETL,ATMS1	Cobalamin-independent synthase family protein	NA
Sapur.01G0134500.1	594.7564841	0.200427461	0.05408613	4.48606	7.26E-06	1.30E-05	grey	-0.32843064	2.46E-05		EMB2777	Sas10/U3 chaperone family protein	NA
Sapur.00G0145600.1	26.10671318	0.586318845	0.130677932	-4.48537	7.28E-06	1.31E-05	grey	-0.38326228	8.50E-07	GO:0005975;GO:0004553	ATSG13560.2	O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase
Sapur.01G0134400.2	20.83953443	0.292341668	0.087433623	-4.484	7.33E-06	1.31E-05	grey	-0.35432005	5.36E-06	GO:0006482;GO:0005491;GO:0003723;GO:0005122	ATSG14920.1	Pseudouridine synthase family protein	DNA pseudouridine synthase
Sapur.T112200.1	1.598439904	0.311639814	0.292523881	-4.4839	7.33E-06	1.32E-05	grey	-0.32763827	2.84E-05		ATSG28620.2	Magnesium transporter CorA-like family protein	NA
Sapur.01G0615500.1	238.6171172	-0.192773881	0.042969659	-4.48377	7.33E-06	1.32E-05	grey	-0.33622603	5.60E-05		ATSG02148.1		NA
Sapur.01B0284600.1	6492.363868	0.205026448	0.045929032	-4.48358	7.34E-06	1.32E-05	grey	-0.35698706	4.44E-06		ATSG58070.1	ATTIL,TIL	temperature-induced lipocalin
Sapur.01G0168900.1	1526.473045	0.319430256	0.071247947	-4.48336	7.35E-06	1.32E-05	grey	-0.35623089	4.67E-06	GO:0003924;GO:0007017;GO:0005874	ATSG19770.1	TUA3	tubulin alpha-3
Sapur.01G0258600.1	4.77618156	1.012551938	0.227577599	4.483654	7.36E-06	1.32E-05	grey	-0.30954782	7.97E-05		ATSG17920.1	Outer cell wall GPI-anchored protein 3	outer arm dynein light chain 1 protein
Sapur.01B0277800.1	34.86048807	-0.33752829	0.075299125	-4.4828	7.37E-06	1.32E-05	grey	-0.33562225	1.76E-05	GO:0005515	ATSG30860.1	ASHR3,SDG4	SET domain group 4
Sapur.01W0078300.1	0.738773553	1.303865456	0.30380654	4.48183	7.38E-06	1.32E-05	grey	-0.36021066	8.58E-05				NA
Sapur.01G0922300.1	2.730746755	-0.88032261	0.19639818	-4.48233	7.38E-06	1.32E-05	grey	-0.40800674	1.13E-07		ATSG22900.1	Protein of unknown function (DUF1191)	transmembrane protein, putative
Sapur.01G0623000.1	784.1120381	0.175207268	0.039237847	-4.48218	7.39E-06	1.33E-05	grey	0.31461175	5.26E-05	GO:0005975;GO:0005506;GO:0046556;GO:0046169;GO:0003824	AHAY1,ATAMY3	alpha-amylase 3	alpha amylase domain family protein
Sapur.01G0620900.1	9.810487407	-0.49443388	0.110780861	-4.48123	7.42E-06	1.33E-05	grey	-0.32859289	2.65E-05	GO:0016491;GO:0008152	ATSG11410.1	NAD(P)-binding Rossmann-fold superfamily protein	short chain dehydrogenase
Sapur.01G0282900.1	24.11562103	-0.656389379	0.147000329	-4.48191	7.42E-06	1.33E-05	grey	-0.26667207	0.000735366		ATSG25130.1		transmembrane protein, putative
Sapur.01G0180400.2	19.28105608	-0.476732026	0.106431024	-4.48002	7.44E-06	1.34E-05	grey	-0.31521411	4.60E-05		ATSG39130.1	Transmembrane amino acid transporter family protein	transmembrane amino acid transporter protein
Sapur.01G0150100.1	2.024669254	1.162144486	0.25941521	4.47956	7.48E-06	1.34E-05	grey	0.3387009	1.26E-05		ATSG38380.1		NA
Sapur.01B0237700.5	3.667654595	0.6306459	0.140666968	4.479123	7.50E-06	1.34E-05	grey	0.46031618	1.31E-09		ATSG25360.1		NA
Sapur.01G0705900.1	62.02812548	0.200575822	0.044826736	4.478684	7.51E-06	1.35E-05	grey	0.27229497	0.005406869	GO:0005515	ATSG07610.1	F-box family protein	F-box protein, putative
Sapur.00T0064600.1	773.8155062	0.195318333	0.08823888	4.478562	7.51E-06	1.35E-05	grey	0.31835589	1.46E-05	GO:0016246;GO:0005975;GO:0004553	BGAL9	beta galactosidase 9	beta-galactosidase 9
Sapur.01G0380600.1	0.725758811	1.600026447	0.357464689	4.477947	7.54E-06	1.35E-05	grey	0.30824235	8.58E-05		ATSG34050.1	Ankyrin repeat family protein	transmembrane protein, putative
Sapur.00T0260100.2	2.381124868	0.761317393	0.165149303	4.477925	7.54E-06	1.35E-05	grey	0.3497037	7.01E-06	GO:0006468;GO:0005524;GO:0004672	ATSG17220.1	Protein kinase superfamily protein	Serine/Threonine-kinase Cx32, putative
Sapur.T010700.1	34.79416251	0.419152295	0.093615132	4.477571	7.55E-06	1.35E-05	grey	0.35056351	6.76E-06		ATSG09320.1	agenet domain-containing protein	NA
Sapur.01G0279100.1	2.428816364	0.918839487	0.20567851	4.47742	7.56E-06	1.35E-05	grey	-0.42826688	2.09E-08		ATSG18150.1	homeobox protein 6	2'-HD homeobox protein cysl/his-rich dimerization domain protein
Sapur.01B0284600.1	4692.363868	0.205026448	0.045929032	-4.48358	7.34E-06	1.32E-05	grey	-0.35698706	4.44E-06		ATSG18730.2	MGDI,MGDA	monogalactosyl diacylglycerol synthase 1
Sapur.01G0168900.1	1526.473045	0.319430256	0.071247947	-4.48336	7.35E-06	1.32E-05	grey	-0.35623089	4.67E-06	GO:0003924;GO:0007017;GO:0005874	ATSG19770.1	TUA3	tubulin alpha-3
Sapur.01G0258600.1	4.77618156	1.012551938	0.227577599	4.483654	7.36E-06	1.32E-05	grey	-0.30954782	7.97E-05		ATSG17920.1	Outer cell wall GPI-anchored protein 3	outer arm dynein light chain 1 protein
Sapur.01B0277800.1	34.86048807	-0.33752829	0.075299125	-4.4828	7.37E-06	1.32E-05	grey	-0.33562225	1.76E-05	GO:0005515	ATSG30860.1	ASHR3,SDG4	SET domain group 4
Sapur.01W0078300.1	0.738773553	1.303865456	0.30380654	4.48183	7.38E-06	1.32E-05	grey	-0.36021066	8.58E-05				NA
Sapur.01G0922300.1	2.730746755	-0.88032261	0.19639818	-4.48233	7.38E-06	1.32E-05	grey	-0.40800674	1.13E-07		ATSG22900.1	Protein of unknown function (DUF1191)	transmembrane protein, putative
Sapur.01G0620900.1	9.810487407	-0.49443388	0.110780861	-4.48123	7.42E-06	1.33E-05	grey	0.31461175	5.26E-05	GO:0005975;GO:0005506;GO:0046556;GO:0046169;GO:0003824	AHAY1,ATAMY3	alpha-amylase 3	alpha amylase domain family protein
Sapur.01G0282900.1	24.11562103	-0.656389379	0.147000329	-4.48191	7.42E-06	1.33E-05	grey	-0.32859289	2.65E-05	GO:0016491;GO:0008152	ATSG11410.1	NAD(P)-binding Rossmann-fold superfamily protein	short chain dehydrogenase
Sapur.01G0180400.2	19.28105608	-0.476732026	0.106431024	-4.48002	7.44E-06	1.34E-05	grey	-0.26667207	0.000735366		ATSG25130.1		transmembrane protein, putative
Sapur.01G0150100.1	2.024669254	1.162144486	0.25941521	4.47956	7.48E-06	1.34E-05	grey	-0.31521411	4.60E-05		ATSG39130.1	Transmembrane amino acid transporter family protein	transmembrane amino acid transporter protein
Sapur.01B0237700.5	3.667654595	0.6306459	0.140666968	4.479123	7.50E-06	1.34E-05	grey	0.3387009	1.26E-05		ATSG38380.1		NA
Sapur.01B0237700.1	62.02812548	0.200575822	0.044826736	4.478684	7.51E-06	1.35E-05	grey	0.46031618	1.31E-09		ATSG25360.1		NA
Sapur.01G0705900.1	773.8155062	0.195318333	0.08823888	4.478562	7.51E-06	1.35E-05	grey	0.27229497	0.005406869	GO:0005515	ATSG07610.1	F-box family protein	F-box protein, putative
Sapur.00T0064600.1	0.725758811	1.600026447	0.357464689	4.477947	7.54E-06	1.35E-05	grey	0.31835589	1.46E-05	GO:0016246;GO:0005975;GO:0004553	BGAL9	beta galactosidase 9	beta-galactosidase 9
Sapur.00T0260100.2	2.381124868	0.761317393	0.165149303	4.477925	7.54E-06	1.35E-05	grey	0.3497037	7.01E-06	GO:0006468;GO:0005524;GO:0004672	ATSG34050.1	Ankyrin repeat family protein	transmembrane protein, putative
Sapur.T010700.1	34.79416251	0.419152295	0.093615132	4.477571	7.55E-06	1.35E-05	grey	0.35056351	6.76E-06		ATSG17220.1	Protein kinase superfamily protein	Serine/Threonine-kinase Cx32, putative
Sapur.01G0279100.1	2.428816364	0.918839487	0.20567851	4.47742	7.56E-06	1.35E-05	grey	-0.42826688	2.09E-08		ATSG09320.1	agenet domain-containing protein	NA
Sapur.01G0622300.3	2.310580358	-0.085912397	0.242626877	-4.47565	7.62E-06	1.37E-05	grey	-0.35492756	5.39E-06	GO:0016758;GO:0009247	ATSG18180.2	homeobox protein 6	2'-HD homeobox protein cysl/his-rich dimerization domain protein
Sapur.01G0620400.1	258.3413307	0.075188737	0.016417158	-4.47493	7.64E-06	1.37E-05	grey	-0.32896613	2.59E-05		ATSG58070.1	ATTIL,TIL	monogalactosyl diacylglycerol synthase 1
Sapur.01G0182300.4	0.080976646	-4.45631403	1.325476339	-4.4744	7.66E-06	1.37E-05	grey	-0.46728101	6.84E-10		ATSG14200.1	Pentatricopeptide repeat (PPR) superfamily protein	salt-inducible protein, putative
Sapur.01W0288100.2	13.44221287	0.521988304	0.116688091	4.473648	7.68E-06	1.38E-05	grey	-0.29871989	0.000146628		ATSG47390.1	myb-like transcription factor family protein	MYB transcription factor, putative
Sapur.01G0236000.1	51.10217157	-0.602751766	0.134761106	-4.47341	7.70E-06	1.38E-05	grey	-0.33267005	2.16E-05		ATSG33030.1	ADR6-like 1	ADR6-like 1
Sapur.00T0681300.1	391.1603217	0.294982694	0.065931599	-4.47339	7.70E-06	1.38E-05	grey	-0.35891221	4.45E-06		ATSG19780.1		NA
Sapur.01G0154900.1	3.20513932	1.829260364	0.408925441	4.473346	7.70E-06	1.38E-05	grey	0.35182053	1.24E-05				NA
Sapur.00G0141700.4	0.557554637	-1.527222813	0.341462214	-4.47389	7.72E-06	1.38E-05	grey	-0.39124034	4.05E-07		ATSG46640.3		hypothetical protein
Sapur.00G0126300.1	2.839358622	-0.48820206	0.107175564	-4.47261	7.76E-06	1.39E-05	grey	-0.31882646	4.68E-05				NA
Sapur.01G0890400.1	3.785729617	-0.801477411	0.179199855	-4.47253	7.73E-06	1.38E-05	grey	-0.31507529	5.94E-05	GO:0005515	ATSG13682.1	LDL2	lysine-specific histone demethylase-like protein
Sapur.01G0802800.1	318.1767799	0.379591631	0.084875256	4.472348	7.74E-06	1.39E-05	grey	0.30546802	0.000202011	GO:0016602	ATSG12120.1	RD2	adenine nucleotide alpha hydrolases-like superfamily protein	universal stress protein
Sapur.01T0020700.1	1.067639805	1.263577479	0.28256628	4.471791	7.76E-06	1.39E-05	grey	0.31841649	4.82E-05	GO:0008152;GO:0003824	ATSG23380.1	AMP-dependent synthetase and ligase family protein	4-coumarate-CoA ligase
Sapur.T145100.1	2.834036471	1.362681927	0.319678317	4.47173	7.78E-06	1.39E-05	grey	-0.36843765	3.52E-06		ATSG41551.1	Forkhead-associated (FHA) domain-containing protein	NA
Sapur.01B0443000.1	700.6879678	-0.247979905	0.055456494	-4.47161	7.78E-06	1.39E-05	grey	-0.33431866	1.87E-05		ATSG28910.2		NA
Sapur.00G0163600.1	3.353692053	0.928314861	0.207550481	-4.47087	7.79E-06	1.40E-05	grey	-0.37794625?	1.06E-06		ATSG19875.1		CMT-type cytosine DNA-methyltransferase 3b, putative
Sapur.00T0251900.4	10.50835157	0.404824015	0.09057763	4.46804	7.86E-06	1.40E-05	grey	0.34277114	6.44E-06				NA
Sapur.01B0264200.1	17.30326621	-0.425704051	0.095294724	-4.46755	7.91E-06	1.42E-05	grey	-0.36105114	3.20E-06		ATSG16490.1	RIC4	WSCD-interacting CRIB motif-containing protein 4	wiscott-aldrich syndrome, carboxy-terminal protein%2C putative
Sapur.01G0275400.1	2.832619851	-1.141929309	0.255603488	-4.46719	7.93E-06	1.42E-05	grey	-0.10830606	0.177476662		ATSG21570.1		remorin protein
Sapur.01G0620700.1	4.473673131	0.717369951	0.160568873	4.466656	7.95E-06	1.42E-05	grey	0.33155603	1.96E-05				hypothetical protein
Sapur.01G0248100.1	0.552609299	1.071141994	0.239248846	4.46425	8.05E-06	1.44E-05	grey	-0.31990545	1.42E-05		ATSG14090.1		hypothetical protein
Sapur.00G0721200.1	286.5414726	0.206280477	0.046219494	4.463062	8.08E-06	1.45E-05	grey	0.35904586	3.88E-06		ATSG15640.1		substrate carrier family protein
Sapur.01W0218100.1	1.34072868	-0.124898469	0.28007929	-4.46274	8.08E-06	1.45E-05	grey	-0.36742008	2.25E-06	AtMYB85,MYB85	AtMYB85,MYB85	myb-domain protein 85	Myb-transcription factor
Sapur.00G0507000.1	58.7694444	-0.413570444	0.09267347	-4.46271	8.08E-06	1.45E-05	grey	-0.33819268	1.38E-05	GO:0005515	ATSG48060.1	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein	NA
Sapur.01G0281700.1	10.10737612	0.364168069	0.08169455	4.46255	8.10E-06	1.45E-05	grey	0.29154771	0.000211627		ATSG10800.1	Protein kinase superfamily protein	hypothetical protein
Sapur.01G0231100.1	2.17801177	-0.85280162	0.191111417	-4.46233	8.11E-06	1.45E-05	grey	-0.39279427	3.61E-07		ATSG22440.1	Protein of unknown function (DUF2223)	DUF2223 family protein
Sapur.01G0203900.1	147.6241656	0.731851982	0.159973166	4.462098	8.13E-06	1.45E-05	grey	0.34113406	1.22E-05	GO:0008837;GO:0005542;GO:0004356	ATSG37600.1	ATGLN1;1.ATGDR1;GLN1;1.(	glutamine synthetase
Sapur.00W0207300.1	0.747490959	1.651489891	0.370139845	4.461684	8.15E-06	1.46E-05	grey	0.36094735	0.000128396	GO:0005524;GO:0005524;GO:0004672	ATSG26750.1	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	receptor-like kinase
Sapur.01G0205400.1	42.92282545	-0.681854528	0.153375528	-4.46098	8.18E-06	1.46E-05	grey	-0.38100589	8.47E-07	GO:0055114;GO:0016491;GO:0005507	ATLAC1,LAC1	laccase 1	laccase
Sapur.01G0206600.1	121.0127747	-0.554668887	0.124630022	-4.46058	8.17E-06	1.46E-05	grey	-0.34758549	8.16E-06	GO:0055114;GO:0045262;GO:0007246	ATSG14630.1	5'/3'-AMP-activated protein kinase beta-2 subunit protein	SNF1-related kinase regulatory subunit beta-2
Sapur.01G0217000.1	12.82501183	-0.66957258	0.150147571	-4.45943	8.23E-06	1.47E-05	grey	-0.34566189	9.37E-06	GO:0055085;GO:0016020;GO:0008811;GO:0005216	ATSG13130.1	ATCNGC1,CNGC1	cyclic nucleotide gated channel 1
Sapur.01G0221200.1	2.334259179	0.918644023	0.205977219	4.46437	8.21E-06	1.47E-05	grey	-0.3855557	2.34E-07		ATSG27240.1	Protein kinase family protein with domain-containing protein	receptor protein Dnd1, putative
Sapur.00G0284900.1	0.452268684	7.712539433	1.694034801	-4.45801	8.27E-06	1.48E-05	grey	-0.40949503	1.01E-07		ATSG47740.2	PPR06 putative thiol peptidase family protein	PPR06 peptidase domain protein, putative
Sapur.01B0258700.5	8.530716659	-0.504906386	0.113173114	-4.45741	8.28E-06	1.48E-05	grey	-0.33848825	1.36E-05		ATSG18490.1	Mitochondrial import membrane translocase subunit Tim17/Tim22/Tim23 family protein	import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
Sapur.01G0296600.1	1.56824991	-1.130423776	0.253635124	-4.45689	8.32E-06	1.48E-05	grey	-0.37413603	1.32E-06		ATSG29020.2	Phosphatidic acid phosphatase (PAP2) family protein	NA
Sapur.01G0118800.1	2.590939944	0.969977973	0.24010658	4.456263	8.34E-06	1.49E-05	grey	0.29382265	0.000187757				hypothetical protein
Sapur.00T0251300.1	220.1764665	-0.346888893	0.077806954	-4.45619	8.34E-06	1.49E-05	grey	-0.28185157	7.76E-08		ATSG12845.1		transmembrane protein, putative
Sapur.00G0285700.4	12.06339845	-0.378606962	0.084976948	-4.45615	8.34E-06	1.49E-05	grey	-0.01115216	0.889717395				Myb-like DNA-binding domain protein
Sapur.T081500.1	30.3515642	-0.567867538	0.126947104	-4.45489	8.36E-06	1.50E-05	grey	-0.32456268	1.87E-05	GO:0008270;GO:0008022;GO:0006625;GO:0005779	ATSG04660.

Sapur.01G0201000.1	1.30264733e-16	1.46830566	0.262307776	-4.37779	1.20E-05	2.13E-05	grey	-0.30483821	0.000103647					NA
Sapur.003G098100.1	3.02047871e-17	-2.059598447	0.46592889	-4.37749	1.20E-05	2.13E-05	grey	-0.34947817	7.25E-06		ATSG64160.1		Disease resistance-responsive (dirigent-like protein) family protein	plant disease resistance response protein, putative
Sapur.006G011500.1	7.76784631e-17	0.611367864	0.13974429	-4.37728	1.20E-05	2.13E-05	grey	-0.31251772	6.48E-05		ATSG64120.1		Pentatricopeptide repeat (PPR)-superfamily protein	auxin response factor
Sapur.008G160300.5	1.32339234e-17	1.17074992	0.26740458	-4.37726	1.20E-05	2.13E-05	grey	0.11079783	0.167138828	GD055085;GD016020;GD006810;GD001517;GD003333	ATSG01170.1	BAT1	bidirectional amino acid transporter 1	NA
Sapur.004G000100.1	7.146601e-17	1.125020153	0.23234131	-4.37606	1.20E-05	2.13E-05	grey	-0.31866734	4.67E-05					NA
Sapur.001G002000.1	10.34328558	-0.483494372	0.11046757	-4.3768	1.20E-05	2.13E-05	grey	-0.33761284	1.53E-05		ATSG13480.1			hypothetical protein
Sapur.012G061100.13	15.3108886	0.334441953	0.076433221	-4.37561	1.21E-05	2.15E-05	grey	0.31832328	6.38E-05	GD035891	ATSG48195.1		Phox (PX) domain-containing protein	differentially in FDCP-like protein, putative
Sapur.004G011200.1	1.56819787e-17	1.166560209	0.26673908	-4.37503	1.21E-05	2.15E-05	grey	0.30763927	8.87E-05	GD054648;GD005524;GD004672	ATSG05530.1		Protein kinase superfamily protein	receptor Ser/ser/Threonine kinase, putative
Sapur.016G270700.1	268.4574885	0.421290598	0.096206232	-4.37458	1.22E-05	2.16E-05	grey	0.31317662	6.52E-05	GD016758;GD008152	ATSG21790.1		UDP-Glycosyltransferase superfamily protein	UDP-glucose flavonoid 3-O-glucosyltransferase, putative
Sapur.005G178600.1	15.36263703	-0.682551891	0.156088189	-4.37438	1.22E-05	2.16E-05	grey	-0.32363138	1E-05		ATSG05020.1		CTP synthase family protein	DUT561 domain protein
Sapur.017G017500.1	16.26128872	-0.439721481	0.100536149	-4.37376	1.22E-05	2.16E-05	grey	-0.31807064	5.24E-05		ATSG04260.1	MPI7;MPI7;PRA1.D	CAAX motif-containing protein interacting protein 7	PRA1 family protein
Sapur.012G121700.1	287.4737322	-0.611231705	0.140238376	-4.37375	1.22E-05	2.16E-05	grey	-0.36197034	3.36E-06	GD016392;GD016023;GD006810	ATSG56020.1		Gnt1/Pbl2-like vesicle transport protein family	protein transport SFT2
Sapur.008G026700.1	101.9182847	0.198012092	0.045277882	-4.37375	1.22E-05	2.16E-05	grey	0.28855927	0.000247311	GD008270	ATSG54826.1		Zim17-type zinc finger protein	DNL zinc finger protein
Sapur.007G052300.1	334.8844536	-0.7884888	0.180466184	-4.37364	1.22E-05	2.16E-05	grey	-0.32616842	2.07E-05		ATSG48042.1		Zinc finger (B-box) family protein	excision-like protein
Sapur.012G097600.1	125.7971885	-0.356351928	0.081488469	-4.37304	1.23E-05	2.17E-05	grey	-0.34503807	9.62E-06		ATSG26081.1	MYB85;MYB85	myb domain protein 85	Myb transcription factor
Sapur.003G032100.1	0.32154267	1.015435664	0.23473664	-4.37299	1.23E-05	2.17E-05	grey	0.42456078	1.56E-08					NA
Sapur.002G153500.1	3.01215492	1.113913419	0.254739135	-4.37293	1.23E-05	2.17E-05	grey	0.31639362	5.42E-05	GD045454;GD015035;GD009055	ATSG62930.1		Thioredoxin superfamily protein	monothiol glutaredoxin-S6 protein
Sapur.T010200.1	0.32078611	1.72068651	0.39357881	-4.37189	1.23E-05	2.18E-05	grey	0.47853819	2.29E-10		ATMG15140.1			NA
Sapur.T094600.1	3.12477937	-0.586753656	0.13923817	-4.37157	1.23E-05	2.18E-05	grey	-0.33432658	1E-05		ATSG38455.1	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.016G089900.1	88.53511185	-0.561982656	0.128538751	-4.37054	1.24E-05	2.19E-05	grey	-0.31668709	7.57E-05		ATSG03190.3	CPUORF47	conserved peptide upstream open reading frame 47	NA
Sapur.017G007600.1	5.52518534e-17	-0.508827827	0.116439669	-4.37004	1.24E-05	2.20E-05	grey	-0.38342416	1.27E-07		ATSG05081.1	NF06	nuclear fusion defective 6	hypothetical protein
Sapur.016G285800.1	196.1452048	0.253424393	0.057759979	-4.37023	1.24E-05	2.20E-05	grey	0.29801363	0.000140302	GD006886	ATSG20410.1	GAMMA-SNAP;GSNAP	gamma-soluble NSF attachment protein	gamma-soluble NSF attachment protein
Sapur.011G026600.1	118.6237348	0.251882796	0.057631502	-4.37028	1.24E-05	2.20E-05	grey	0.37730759	1E-05		ATSG02020.1	EZA1;SDG10;SWN	SET domain-containing protein	NA
Sapur.001G053300.1	34.41514832	-0.364778764	0.083597334	-4.36948	1.25E-05	2.20E-05	grey	-0.35059253	6.75E-06	GD047755;GD016135;GD016021	ATSG00550.1	HYD1	C-8,7 sterol isomerase	sterol Δ8,Δ7-isomerase
Sapur.006G069300.1	896.6109422	0.788458866	0.180147172	-4.36768	1.25E-05	2.21E-05	grey	0.26646507	0.000743941	GD080611;GD016998;GD006022;GD004568	ATSG54320.1	ATCHITIV;ATEP3;CHIV;EP3	Chitinase family protein;Pathogenesis-related protein 3;chitinase	class IV endochitinase
Sapur.016G140500.1	445.4887917	0.314066513	0.071917514	-4.36708	1.26E-05	2.22E-05	grey	0.29344933	0.000159449	GD016788	ATSG07230.1	NPC1	non-specific phosphoesterase C1	acting on ester bonds hydrolase, putative
Sapur.016G142900.1	3.08929975	-1.069152299	0.243008039	-4.36587	1.27E-05	2.24E-05	grey	-0.33454583	1.85E-05		ATSG13360.1	AGT;AGT1;SGAT	alanine:glyoxylate aminotransferase	serine-glyoxylate aminotransferase
Sapur.003G188700.2	0.65454549	-2.462082633	0.134898622	-4.36512	1.27E-05	2.24E-05	grey	-0.36431926	2.75E-06	GD005524	ATSG14570.1		Protein kinase superfamily protein	robust large subunit-binding protein subunit beta
Sapur.016G114400.1	107.0326059	-0.249943028	0.057266703	-4.36455	1.27E-05	2.25E-05	grey	-0.36276118	2.31E-06	GD016149;GD006415;GD005737	ATSG26618.1	ERF1-3	eukaryotic release factor 1-3	eukaryotic peptide chain release factor subunit 1-3
Sapur.T103000.1	0.33683223	1.811192184	0.419617226	-4.36369	1.28E-05	2.26E-05	grey	0.41963136	4.48E-08					NA
Sapur.002G049900.1	1.019815565	-1.135610771	0.260288422	-4.36295	1.28E-05	2.27E-05	grey	-0.31266425	6.70E-05		ATSG22750.4			NA
Sapur.006G020800.1	11.414671	-0.455014152	0.093860757	-4.36277	1.28E-05	2.27E-05	grey	-0.31661374	1.40E-05		ATSG05081.1	ATUBC22;UBC22	ubiquitin-conjugating enzyme 22	ubiquitin-conjugating enzyme E2
Sapur.I59G011400.1	257.4294707	0.197427588	0.045255767	-4.362485	1.29E-05	2.28E-05	grey	0.31772789	5.01E-05	GD055515;GD016773	ATSG42240.1		Phosphatidylinositol 3- and 4-kinase ;Ubiquitin family protein	phosphatidylinositol 3- and 4-kinase family protein
Sapur.I59G147200.1	365.647931	0.242723113	0.055645267	-4.36372	1.28E-05	2.28E-05	grey	-0.27808329	0.000445039		ATSG22180.1			transmembrane protein 81A,B,C
Sapur.004G044300.1	5.13975204	0.87633306	0.200912998	-4.361754	1.28E-05	2.28E-05	grey	0.32548507	3.19E-05					NA
Sapur.006G044000.2	4.82364009	-0.294374827	0.13005162	-4.36112	1.29E-05	2.29E-05	grey	-0.34838376	5.32E-06		ATSG15572.1		3-phosphoinositide-dependent protein kinase-1, putative	3-phosphoinositide-dependent kinase-1 protein, putative
Sapur.013G105900.1	210.5547524	0.190083188	0.043731531	-4.361311	1.29E-05	2.29E-05	grey	0.33395722	5.92E-05	GD005515;GD006468;GD005524;GD004672	ATSG34420.1		leucine-rich repeat transmembrane protein kinase family protein	LRR receptor-like kinase
Sapur.013G020800.1	0.69268178	2.778047491	-0.406682288	-4.36118	1.29E-05	2.29E-05	grey	0.3013095	0.000127589		ATSG38280.1	PRSK	PRS-like receptor kinase	NA
Sapur.014G087600.1	6.24118493	-0.621468361	0.141573602	-4.35884	1.30E-05	2.31E-05	grey	-0.34242048	1.18E-05	GD003824;GD006470;GD004722	ATSG46920.2	PDI1	Protein phosphatase 2C family protein	protein phosphatase 2C, putative
Sapur.006G021200.1	798.9375343	0.315757811	0.072445658	-4.35854	1.31E-05	2.32E-05	grey	0.30551175	9.97E-05	GD005329	ATSG41410.1		Calcium-binding EF-hand family protein	calcium-binding protein CML36, putative
Sapur.I59G065100.1	1.59953864	-0.15979923	0.3542612	-4.3565	1.31E-05	2.33E-05	grey	-0.37519667	1.66E-06	GD050528;GD006190	ATSG03220.1		Eukaryotic aspartyl protease family protein	eglin/plasm specific endopepsin inhibitor
Sapur.007G041000.1	167.828863	-0.336058831	0.077140988	-4.35684	1.32E-05	2.33E-05	grey	-0.33522658	1.77E-05	GD016753;GD016021	ATSG22900.1		Galactosyl transferase GMA12/MNN10 family protein	galactomannan galactosyltransferase
Sapur.007G089700.1	73.6861322	-0.606587927	0.135374834	-4.35522	1.33E-05	2.35E-05	grey	-0.29970279	0.000106885	GD050528;GD006190	ATSG34490.2		Eukaryotic aspartyl protease family protein	aspartyl protease family protein
Sapur.006G075400.1	5.42665795e-17	0.813139128	0.180708029	-4.35514	1.33E-05	2.35E-05	grey	-0.30972588	7.90E-05					NA
Sapur.I59G147300.1	12.7501796	0.156110001	0.034857223	-4.35479	1.33E-05	2.35E-05	grey	-0.30294195	0.000128475					transmembrane protein, putative
Sapur.016G138300.1	1.59596631	1.164774991	0.267554677	-4.35349	1.34E-05	2.37E-05	grey	-0.31328148	7.66E-05		ATSG07180.1		Neutral/alkaline non-lysosomal ceramidase	neutral/alkaline nonlysosomal ceramidase
Sapur.012G088800.1	0.72625384	1.418904281	0.32598101	-4.35283	1.34E-05	2.38E-05	grey	0.31735487	5.01E-05		ATSG03500.1		Ankyrin-repeat family protein	ankyrin-like protein, putative
Sapur.016G088300.1	89.31516689	-0.687763755	0.144931046	-4.35248	1.35E-05	2.38E-05	grey	-0.31931242	2.17E-05	GD005524;GD005515	ATSG27190.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.004G072800.1	970.3507937	0.177951365	0.04080512	-4.351784	1.35E-05	2.39E-05	grey	0.31935251	4.61E-05		ATMES11;MES11		methyl esterase 11	esterase
Sapur.010G160800.1	0.49759489	-0.784661882	0.180461487	-4.35152	1.35E-05	2.39E-05	grey	-0.36601046	2.42E-06		ATSG16050.1		Cysteine/histidine-rich C1 domain family protein	transmembrane protein, putative
Sapur.005G024000.1	26.6614708	-0.453027938	0.104233282	-4.35116	1.35E-05	2.39E-05	grey	-0.35451079	5.35E-06	GD017053;GD007049;GD006351	ATSG27630.1	ALY1;ATALY1	DNRF ;Myb-like DNA-binding domain	transcription factor
Sapur.I59G047000.1	1.38934809	-0.215512214	0.137876971	-4.35147	1.35E-05	2.39E-05	grey	0.24318061	0.001015255	GD055515;GD006468;GD005524	ATSG47535.1		Leucine-rich repeat protein kinase family protein	tyrosine kinase domain protein
Sapur.002G134500.1	0.87287891	1.344296586	0.308962634	-4.351	1.36E-05	2.40E-05	grey	-0.34210589	1.16E-05	GD005975;GD004553	ATSG66460.1		Glycosyl hydrolase superfamily protein	1-4, beta-mannan endohydrolase (mannan endo-1%2C4-beta-mannosidase), putative
Sapur.003G158800.6	11.60145439	0.185091386	0.08134278	-4.35049	1.36E-05	2.40E-05	grey	-0.29217439	0.000204786	GD016020;GD015171;GD003333	ATSG50440.1	CAT9	cysteine synthase 9;cysteine synthase 9	cytosolic serine acetyltransferase
Sapur.016G292200.6	1.30251646	-0.035306432	0.237690383	-4.35015	1.36E-05	2.40E-05	grey	-0.36659477	2.33E-06	GD008270	ATSG46530.1		RING/U-box superfamily protein	RING/U-box superfamily protein
Sapur.I59G080018.8	4.20913882	-0.612021368	0.1384117	-4.34988	1.36E-05	2.41E-05	grey	0.06863327	0.393024025	GD015969	ATSG14050.1	AT-RSH2;ATRSH2;RSH2	RELA/SPOT homolog 2	guanosine-3%2C5-bis(diphosphate) 3'-pyrophosphohydrolase, putative
Sapur.006G158100.1	8.58283479	0.707467722	0.162614224	-4.34874	1.37E-05	2.42E-05	grey	0.31308889	6.55E-05					NA
Sapur.013G117800.2	49.8078291	0.594566348	0.136743942	-4.34802	1.37E-05	2.43E-05	grey	0.29285455	0.000197591	GD006468;GD005524;GD004672	ATSG07180.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.008G026800.1	261.3137941	-0.456301163	0.095173848	-4.34767	1.38E-05	2.43E-05	grey	0.34896497	8.52E-06	GD016916;GD008324	ATSG42910.1		Phosphorylase superfamily protein	phosphorylase family protein
Sapur.009G021100.1	950.6724739	0.163151216	0.037530273	-4.34719	1.38E-05	2.44E-05	grey	-0.29647873	0.000163045	GD008152;GD006807	ATSG55440.1	ATTCTIMC;CYTOTPI;TPI	triosephosphate isomerase	triosephosphate isomerase
Sapur.I16G176600.1	10.70175364	-0.190174929	0.07321676	-4.34609	1.39E-05	2.45E-05	grey	-0.31303132	5.76E-05	GD005525	ATSG60190.3		Cytokinin-responsive factor Tu family protein	NA
Sapur.003G186300.2	2.08129139	0.993631217	0.228638868	-4.34358	1.39E-05	2.46E-05	grey	0.30629879	9.58E-05	GD016192;GD016021	ATSG39120.1	ATVAMP72;SAR1;VAMP72;	synaptobrevin-related protein 1	vesicle-associated membrane protein, synaptobrevin 7B, putative
Sapur.006G171200.1	1.64800039	0.940977191	0.216528664	-4.34174	1.39E-05	2.46E-05	grey	0.30581237	9.82E-05		ATSG42620.1			transmembrane protein
Sapur.004G183800.1	0.61942844	1.389003289	0.319641161	-4.34593	1.39E-05	2.45E-05	grey	0.27353874	0.00052749		ATSG22890.1		C2H2 and C2HC zinc fingers superfamily protein	C2-H2 zinc finger protein
Sapur.006G077200.1	796.2213024	-0.460.68394	0.112564122	-4.34526	1.39E-05	2.46E-05	grey	-0.31681602	5.38E-05		ATSG30120.1		Transmembrane protein family protein	NA
Sapur.010G102600.1	148.9654561	-0.410108948	0.092302038	-4.34449	1.40E-05	2.46E-05	grey	-0.31827874	4.86E-05					hypothetical protein
Sapur.016G000300.1	4.58334331	-0.556230703	0.128468733	-4.34367	1.40E-05	2.47E-05	grey	-0.22454833	0.004698943	GD006323;GD005750	ATSG25450.1		Cytochrome b4 ubiquinol oxidase, b6f/b6 subunit	cytochrome B-c1 complex subunit 7
Sapur.016G157700.1	7.26606077	-0.462888231	0.10564607	-4.34369	1.40E-05	2.47E-05	grey	0.36531464	2.55E-06	GD006777	ATSG43760.3		molybdopterin biosynthesis Mod1 family protein	molybdopterin synthase large subunit, putative
Sapur.006G195200.1	233.4204825	0.321881373	0.076286809	-4.34351	1.40E-05	2.47E-05	grey	0.29757362	0.000157779	GD005515;GD006468;GD005524;GD004672	ATSG25930.1		Protein kinase family protein with leucine-rich repeat domain	receptor-like kinase
Sapur.016G127500.1	104.7653909	-0.625319266	0.148179947	-4.34302	1.41E-05	2.48E-05	grey	-0.35272171	5.88E-06	GD008270	ATSG59120.1		Zinc finger superfamily protein	zinc finger protein, putative
Sapur.010G122800.1	266.4548666	0.142451759	0.032800513	-4.34021	1.41E-05	2.48E-05	grey	-0.28460536	0.000306235		ATSG13870.1	DRL1	calmodulin-binding purine nucleotide binding	chromatin associated protein KTI12
Sapur.003G116800.1	1.44076927	-1.185391386	0.27301781	-4.34325	1.41E-05	2.48E-05	grey	-0.27833131	0.000441264		ATMG01090.1			hypothetical protein
Sapur.010G097800.1	7.40225029	0.406890153	0.324050029	-4.34158	1.41E-05	2.50E-05	grey	0.34784284	8.05E-06					NA
Sapur.003G181400.1	597.8984661	0.316844527	0.07306542	-4.34122	1.42E-05	2.50E-05	grey	0.31813604	1.48E-05	GD005975;GD004553	ATSG07320.1		O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase, putative
Sapur.013G104300.1	3.20426955	0.890789663	0.205131437	-4.33874	1.43E-05	2.52E-05	grey	0.28981679	0.000231674	GD043565;GD006355;GD007030;GD003677	ATSG06730.1	HAT14	homeobox from Arabidopsis thaliana	homeobox leucine zipper protein, putative
Sapur.003G091100.1	1422.973438	-0.661661101	0.152488072	-4.33831	1.43E-05	2.52E-05	grey	0.30988706	7.79E-05	GD003924;GD007017;GD005874	ATSG22320.1	TU8B	Kinesin-like protein	nucleus, beta chain
Sapur.013G168100.2	42.54074844	0.340959079	0.07659476	-4.33819	1.44E-05	2.52E-05	grey	0.00348053	0.945496971		ATSG13480.1			hypothetical protein
Sapur.004G099600.1	274.452892	0.120085157	0.029235925	-4.33804	1.44E-05	2.54E-05	grey	-0.35383485	4.19E-06	GD016392;GD016023;GD006810	ATSG23530.1		Gnt1/Pbl2-like vesicle transport protein family	Gnt1/Pbl2-like vesicle transporter
Sapur.005G039200.1	163.4361214	-0.240497867	0.059149654	-4.33802	1.44E-05	2.54E-05	grey	-0.31769762	5.61E-05	GD006468;GD005524;GD004672	ATSG42630.1		Protein kinase superfamily protein	transmembrane receptor 1-associated receptor kinase, putative
Sapur.I16G111000.3	18.05138604	-0.586399174	0.13127833	-4.33624	1.45E-05	2.56E-05	grey	-0.01009754	0.900153931		ATSG26980.1	ATNBG1;NBS1	nijmegen breakage syndrome 1	NA
Sapur.I59G053000.1	2.05018859e-17	1.512353232	0.34879725	-4.33561	1.45E-05	2.56E-05	grey	0.26879658	0.000419973	GD055114;GD020037;GD016705;GD005506	ATSG45163.1	CYP704A2	cytochrome P450, family 704, subfamily A, polypeptide 2	NA
Sapur.I01G161200.1	4.77263773	-1.804368841	0.4142594	-4.33472	1.46E-05	2.57E-05	grey	-0.38295657	7.42E-07		ATSG16630.1			NA
Sapur.I21G069300.2	21.02602585	-0.383814651	0.205609633	-4.33467	1.46E-05	2.57E-05	grey	0.21719015	0.006306291	GD048544	ATSG11140.1		S-locus lectin protein kinase family protein	NA
Sapur.T161200.1	0.40917129	1.727671677	0.398612233	-4.33417	1.46E-05	2.58E-05	grey	0.36461193	2.71E-06					NA
Sapur.I59G151000.2	1.35886051	-1.289350025	0.297408847	-4.33408	1.46E-05	2.58E-05	grey	-0.11119166	0.607171827		ATSG36620.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR domain protein, putative
Sapur.I59G125000.1	8.05761791	-0.699004759	0.161334373	-4.33294	1.47E-05	2.59E-05	grey	-0.27261948	0.00054422		ATSG45470.1		Protein of unknown function (DUF594)	NA
Sapur.I05G037700.1	135.8047636	-0.658014461	0.152488157	-4.33184	1.48E-05	2.61E-05	grey	0.31316052	0.000288626					hypothetical protein
Sapur.I01G143400.2	4.06622749	0.607614487	0.140324276	-4.33035	1.49E-05	2.62E-05	grey	0.29882554	0.000143771	GD005515	ATSG02020.1	EZA1;SDG10;SWN	SET domain-containing protein	histone-lysine N-methyltransferase, putative
Sapur.008G031000.1	2.76581951	0.869004759	0.161334373	-4.33294	1.47E-05	2.59E-05	grey	0.32754372	2.82E-05					NA
Sapur.I05G143800.1	0.97906434	1.254283877	0.289667005	-4.33007	1.49E-05	2.63E-05	grey	0.30052003	0.000131008					NA
Sapur.I01G122800.1	89.81747966	-0.262415944	0.060615585	-4.32922	1.50E-05	2.64E-05	grey	-0.30945841	8.71E-05		ATSG13200.1		GRAM domain family protein	NA
Sapur.I05G087200.1	14.00216546	-0.495681043	0.11456542	-4.3289	1.50E-05	2.64E-05	grey	-0.30454388	0.000202020		ATSG45160.1		Root hair defective 3 GTP-binding protein (RHD3)	Root hair defective 3 GTP-binding protein (RHD3)
Sapur.T086600.1	1.22625872	2.963872757	0.218054895	-4.32602	1.51E-05	2.66E-05	grey	0.38060109	8.87E-07					NA
Sapur.I05G054500.1	15.7523571	0.559221491	0.129218995	-4.32772	1.51E-05	2.65E-05	grey	0.31108382	7.32E-05		ATSG13540.1	ATMYB5;MYB5	myb domain protein 5	MYB transcription factor, putative
Sapur.I01G137900.1	1.86658582e-16	0.995598875	0.230047741	-4.32486	1.53E-05	2.69E-05	grey	-0.32103332	4.14E-05	GD005975;GD004553	ATSG45620.1	ATGH9A2;XDR2	Glycosyl hydrolases family protein	endo-1%2C4-beta-glucanase
Sapur.I05G082200.2	1.32893707	-0.091148704	0.2121423	-4.32456	1.53E-05	2.69E-05	grey	-0.32203663	0.000168477		ATSG21260.1	ARGK;ATARG9	autophagy 9 family protein	autophagy protein kinase 9 containing protein
Sapur.I01G148900.1	5.62745412	0.569942226	0.131795588	-4.32444	1.53E-05	2.69E-05	grey	-0.29285132	0.000175603		ATSG05680.1	MOS7	nuclear pore complex protein-related	nuclear pore complex-like protein
Sapur.I05G148900.1	688.0120937	0.562237947	0.138404165	-4.32388	1.53E-05	2.70E-05	grey	-0.31705145	5.23E-05		ATSG66510.1		mitochondrial ribosomal protein L51/S25/CI-B8 family protein	ribosomal protein L51/S25/CI-B8 family protein
Sapur.I05G062800.1	434.4945728	0.155881465	0.038009791	-4.32351	1.53E-05	2.70E-05	grey	-0.32463616	3.36E-05		ATSG22530.1		Protein of unknown function (DUF581)	DUF581 family protein
Sapur.I01G167300.1	3.11997594	-0.703251393	0.162688662	-4.32278	1.54E-05	2.71E-05	grey	-0.32158843	6.01E-05		ATSG61190.1		putative endosulfanase or glycosyl hydrolase with C2H2-type zinc finger domain	NA
Sapur.I01G136400.1	4.28657875	-1.142938532	0.264198602	-4.32244	1.54E-05	2.71E-05	grey	-0.31182153	5.76E-05	GD016829;GD010333;GD008152;GD000287	ATSG29120.1	TPS10	terpene synthase 10	NA
Sapur.I01G077700.2	17.16618579	0.539793755	0.124883046	-4.32194	1.54E-05	2.72E-05	grey	-0.28209102	0.000344491	GD005515	ATSG05460.1		RNA-like superfamily protein	5'-5'-phosphate and NAD+ dependent RNA helicase DHR9
Sapur.I05G132200.1	726.2924844	0.229209885	0.053014335	-4.32166	1.55E-05	2.73E-05	grey	-0.34884161	1.25E-05	GD055515;GD003676;GD004386	ATSG24960.1	EMB2733;EP3	RNA helicase family protein	ATP-dependent RNA helicase DHR8
Sapur.I05G051200.1	1.57274699	-0.000386264	0.23115334	-4.32037	1.56E-05	2.76E-05	grey	-0.30863718	8.40E-05	GD006351;GD003899	ATSG25910.1		RNA polymerase II, RpbK core protein	RNA polymerase RpbK
Sapur.I05G112000.1	50.5818116	0.230281015	0.07646606	-4.31976	1.56E-05	2.76E-05	grey	-0.34835195	7.77E-06	GD043565;GD006355;GD003700	ATSG55130.1	AtbZIP18;bZIP18	basic region/leucine zipper transcription factor 16	BZIP transcription factor
Sapur.I01G079400.1	151.9779578	0.173387347	0.040184595	-4.31974	1.56E-05	2.76E-05	grey	0.35325989	4.96E-06		ATSG79310.1	ATRNL;RNL	RNAligase	NA
Sapur.I05G145400.1	221.488855	0.290218836	0.06637588	-4.31953	1.56E-05	2.76E-05	grey	-0.30730379	1.02E-05		ATSG59680.2			hypothetical protein
Sapur.I08G058800.1	1.39164585	1.051579224	0.241509416	-4.31694	1.58E-05	2.79E-05	grey	0.29831699	0.00016685		ATSG40260.1		Homeodomain-like superfamily protein	Myb-like DNA-binding domain protein
Sapur.I01G013500.1	6.86314829	-1.167786326	0.270534165	-4.31659	1.58E-05	2.79E-05	grey	-0.31233953	6.86E-05		ATSG05320.1	ATEHD2;EHD2	EPS15 homology domain 2	EPS15 homology domain 2
Sapur.I01G175800.1	611.6260768	0.165026736	0.024686565	-4.31602	1.59E-05	2.80E-05	grey	0.31561299	5.01E-05		ATSG20120.1		DNA heat shock transcriptional domain-containing protein	heat shock protein binding protein-related
Sapur.I01G165200.1	42.9737874	0.434341986	0.100649124	-4.31408	1.59E-05	2.80E-05	grey	0.34946001	7.26E-06	GD006355;GD003677	ATSG22380.1	anac006;NAC006	NAC domain containing protein 90	NAC transcription factor
Sapur.I05G058400.1	219.0849014	-0.567853788	0.134668	-4.31405	1.59E-05	2.81E-05	grey	0.30240498	1.66E-05	GD042391;GD016767;GD005524;GD003677	ATSG60510.1	ATCHR12	Homeotic gene regulator	chromatin remodeling subunit
Sapur.I16G051900.1	371.0047628	0.228545933	0.052976185	-4.31492	1.60E-05	2.82E-05	grey	0.29815264	0.000149609		ATSG06700.1	TBR	Plant protein of unknown function (DUF828)	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.I01G112700.1	0.61618291	-1.453897487	0.56891031	-4.31346	1.60E-05	2.82E-05	grey	0.28378969	0.000127					hypothetical protein
Sapur.I07G086400.1	310.5948827	-0.125026735	0.028985415	-4.31344	1.61E-05	2.83E-05	grey	-0.33781566	1.51E-05		ATSG52530.1			transmembrane protein, putative
Sapur.I07G201200.1	8.90466799	-0.664663291	0.154186841	-4.31321	1.61E-05	2.83E-05	grey	-0.33432667	1.87E-05		ATSG27230.1			transmembrane protein, putative
Sapur.I01G112500.1	3.19250951	-0.64632371	0.149693891	-4.31303	1.61E-05	2.83E-05	grey	-0.32647802	3.01E-05				Uncharacterized protein family (UPF0497)	NA
Sapur.I05G080900.1	296.5362435	0.155931619	0.036809462	-4.31241	1.61E-05	2.84E-05	grey	-0.29631842	0.000225577		ATSG07020.1			hypothetical protein
Sapur.I01G098500.1	2.59701798	0.706645059	0.164572387	-4.31245	1.61E-05	2.84E-05	grey	-0.32773829	2.79E-05	GD005156;GD003824;GD015139;GD016992;GD009107	ATSG08415.1		Radical SAM superfamily protein	Elongator protein 3
Sapur.I01G021500.1	5.46023343	0.801091543	0.189480784	-4.31011	1.63E-05	2.87E-05	grey	-0.35230767	6.94E-06		ATSG56430.1		Carbohydrate-binding-like domain superfamily protein	carbohydrate-binding module family protein
Sapur.I05G070500.1	220.4412463	-0.188481038	0.043727281	-4.30809	1.64E-05	2.88E-05	grey	-0.37547164	2.07E-06		ATSG24540.1		RNI-like superfamily protein	glucose regulated repressor protein, putative
Sapur.I01G067500.1	172.582746	0.167305531	0.038779353	-4.30924	1.64E-05	2.88E-05	grey	-0.34021292	1.30E-05		ATSG46060.1		transmembrane protein-related	transmembrane protein BB
Sapur.I08G155600.1	0.68887924	-0.252381973	0.058488	-4.30919	1.64E-05	2.88E-05	grey	-0.37984614	1.41E-06		ATSG68360.1		C2H2 and C2HC zinc fingers superfamily protein	zinc finger protein, putative
Sapur.I01G130800.4	0.78155871	-1.224601479	0.284347954	-4.30671	1.66E-05	2.91E-05	grey	0.07564831	0.321841487		ATSG11860.4	SSP5	SCP1-like small phosphatase family protein	CTD small phosphatase-like protein
Sapur.I05G080100.1	1.60667674	0.913

Sapur.01G0089400.1	62.63420108	-6.36675499	0.086539217	-4.23876	2.25E-05	3.92E-05	grey	-0.309311792	8.86E-04	ATSG31240.1		Bromodomain transcription factor	NA
Sapur.004G154300.1	97.44932826	-0.186489138	0.04600024	-4.23837	2.25E-05	3.93E-05	grey	-0.318951599	4.67E-05	AtHSC15270.1		Plant regulator RWP-RK family protein	transcription factor, putative
Sapur.01G0100300.1	118.0864159	0.033542204	0.149018225	-4.23755	2.26E-05	3.94E-05	grey	-0.340039138	1.29E-05	AtHSC18130.1		Ribosomal protein L7 family	NA
Sapur.005G028400.1	4.585901968	0.533382073	0.125897148	-4.23665	2.27E-05	3.96E-05	grey	-0.349846693	7.08E-06	AtHSC62550.1		RING/U-box superfamily family protein	RING-zinc finger protein
Sapur.01G0200400.1	3356.015369	0.365320858	0.087170584	-4.23637	2.28E-05	3.96E-05	grey	-0.31628848	5.45E-05	AtHSC24220.1	AW031_VEP1	NAD(P)-binding Rossmann-fold superfamily protein	progesterone 5-beta-reductase, putative
Sapur.01G0130300.1	60.98127008	0.230165689	0.05432909	-4.26509	2.27E-05	3.96E-05	grey	-0.342438852	1.13E-05				hypothetical protein
Sapur.01G0287200.1	2.670802002	-0.679720258	0.160465789	-4.23592	2.28E-05	3.97E-05	grey	-0.347439825	8.36E-06	GO:0008270;GO:0005515	RHB1A	RING-H2 finger B1A	RING-H2 finger B1A
Sapur.004G222600.1	116.4078808	0.187858984	0.044160545	-4.23543	2.28E-05	3.98E-05	grey	-0.348376269	7.58E-06		ATCGC14.CCHGC14	cyclic nucleotide-gated channel 14	NA
Sapur.008G051300.1	425.3838989	0.165024496	0.039078666	-4.23514	2.28E-05	3.99E-05	grey	-0.34862189	7.66E-06	GO:0016021;GO:0008233;GO:0006460;GO:0005787		Microsomal signal peptidase 25 kDa subunit (SPC25)	NA
Sapur.002G017400.2	0.78282957	0.573138839	0.136437536	-4.23427	2.29E-05	4.00E-05	grey	-0.078548531	4.11E-04	GO:0006355;GO:0005667;GO:0003700	AtTEF2;AtTEF2C;E2FC	winged-helix DNA-binding transcription factor family protein	transcription factor E2F
Sapur.01G0206600.3	2.10153931	0.703545021	0.180338354	-4.23411	2.29E-05	4.00E-05	grey	-0.130754074	0.08086349			DCD (Development and Cell Death) domain protein	Gda-1, putative
Sapur.004G157800.1	0.651887571	0.404983063	0.137906483	-4.23452	2.30E-05	4.00E-05	grey	-0.315188751	3.91E-05	GO:0016021;GO:0005215		Drug/metabolite transporter superfamily protein	NA
Sapur.017G024700.1	5.654653097	0.581726645	0.137427281	-4.23298	2.31E-05	4.02E-05	grey	-0.304945454	0.001004468	GO000123			DNA-binding domain protein, putative
Sapur.006G369800.1	7.897470605	0.618604229	0.147128384	-4.23301	2.31E-05	4.02E-05	grey	-0.318300419	0.000406008			Tetratricopeptide repeat (TPR)-like superfamily protein	DnaJ homologue, putative
Sapur.012G096300.3	5.061375467	0.598324154	0.141385614	-4.23186	2.32E-05	4.04E-05	grey	-0.09630618	0.232032985			clathrin adaptor complexes medium subunit family protein	clathrin-adaptor complexes medium subunit family protein
Sapur.004G204300.1	5.589693372	0.867800382	0.205097943	-4.23169	2.32E-05	4.05E-05	grey	-0.277848993	0.000426287			P-loop containing nucleoside triphosphate hydrolases superfamily protein	P-loop containing nucleoside triphosphate hydrolases family-like protein
Sapur.005G198700.1	265.1572729	0.330338551	0.078068124	-4.231414	2.32E-05	4.05E-05	grey	-0.312950183	6.59E-05	GO:0009415;GO:0006950	AtCOR47,COR47,RD17	cold-regulated 47	dehydrin
Sapur.007G105400.1	12.55338903	0.728696264	0.172129459	-4.23005	2.34E-05	4.07E-05	grey	-0.317995658	4.94E-05				hypothetical protein
Sapur.005G028300.1	4.553577786	0.852663416	0.150023018	-4.22975	2.34E-05	4.08E-05	grey	-0.14673454	0.006376922		HMGB1,NFD01,NFD3	high mobility group B3	NA
Sapur.008G141300.1	490.5569579	0.263751022	0.062357526	-4.22966	2.34E-05	4.08E-05	grey	-0.290529653	0.000223217		SMAP1	small acidic protein 1	hypothetical protein
Sapur.005G172400.3	31.59648884	0.625025504	0.148239166	-4.22862	2.35E-05	4.09E-05	grey	-0.129803497	0.101361164	GO003676		RNA-binding (RNA9B/RNP motif) family protein	RNA recognition motif 2 in RNA-binding protein musashi-like musashi protein
Sapur.01G0201600.1	137.3727214	0.288265451	0.068171794	-4.22851	2.35E-05	4.10E-05	grey	-0.155922484	0.046001107				arginine and glutamate-rich 1 protein
Sapur.004G207800.1	1264.151949	0.129317422	0.030588802	-4.22767	2.36E-05	4.11E-05	grey	-0.275882275	0.000469771	GO:0003170;GO:0008483	AGT2	alanine:glyoxylate aminotransferase 2	alanine:glyoxylate aminotransferase, putative
Sapur.001G071700.1	237.5918881	0.384947977	0.091002229	-4.227307	2.37E-05	4.12E-05	grey	-0.191027237	0.016504123			Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.004G225200.1	0.466454963	1.414527378	0.340501984	-4.2272	2.37E-05	4.12E-05	grey	-0.51728	2.06E-05	GO:0005515;GO:0006468;GO:0004672		Leucine-rich repeat protein kinase family protein	NA
Sapur.01G0690200.1	300.1460913	0.238097568	0.056360365	-4.227077	2.37E-05	4.13E-05	grey	-0.33938432	1.37E-05				hypothetical protein
Sapur.01G0122200.6	0.818354982	0.336004292	0.316001067	-4.22704	2.37E-05	4.13E-05	grey	-0.301108043	0.005126669			DTW domain-containing protein	DTW domain protein
Sapur.017G027200.1	6.896475429	0.456451406	0.108075033	-4.22688	2.37E-05	4.13E-05	grey	-0.302520286	0.00011765	GO:0016192		Golgi/SNP2-like vesicle transport protein family	vesicle transporter GOT1B, putative
Sapur.01B0119200.3	0.930322759	-1.208859517	0.286026136	-4.22687	2.37E-05	4.13E-05	grey	-0.298631361	0.000145281			hydroxyproline-rich glycoprotein family protein	plastid DNA-binding protein, putative
Sapur.01W0018880.1	17.34637273	0.454988251	0.108812121	-4.226425	2.37E-05	4.14E-05	grey	-0.263464823	0.000312263				DUF1543 family protein
Sapur.01G0482000.1	0.290955716	1.88761235	0.446623865	-4.226403	2.37E-05	4.14E-05	grey	-0.479609692	2.06E-10			Protein protein of unknown function (DUF889)	NA
Sapur.005G115300.1	45.34719325	-0.542384093	0.057172969	-4.22568	2.37E-05	4.14E-05	grey	-0.301562799	0.000123664	GO:0005739;GO:0004129	ATCOXIIA2,COXIIA9	cytochrome oxidase C subunit VIb	cytochrome oxidase C subunit VIb
Sapur.005G080300.1	28.27799363	0.298270797	0.070560015	-4.225037	2.38E-05	4.16E-05	grey	-0.353460305	5.60E-06	GO0016765		Undecaprenyl pyrophosphate synthetase family protein	undecaprenyl pyrophosphate synthase
Sapur.004G162700.1	4.270144661	-0.674164519	0.158968854	-4.22502	2.38E-05	4.16E-05	grey	-0.29274054	0.000269769				NA
Sapur.006G266000.1	2563.332775	0.179616515	0.042154654	-4.224834	2.38E-05	4.17E-05	grey	-0.284148428	0.000103296			Proteasome maturation factor UMP1	proteasome maturation factor UMP1 family protein
Sapur.004G208700.1	13.84568745	-0.612328844	0.144216164	-4.224668	2.38E-05	4.17E-05	grey	-0.313458886	5.70E-06			myb-like HTH transcriptional regulator family protein	NA
Sapur.T034300.1	52.3829954	0.292620936	0.069271675	-4.224251	2.40E-05	4.18E-05	grey	-0.369375324	1.93E-06				NA
Sapur.007G137500.1	94.71008883	0.895038724	0.164539126	-4.224143	2.40E-05	4.18E-05	grey	-0.357579876	4.27E-06	GO:0003247;GO:0006468;GO:0005524;GO:0004672		protein serine/threonine kinases;protein kinases;ATP binding;sugar binding;kinases;carbohydrate binding	NA
Sapur.01B0193800.1	93.61092603	0.146502093	0.034786683	-4.22367	2.40E-05	4.19E-05	grey	-0.314846458	1.24E-06				hypothetical protein
Sapur.01G0238400.1	371.76191	0.287484937	0.068008886	-4.223441	2.41E-05	4.19E-05	grey	-0.289205431	0.000239161	GO0006229;GO0005108;GO:0004190	APA1,ATAPA1	aspartic proteinase A1	aspartic proteinase
Sapur.01G0062300.1	306.4727985	0.251279152	0.059668655	-4.223007	2.41E-05	4.20E-05	grey	-0.32061768	4.29E-05				hypothetical protein
Sapur.007G089200.1	2.516862296	-0.683819249	0.161924146	-4.22261	2.41E-05	4.21E-05	grey	-0.341839564	1.18E-05			Plant protein of unknown function (DUF868)	filament-like plant protein, putative
Sapur.01G0284700.1	2.806418837	0.726109296	0.171918315	-4.22262	2.41E-05	4.21E-05	grey	-0.00925047	0.000688737	GO0008837;GO0030145	SEC6	SEC6	exocyst complex subunit, putative
Sapur.01G0070300.1	335.7013055	0.163625991	0.038766129	-4.22085	2.43E-05	4.24E-05	grey	-0.318849763	1.45E-05				T6.10 protein, putative
Sapur.004G201000.1	10.85195702	0.914296591	0.216616	-4.220625	2.43E-05	4.24E-05	grey	-0.292022254	0.000368887	GO0006229	FAD2	Fatty acid desaturase	delta-12 fatty acid desaturase
Sapur.01G0072000.1	4.716451008	0.573545284	0.135888551	-4.22077	2.43E-05	4.24E-05	grey	-0.314883424	5.87E-05			RNA-binding KH domain-containing protein	T1.4 protein, putative
Sapur.01G0151100.1	27.56808696	0.704062473	0.166815491	-4.220606	2.44E-05	4.24E-05	grey	-0.305205059	0.000102444			Thioredoxin superfamily protein	NA
Sapur.01G0102300.1	435.341852	-0.260830366	0.06054807	-4.22046	2.44E-05	4.25E-05	grey	-0.320774015	4.20E-05	LRP1		Lateral root primordium (LRP) protein-related	transcription factor, putative
Sapur.017G061400.1	33.72442909	-0.439181832	0.104074292	-4.21976	2.45E-05	4.26E-05	grey	-0.289055662	0.000241029				NA
Sapur.006G044200.4	1.710711168	0.452217924	0.108145	-4.21946	2.45E-05	4.26E-05	grey	-0.142884212	0.079424619			nucleolar protein gar2-related	L6G protein
Sapur.005G130100.1	0.528101857	1.175429014	0.515622895	-4.21903	2.45E-05	4.27E-05	grey	-0.383372952	8.51E-07	GO:0005992;GO:0003824		Haloacid dehalogenase-like hydrolase (HAD) superfamily	trehalose-phosphate phosphatase, putative
Sapur.005G082100.1	2.768858857	0.551481447	0.154960073	-4.218875	2.46E-05	4.29E-05	grey	-0.356690633	4.56E-06	GO:0004488;GO:0004672	CRK10,RLK4	cysteine-rich RLK (RLK) subfamily protein	NA
Sapur.01G0050400.5	2.185675671	-0.818180033	0.193955708	-4.21839	2.46E-05	4.28E-05	grey	-0.07854831	0.32814687			2o-dependent oxoglutarates superfamily protein	NGE2-2o-peptidase family protein
Sapur.004G087300.1	1.367950751	-0.364591	0.086455291	-4.218429	2.47E-05	4.30E-05	grey	-0.328382006	2.68E-05			AGC kinase superfamily protein	transportin, putative
Sapur.006G199200.2	0.923926557	1.173816163	0.278279312	-4.21728	2.47E-05	4.30E-05	grey	-0.288631864	6.31E-05			peroxin4	ubiquitin-conjugating enzyme E2, putative
Sapur.004G204200.1	1.006763126	1.12257862	0.266248278	-4.217236	2.48E-05	4.31E-05	grey	-0.317374831	1.56E-05	GO:0043565;GO:0006355;GO:0003700	ATWRKY60,WRKY65	WRKY DNA-binding protein 65	WRKY transcription factor, putative
Sapur.01G0231800.2	177.6300313	0.249893045	0.059289174	-4.21624	2.48E-05	4.32E-05	grey	-0.374600656	1.36E-06	GO0005515		F-box family protein	F-box protein
Sapur.006G132800.1	369.8923817	0.12466788	0.029570394	-4.215942	2.49E-05	4.33E-05	grey	-0.343426367	1.06E-05		UBC27	ubiquitin-conjugating enzyme 37	ubiquitin-conjugating enzyme E2 T
Sapur.011G0260001.1	123.3667511	-0.257974189	0.28891682	-4.21566	2.49E-05	4.33E-05	grey	-0.460892555	1.26E-09			NAD(P)-binding Rossmann-fold superfamily protein	NA
Sapur.15W0G012200.1	601.9571173	0.283265769	0.067194829	-4.214348	2.51E-05	4.36E-05	grey	-0.27759727	0.000428187				UPF0368 protein C5orf57-like protein, putative
Sapur.01G0070001.1	16.67832175	0.86466918	0.151882	-4.21333	2.52E-05	4.38E-05	grey	-0.269181834	0.011398285	GO0005515		receptor like protein 6	NA
Sapur.01G0089800.1	21.41996078	0.332322683	0.078690421	-4.21177	2.53E-05	4.41E-05	grey	-0.305025059	0.000102444			Thioredoxin superfamily protein	DUF3511 domain protein
Sapur.01G0102300.1	435.341852	-0.260830366	0.06054807	-4.21096	2.44E-05	4.25E-05	grey	-0.320774015	4.20E-05	LRP1		Lateral root primordium (LRP) protein-related	transcription factor, putative
Sapur.017G061400.1	33.72442909	-0.439181832	0.104074292	-4.21976	2.45E-05	4.26E-05	grey	-0.289055662	0.000241029				NA
Sapur.006G044200.4	1.710711168	0.452217924	0.108145	-4.21946	2.45E-05	4.26E-05	grey	-0.142884212	0.079424619			nucleolar protein gar2-related	L6G protein
Sapur.005G130100.1	0.528101857	1.175429014	0.515622895	-4.21903	2.45E-05	4.27E-05	grey	-0.383372952	8.51E-07	GO:0005992;GO:0003824		Haloacid dehalogenase-like hydrolase (HAD) superfamily	trehalose-phosphate phosphatase, putative
Sapur.005G082100.1	2.768858857	0.551481447	0.154960073	-4.218875	2.46E-05	4.29E-05	grey	-0.356690633	4.56E-06	GO:0004488;GO:0004672	CRK10,RLK4	cysteine-rich RLK (RLK) subfamily protein	NA
Sapur.01G0050400.5	2.185675671	-0.818180033	0.193955708	-4.21839	2.46E-05	4.28E-05	grey	-0.07854831	0.32814687			2o-dependent oxoglutarates superfamily protein	NGE2-2o-peptidase family protein
Sapur.004G087300.1	1.367950751	-0.364591	0.086455291	-4.218429	2.47E-05	4.30E-05	grey	-0.328382006	2.68E-05			AGC kinase superfamily protein	transportin, putative
Sapur.006G199200.2	0.923926557	1.173816163	0.278279312	-4.21728	2.47E-05	4.30E-05	grey	-0.288631864	6.31E-05			peroxin4	ubiquitin-conjugating enzyme E2, putative
Sapur.004G204200.1	1.006763126	1.12257862	0.266248278	-4.217236	2.48E-05	4.31E-05	grey	-0.317374831	1.56E-05	GO:0043565;GO:0006355;GO:0003700	ATWRKY60,WRKY65	WRKY DNA-binding protein 65	WRKY transcription factor, putative
Sapur.01G0231800.2	177.6300313	0.249893045	0.059289174	-4.21624	2.48E-05	4.32E-05	grey	-0.374600656	1.36E-06	GO0005515		F-box family protein	F-box protein
Sapur.006G132800.1	369.8923817	0.12466788	0.029570394	-4.215942	2.49E-05	4.33E-05	grey	-0.343426367	1.06E-05		UBC27	ubiquitin-conjugating enzyme 37	ubiquitin-conjugating enzyme E2 T
Sapur.011G0260001.1	123.3667511	-0.257974189	0.28891682	-4.21566	2.49E-05	4.33E-05	grey	-0.460892555	1.26E-09			NAD(P)-binding Rossmann-fold superfamily protein	NA
Sapur.15W0G012200.1	601.9571173	0.283265769	0.067194829	-4.214348	2.51E-05	4.36E-05	grey	-0.27759727	0.000428187				UPF0368 protein C5orf57-like protein, putative
Sapur.01G0070001.1	16.67832175	0.86466918	0.151882	-4.21333	2.52E-05	4.38E-05	grey	-0.269181834	0.011398285	GO0005515		receptor like protein 6	NA
Sapur.01G0089800.1	21.41996078	0.332322683	0.078690421	-4.21177	2.53E-05	4.41E-05	grey	-0.305025059	0.000102444			Thioredoxin superfamily protein	DUF3511 domain protein
Sapur.01G0102300.1	171.5143668	0.218784997	0.051939559	-4.21114	2.54E-05	4.42E-05	grey	-0.341818154	1.18E-05			Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.007G021300.1	1.578131552	0.908213261	0.215649968	-4.21064	2.55E-05	4.43E-05	grey	-0.316162739	5.49E-05				NA
Sapur.01G0284300.1	1.095.799319	0.405.6.8.8.1	0.096650147	-4.2105	2.55E-05	4.43E-05	grey	-0.332936196	7.46E-06	GO:0005114;GO:0016491		ferric reduction oxidase 6	heme-c-chelate reductase, putative
Sapur.007G065900.1	0.358605598	1.988394207	0.472267648	-4.210312	2.55E-05	4.43E-05	grey	-0.444864057	5.31E-09	GO0008270;GO0005515	ATRING,FRO6	Zinc finger, C3HC4 type (RING finger) family protein	RING-H2 zinc finger protein
Sapur.01G0280900.1	438.9837777	0.235854071	0.056025129	-4.209875	2.56E-05	4.44E-05	grey	-0.29875452	0.000187775			TCP family transcription factor	TCP transcription factor
Sapur.01G0848800.1	2065.417589	0.329585279	0.078293836	-4.209594	2.56E-05	4.45E-05	grey	-0.292713251	0.000199067			cellulose synthase family protein	cellulose synthase A
Sapur.008G205900.1	8.324923855	-0.897165462	0.213192763	-4.20824	2.57E-05	4.47E-05	grey	-0.378634414	1.02E-06				hypothetical protein
Sapur.005G203000.1	111.5417086	-0.485318491	0.115059503	-4.20793	2.58E-05	4.48E-05	grey	-0.355021513	4.87E-06	GO0007165;GO0005515;GO:0043531		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.01G0207700.1	696.2763837	-0.281814229	0.066985942	-4.20707	2.58E-05	4.50E-05	grey	-0.12465979	3.35E-05			alpha/beta-Hydrolases superfamily protein	sigma factor sigb regulation protein rsbq protein
Sapur.01G0264700.1	12.33870904	-0.225568809	0.05264648	-4.20671	2.58E-05	4.50E-05	grey	-0.287850142	0.000245627	GO:0017069;GO:0000398			NA
Sapur.01G0292600.3	37.86398816	-0.394267453	0.09372351	-4.20671	2.58E-05	4.50E-05	grey	-0.081608864	0.309590942	GO:0016021;GO:0004190	ATSPP1,2,SPP1,2	SIGNAL PEPTIDE PEPTIDASE-LIKE 2	signal peptide peptidase-like protein
Sapur.01G0205000.1	36.24664658	0.411314202	0.09826429	-4.20529	2.59E-05	4.51E-05	grey	-0.342610596	1.12E-05	GO:0016866		Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	allinin lyase-like protein
Sapur.006G012100.1	760.3949675	0.26684519	0.063455579	-4.205228	2.61E-05	4.53E-05	grey	-0.267847086	0.000695161			Uncharacterised protein family (UPF0497)	CASP-like protein PORTPORDRAFT-81895 protein
Sapur.004G207200.1	270.8439454	0.181725892	0.043218514	-4.204769	2.61E-05	4.54E-05	grey	-0.305273057	0.000100627	GO0008289		Polykeratin conserved domain and lipid transport superfamily protein	mammalian STARD7-like lipid-binding START domain protein, putative
Sapur.017G127500.1	215.0664706	0.582361176	0.138598695	-4.202962	2.63E-05	4.58E-05	grey	-0.260419192	0.000127926			Kunitz family trypsin and protease inhibitor family protein	kunitz-type trypsin inhibitor
Sapur.01G0213900.6	1.37793349	0.961092104	0.228678786	-4.202786	2.64E-05	4.58E-05	grey	-0.326113489	3.07E-05			RING/U-box superfamily family protein	baculovirus IAP repeat protein, putative
Sapur.15W0G018180.1	52.5109846	-0.319381924	0.075178954	-4.20268	2.64E-05	4.58E-05	grey	-0.292979516	4.17E-05	GO:0006355;GO:0003700	CRF4	cytokinin response factor 4	AP2/EREBP domain transcription factor
Sapur.01G0434000.1	8.613664674	0.499230428	0.118831119	-4.201176	2.66E-05	4.61E-05	grey	-0.288813875	0.002344074		IqD9	IQ-domain 9 protein	IQ-domain 9 protein
Sapur.003G167000.1	4.004923164	0.611881986	0.145618373	-4.20064	2.66E-05	4.62E-05	grey	-0.321687739	1.99E-05				NA
Sapur.003G140000.1	0.914323506	1.349174009	0.321600092	-4.197019	2.70E-05	4.70E-05	grey	-0.283003497	0.000328917	GO:0016758;GO:0008152		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase family protein
Sapur.007G027300.1	0.56972986	1.802066429	0.448497756	-4.196335	2.71E-05	4.71E-05	grey	-0.32221053	1.87E-05				NA
Sapur.T006100.1	4.273595825	0.880241302	0.209765989	-4.195901	2.72E-05	4.72E-05	grey	-0.221495879	0.053205548				transmembrane protein, putative
Sapur.01G0181400.1	106.4073989	0.674825773	0.161134903	-4.19542	2.72E-05	4.73E-05	grey	-0.264121058	0.000822337				transmembrane protein, putative
Sapur.001G135200.1	3.738695339	-0.993131851	0.236857292	-4.19295	2.75E-05	4.78E-05	grey	-0.312139973	6.90E-05	GO:0004857;GO:0042545;GO:0030599;GO:0005618		pectin methylesterase 3	NA
Sapur.01G0301000.1	20.42218322	-0.679278466	0.162018514	-4.190478	2.76E-05	4.79E-05	grey	-0.329278944	0.000160606	GO0005524;GO0007165;GO0005515		Polykeratin conserved domain (TIR-NBS-LRR class) family	disease resistance protein
Sapur.T050200.1	128.7288946	-0.226680808	0.054084743	-4.19061	2.78E-05	4.81E-05	grey	-0.326586468	2.96E-05		AtRI,RI1	a-ray induced transport 1	XRI1
Sapur.003G194400.1	452.5154729	0.362934956	0.082765547	-4.190496	2.78E-05	4.83E-05	grey	-0.329817553	2.95E-05	GO:0006355;GO:0003700			NA
Sapur.01B0264500.3	2.175107907	0.616824213	0.147306365	-4.188724	2.81E-05	4.87E-05	grey	-0.014527876	0.627702084	GO0007275;GO:0005524;GO:0048835;GO:0005516;GO:0004196;GO:0005667	ATHIK2,HIK2	hexokinase 2	hexokinase
Sapur.017G061000.3	1.629123976	0.916060126	0.218727043	-4.18865	2.81E-05	4.88E-05	grey	-0.33113826	2.27E-05	GO0008270;GO0005515		RING/U-box superfamily protein	zinc finger protein
Sapur.017G079000.1	39.17908836	1.353803517	0.323753233	-4.18777	2.82E-05	4.89E-05	grey	-0.34882527	2.50E-07				transmembrane protein, putative
Sapur.01G0121200.1	56.16036729	0.296307498	0.070827879	-4.187581	2.82E-05	4.89E-05	grey	-0.289622126	0.000234033			RNI-like superfamily protein	atFBI3 F-box protein, putative
Sapur.005G081000.1	51.16117974	-0.251324864	0.062368527	-4.18691	2.83E-05	4.91E-05	grey	-0.320012112	0.000310848			Transferase family protein	nucleoside-triphosphatase, putative
Sapur.01G0186900.1	162.5299119	0.193261137	0.046164435	-4.18647	2.83E-05	4.92E-05	grey	-0.326334989	3.03E-05			aspartate/glutamate/uridylate kinase family protein	uridylate kinase
Sapur.004G184600.1	0.42941463	1.617708568	0.386447247	-4.18616	2.84E-05	4.92E-05	grey	-0.404908358	1.46E-07		AtMYB88,MYB88	myb-domain protein 88	Myb-like DNA-binding domain protein
Sapur.012G017000.1	0.49031669	2.010534851	0.528152768	-4.185443	2.85E-05	4.94E-05	grey	-0.389364552	4.66E-07				NA
Sapur.004G144900.1	3.563844023	0.662324026	0.159228893	-4.183208	2.88E-05	4.99E-05	grey	-0.324442223	2.52E-05		AtcDO4,cDO4	indeterminate(ID)-domain 4	C2H2-type zinc finger protein
Sapur.01G0276000.2	18.72612065	0.332761183	0.079606424	-4.18008	2.91E-05	5.05E-05	grey	-0.33215696	2.08E-05			Ubiquitin-like superfamily family protein	telomere stability/silencing protein
Sapur.004G100100.1	21.97984236	-0.408759977	0.145628812	-4.17984	2.92E-05	5.06E-05	grey	-0.307026256	9.18E-05	GO0031047	AtSGS1,SGS3	XS domain-containing protein / XS zinc finger domain-containing protein-related	suppressor Of protein silencing protein
Sapur.T021700.1	1.653178673	-0.367817587	0.235476605	-4.17966	2.92E-05	5.06E-05	grey	-0.297176205	0.000152361				NA
Sapur.009G111600.1	10.91131378	0.453189461	0.108430243	-4.179525	2.92E-05	5.07E-05	grey	-0.363913538	2.80E-06	GO0005089		rho guanyl-nucleotide exchange factor, putative	Rop guanine nucleotide exchange factor, putative
Sapur.006G157600.1	25.28224693	0.509226576	0.121854606	-4.179969	2.98E-05	5.16E-05	grey	0.31.3.5.23	0.000.8.8.8.8		AGP25,AT4G0F25	arabinogalactan protein 25	NA
Sapur.T040700.1	2.036428036	-0.710818551	0.170094534	-4.17896	2.93E-05	5.08E-05	grey	-0.327737564	2.79E-05		CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.01G0130200.1	185.6975234	0.308851967	0.059610184	-4.17801	2.94E-05	5.10E-05	grey	-0.336137978	1.64E-05	GO0005634;GO0003677		Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein	LIGULELESS 1 protein, putative
Sapur.004G192300.1	10.04933321	0.927701579	0.22132671	-4.176452	2.96E-05	5.13E-05	grey	-0.327308004	1.57E-06	GO0005158;GO0009555			ferredoxin-3 protein
Sapur.01G0283200.2	18.42218322	0.673705862	0.161442318	-4.17573	2.97E-05	5.15E-05	grey	-0.332708862	2.60E-05		NPG2	no pollen germination related 2	O-linked N-acetylglucosamine transferase, ogt protein%2C putative
Sapur.01G0289400.1	13.48051519	-0.635081837	0.152097278	-4.17549	2.97E-05	5.15E-05	grey	-0.304890557	0.000105611		TBL19	TRICHOME BIREFRINGENCE-LIKE 19	Pmr5/CaLn/GDSL/SGNH-like acyl-esterase family protein
Sapur.01T0232200.2	2.33004949	0.65062485	0.155888759	-4.17368	3.00E-05	5.20E-05	grey	-0.285417274	0.000290804				CCR associated protein
Sapur.01G0205000.3	0.7956246	-1.234275896	0.295835612	-4.172021	3.02E-05	5.24E-05	grey	-0.306614079	6.60E-05	GO0008270		DHHC-type zinc finger family protein	zinc finger protein
Sapur.005G101700.1	242.9937072	0.283365401	0.067923934	-4.171805	3.02E-05	5.24E-05	grey	-0.26321287	0.003798224				NA
Sapur.016G051300.1	5.580937342	0.625020485	0.126869339	-4.171179	3.03E-05	5.26E-05	grey	-0.248746823	0.000146381	GO0007165;GO0005515;GO:0043531		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.007G076700.2	17.81782369	0.271214838	0.08600165	-4.1709	3.03E-05	5.26E-05	grey	-0.162733289	0.047315862				ATP/GTP-binding protein
Sapur.01G0100500.1	2.351620793	0.814320391	0.200034654	-4.17041	3.04E-05	5.27E-05	grey	-0.32834827	2.62E-05	GO0005524		ATPase, AAA-type, CDC48 protein	NA
Sapur.01B0284800.5	7.705008801	0.553737137	0.132796614	-4.16988	3.05E-05	5.28E-05	grey	-0.336907113	1.60E-05	GO0009432;GO0006281;GO0005524;GO:0003697		recA DNA recombination family protein	DNA repair protein RecA
Sapur.01G0262300.1	10.51862237	0.508856562	0.126282756	-4.169523	3.05E-05	5.29E-05	grey	-0.324882564	2.93E-05	GO0016021	ATHIR1,HIR1	SPFH/Band 7/PHB domain-containing membrane-associated protein family	hypersensitive induced response protein
Sapur.002G013400.1	4.120074266	0.955078546	0.229200246	-4.167005	3.09E-05	5.35E-05	grey	-0.278453005	0.000431617			SBP (S-ribonuclease binding protein) family protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.01G0215100.1	63.28563835	0.490591336	0.118035517	-4.166417	3.09E-05	5.36E-05	grey	-0.318076658	7.75E-05		LUX,PCL1	Homeodomain like superfamily protein	myb-like DNA-binding domain protein
Sapur.003G163500.1	9.32897269	0.501791866	0.120451247	-4.165933	3.10E-05	5.37E-05	grey	-0.305802884	9.77E-05	GO0005515		F-box family protein	F-box protein interaction domain protein
Sapur.15W0G124300.1	176.8358413	0.265330429	0.063609

Sapur.0104G61200.1	968.8597532	0.127440243	0.031101828	4.097516	4.18E-05	7.17E-05	grey	0.292601671	0.00032024	AT4G00510.1	DGD2	digalactosyl diacylglycerol deficient 2	digalactosyldiacylglycerol synthase
Sapur.0096G03300.1	269.0145864	0.185232144	0.045205849	4.097323	4.18E-05	7.18E-05	grey	0.273153641	0.00058869	AT2G29700.1	ATPKL.PH1	pleckstrin homologue 1	pleckstrin-like (PH) domain protein
Sapur.0036G16800.1	0.58491285	0.612604026	0.193018925	-4.09723	4.18E-05	7.18E-05	grey	0.318372718	3.36E-06	GO:0003700	HRI2	Integrase-type DNA-binding superfamily protein	AP2/EREBP domain transcription factor
Sapur.0032G04500.1	2.69288353	-0.691663313	0.168817002	-4.09712	4.18E-05	7.19E-05	grey	-0.28973075	0.000232325	GO:0008080		Acyl-CoA N-acyltransferases (NAT) superfamily protein	NA
Sapur.0062G03100.1	746.2293806	0.17247834	0.042102348	4.096552	4.21E-05	7.23E-05	grey	0.296105052	0.00016768		KAS I,KAS1	3-ketoacyl-acyl carrier protein synthase I	3-oxoacyl-[acyl-carrier] synthase I
Sapur.0096G10900.1	465.4262945	0.31998917	0.078128211	4.095693	4.21E-05	7.23E-05	grey	0.287312249	0.000246275	GO:0009733		SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.0096G04200.1	972.8731501	0.318595631	0.07779287	4.09538	4.22E-05	7.24E-05	grey	0.33732579	1.56E-05	GO:0003779		villin 6	NA
Sapur.0050G19900.2	3.70980657	0.623288894	0.15444759	-4.0942	4.24E-05	7.28E-05	grey	0.301460697	0.000124766		LCV2	like CDV 2	CDV1-like protein
Sapur.0096G06300.1	0.717231666	1.390310504	0.339719361	4.092495	4.27E-05	7.33E-05	grey	0.268457594	0.000675134			Lateral organ boundaries (LOB) domain family protein	LOB domain protein
Sapur.0050J18700.2	15.37415718	0.447929843	0.109387967	-4.09159	4.29E-05	7.37E-05	grey	0.266019355	0.000327829	GO:0016020;GO:0006897		ATNAP4,NAP4	adaptin ear-binding coat-associated protein, putative
Sapur.0196G12400.1	1.032843521	-0.687244972	0.412488331	-4.09041	4.31E-05	7.39E-05	grey	-0.324616276	3.36E-05				NA
Sapur.0102G09100.1	1.403050523	-0.591615613	0.12874826	-4.09023	4.31E-05	7.40E-05	grey	0.315012142	5.86E-05			Metallo-hydrolase/oxidoreductase superfamily protein	NA
Sapur.0105G07600.1	8384.230075	0.290022443	0.070913634	4.089798	4.32E-05	7.41E-05	grey	0.267912169	0.000692993		MLP423	MLP-like protein 423	pathogenesis-related protein Bet V I family protein
Sapur.0096G08300.1	13.11204946	0.328008265	0.097785958	-4.08937	4.32E-05	7.41E-05	grey	-0.281683033	0.000312361	GO:0008270		C2H2 and C2HC zinc fingers superfamily protein	nucleic acid-binding protein
Sapur.0096G03000.2	5.394560884	0.630108425	0.154077541	4.089554	4.32E-05	7.42E-05	grey	0.315210926	5.79E-05			Plant protein of unknown function (DUF641)	DUF641 family protein
Sapur.0070G08700.1	0.565375825	0.424801333	0.103621183	4.089073	4.33E-05	7.43E-05	grey	0.302891028	0.000205708				NA
Sapur.0062G07800.1	172.0708053	0.138857549	0.033970016	4.087542	4.36E-05	7.48E-05	grey	0.309393803	8.05E-05	GO:0008242		isoephin family protein	ataxin-3 protein
Sapur.0192G06300.1	0.523977244	-1.323715154	0.323842112	-4.08675	4.36E-05	7.48E-05	grey	-0.33657246	1.36E-05				hypothetical protein
Sapur.0105J17500.1	109.7543014	0.275316515	0.067416054	4.086892	4.37E-05	7.49E-05	grey	0.292508564	0.000172878	GO:0016021;GO:0006952		Seven transmembrane MLO family protein	MLO-like protein
Sapur.0096G03900.1	1050.183909	-0.173058898	0.042151348	-4.08629	4.38E-05	7.52E-05	grey	-0.327980923	2.75E-05	GO:0003924;GO:0007017;GO:0005874		TUB8	tubulin beta 8
Sapur.0096G04600.1	220.2133393	0.368257264	0.09044709	-4.08559	4.40E-05	7.54E-05	grey	-0.326188271	2.7E-05		ATSEN1,DIN1,SEN1	Rhodanese/Cell cycle control phosphatase superfamily protein	senescence-associated protein DIN1
Sapur.0163G30800.1	50.32470528	-0.338759206	0.082932634	-4.08475	4.41E-05	7.57E-05	grey	-0.317830505	4.99E-05				NA
Sapur.0061G17000.1	2.944564731	-0.626255612	0.15178885	-4.08383	4.42E-05	7.58E-05	grey	-0.28071917	0.000160802				DUF1777 family protein
Sapur.0152G02600.2	1.362715437	0.974022746	0.238541582	4.083241	4.44E-05	7.62E-05	grey	0.294688987	0.000176333			Outer arm dynein light chain 1 protein	outer arm dynein light chain 1, putative
Sapur.0196G02800.1	1069.145489	0.600902021	0.147144429	4.082662	4.45E-05	7.64E-05	grey	-0.424878554	3.22E-08			Nucleotide NAD/NADP transporter	NA
Sapur.0080G02400.1	5118.672545	-0.163945317	0.040165099	-4.08179	4.47E-05	7.67E-05	grey	-0.320183873	4.37E-05	GO:0000128;GO:0005515	ATRAD21.1;SYN4	sister chromatid cohesion 1 protein 4	cohesin subunit
Sapur.0120G06100.1	6.342867892	0.640387846	0.156842433	4.081725	4.47E-05	7.67E-05	grey	0.298930893	0.000142911	GO:0016787		Calcineurin-like metallo-phosphoesterase superfamily protein	manganese-dependent ADP-ribose/CDP-alcohol diphosphatase
Sapur.0080J06600.1	1.800680271	-0.445347579	0.109185051	-4.08152	4.47E-05	7.67E-05	grey	-0.319344554	1.99E-05			pentatricopeptide repeat (PPR) protein	NA
Sapur.0061J08900.5	18.67838293	0.390622361	0.09572183	-4.08112	4.48E-05	7.69E-05	grey	-0.114576403	0.153059866	GO:0044237		KagA/RpiA/CoA transferase-like superfamily protein	methylthioribose-1-phosphate isomerase
Sapur.0142G08800.1	3.462273892	-0.702102394	0.186816542	-4.08087	4.48E-05	7.70E-05	grey	-0.357931292	4.17E-06	GO:0005515		WD40/YVTN repeat-like-containing domain protein	WD40/YVTN repeat-containing domain protein
Sapur.0092H07600.2	1.280310992	0.901158256	0.220872883	-4.07999	4.50E-05	7.72E-05	grey	-0.357697885	4.30E-06			magnesium transporter 4	magnesium transporter
Sapur.0086J15100.1	10.01329276	0.768872451	0.188063296	-4.07893	4.52E-05	7.75E-05	grey	-0.263210337	0.000772809			basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH111, putative
Sapur.0036J16300.1	95.0505853	-0.204612932	0.05706489	-4.07859	4.53E-05	7.77E-05	grey	-0.328497528	2.67E-05			Calcineurin-like phosphoesterase protein (DUF3664)	6-phosphogluconate dehydrase
Sapur.0104G04100.1	330.9537179	0.17845941	0.042765427	4.077821	4.55E-05	7.79E-05	grey	0.304884846	0.000102371	GO:0008270;GO:0005515	SIS3	GLGAN-IN-REPEAT 3	zinc finger protein
Sapur.0040B00.1	1.664918958	0.780753067	0.191481251	-4.07744	4.55E-05	7.80E-05	grey	-0.33970793	1.34E-05				NA
Sapur.0052J08700.1	0.916463508	0.486682781	0.34471945	4.07657	4.56E-05	7.81E-05	grey	0.290296809	0.000155114	GO:0005515;GO:0102777;GO:0051537;GO:0016491		ATCAO,CAO,CH1	Phosphorbide a oxygenase family protein with Rieske [2Fe-2S] domain	chlorophyllide A oxygenase
Sapur.0170G13400.1	3.347227789	-0.822431363	0.218822872	-4.07471	4.61E-05	7.90E-05	grey	-0.284907416	0.000269466			HAD superfamily, subfamily IIIB acid phosphatase	acid phosphatase class B family protein
Sapur.0130J07900.1	3.5318045	0.700492501	0.173027818	-4.07197	4.68E-05	7.99E-05	grey	0.277585895	0.000419308	GO:0005085;GO:0016020;GO:0015297;GO:0015238;GO:0006855		MATE efflux family protein	NA
Sapur.0196G12700.1	10.41838153	0.703164277	0.172707461	-4.07167	4.68E-05	7.99E-05	grey	0.292577613	0.000203493			RmlC-like cupins superfamily protein	germin-like protein 11-1
Sapur.0062B05000.1	0.517687945	1.570201342	0.385777776	4.071216	4.68E-05	8.01E-05	grey	0.319272323	4.59E-05	GO:0004871;GO:0000160	AHP5	histidine-containing phosphotransfer factor 5	histidine phosphotransfer protein
Sapur.0060J11200.1	16.77589921	0.463068031	0.113746214	-4.07083	4.68E-05	8.02E-05	grey	0.289417003	0.000230593			Yippee family putative zinc-binding protein	yippee zinc-binding/DNA-binding/Mis18, centromere assembly protein
Sapur.T122300.1	0.392612009	1.379904794	0.338967656	4.071022	4.68E-05	8.02E-05	grey	0.388317106	5.02E-07		ATCRM1.ATXPO1.HT2.XPO	exportin 1A	NA
Sapur.0170G03800.1	7.990479968	0.605804659	0.152216222	-4.07097	4.68E-05	8.02E-05	grey	-0.315238674	5.76E-05	GO:0005515;GO:0045531		LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.0130J07400.1	807.2410151	0.204760787	0.052079569	4.070959	4.68E-05	8.02E-05	grey	0.307323936	9.08E-05			Sec14p-like phosphatidylinositol transfer family protein	CRAL/TRIO domain protein
Sapur.0114G09700.1	11.68228173	0.360595225	0.088679641	-4.07058	4.69E-05	8.03E-05	grey	-0.281276169	0.000235537			Pentatricopeptide repeat (PPR) superfamily protein	PPR containing protein
Sapur.0191G04600.2	7.553914517	-0.446113837	0.109619663	-4.06965	4.71E-05	8.06E-05	grey	-0.314667505	5.98E-05	GO:0015979;GO:0010207		photosystem II reaction center PSB29 protein	thylakoid FORMATION protein
Sapur.0196J06400.1	49.82179824	-0.209182606	0.051495584	-4.06914	4.71E-05	8.06E-05	grey	-0.299836321	0.000135721			Remorin family protein	remorin, carboxy-terminal region protein
Sapur.0010G09100.1	20.36588894	-0.121260711	0.250982331	-4.06904	4.72E-05	8.08E-05	grey	-0.318226931	4.87E-05	GO:0005085;GO:0016020;GO:0015297;GO:0015238;GO:0006855			NA
Sapur.0161H06300.1	0.779172201	2.151806946	0.528798459	4.068385	4.73E-05	8.11E-05	grey	0.228191354	0.002664215				NA
Sapur.0082B05200.1	266.6658217	0.310102046	0.081165434	-4.067666	4.74E-05	8.12E-05	grey	0.260207734	0.000464344			TRICHOME BIREFRINGENCE-LIKE 33	trichome birefringence-like protein
Sapur.0030G07900.1	102.9102579	-0.263438202	0.064758157	-4.06664	4.77E-05	8.17E-05	grey	-0.32802177	8.22E-05			alpha/beta-hydrolases superfamily protein	NA
Sapur.0060J11200.1	212.2101266	0.252017222	0.061523467	-4.06018	4.78E-05	8.19E-05	grey	-0.305729478	9.87E-05	GO:0016021;GO:0008963		Glycosyl transferase family 8 protein	UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase
Sapur.0180H09900.1	5.139464686	-0.613385161	0.150963311	-4.06446	4.81E-05	8.24E-05	grey	-0.303418253	0.000106651			Exostosin family protein	NA
Sapur.0070G01200.1	10.04619919	-0.354802799	0.088054692	-4.06409	4.82E-05	8.25E-05	grey	-0.310691161	5.26E-05			Plant protein of unknown function (DUF247)	NA
Sapur.0101G13000.2	9.674034944	-0.405739397	0.099844022	-4.06371	4.83E-05	8.27E-05	grey	-0.277560721	0.000432345	GO:0006284;GO:0006281;GO:0004844	ATUNG,UNG	uracil-DNA glycosylase	uracil-DNA glycosylase
Sapur.0050B06900.1	0.686688849	-1.344811399	0.330968389	-4.06363	4.83E-05	8.28E-05	grey	-0.292145459	0.000204016			Protein of unknown function (DUF3527)	DUF3527 domain protein
Sapur.T000100.1	0.450076567	1.986566788	0.488918805	4.06319	4.84E-05	8.29E-05	grey	0.344882608	7.06E-06	GO:0016829;GO:0010333;GO:0008152;GO:0000287	ATTPS21,TPS21	terpene synthase 21	terpene synthase, putative
Sapur.0031J15800.1	55.45728127	0.229280286	0.056900115	-4.06247	4.86E-05	8.31E-05	grey	-0.32230749	3.87E-05			adenylate cyclases	adenylate cyclase
Sapur.0135D05100.2	0.18301581	1.604197642	0.394656702	4.06177	4.87E-05	8.33E-05	grey	0.281345641	0.001088239			185pre-ribosomal assembly protein gar2-related	hypothetical protein
Sapur.0180Z08800.3	2.757079988	-0.689317862	0.16968541	-4.06163	4.87E-05	8.34E-05	grey	-0.294215548	0.000181894	GO:0008168		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosylmethionine-dependent methyltransferase
Sapur.0051T14G00.1	5.249638917	0.37E-05	0.091159187	4.06086	4.88E-05	8.35E-05	grey	0.078548531	0.32814907			Remorin family protein	remorin, carboxy-terminal region protein
Sapur.0061B07700.1	229.421874	0.10451617	0.025738843	4.060482	4.90E-05	8.38E-05	grey	0.31881519	6.39E-05	GO:0016811;GO:0016021;GO:0006672		Alkaline phosphoesterase (aPHC)	alkaline phosphoesterase (APHC)
Sapur.0170J07200.1	44.66108809	0.330364765	0.081362854	-4.06059	4.90E-05	8.39E-05	grey	-0.303151565	0.000113693	GO:0005515;GO:0005622;GO:0005975;GO:0006553			NA
Sapur.0070G09400.1	9.852836601	0.445102023	0.109620871	4.060377	4.90E-05	8.38E-05	grey	0.298897053	0.000135607	GO:0005525	ATRAB8-C,ATRAB18,ATRAB	RAB GTPASE HOMOLOG B18	small GTPase family Rab protein
Sapur.0180J06100.1	195.1414165	0.205021821	0.097609175	-4.0603	4.90E-05	8.38E-05	grey	-0.313870903	1.93E-05	GO:0016020	HYR1	UDP-glucose flavonoid 7-O-glucosyltransferase superfamily	UDP-glucose flavonoid 7-O-glucosyltransferase, putative
Sapur.0130H15500.1	6.059452746	0.753132278	0.185677392	4.057211	4.97E-05	8.50E-05	grey	0.317998858	4.94E-05	GO:0006629		Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein	NA
Sapur.0060B05700.1	45.55692673	-0.304061385	0.074909383	-4.0543	5.03E-05	8.61E-05	grey	-0.305327241	7.12E-06			Tautomerase/MIF superfamily protein	macrophage migration inhibitory factor family protein
Sapur.0051G18900.1	8.071125852	0.953926534	0.236637678	4.054031	5.03E-05	8.61E-05	grey	0.262681849	0.000888455				transmembrane protein, putative
Sapur.0142B06300.1	3388.353059	0.620080868	0.153177223	4.054003	5.03E-05	8.61E-05	grey	0.310787603	7.45E-05	GO:0046983;GO:0008171		O-methyltransferase 1	caffeic acid O-methyltransferase
Sapur.0170Z09800.1	27.00738977	-0.282654549	0.069645658	-4.05362	5.04E-05	8.62E-05	grey	-0.302509999	1.38E-07				NA
Sapur.0050J01700.1	9.16517872	0.481869446	0.11887451	4.053598	5.04E-05	8.63E-05	grey	0.317579713	5.96E-05	GO:0007165;GO:0005515;GO:0043531		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.0115G01200.1	9.709639864	0.458832294	0.113230806	4.053069	5.04E-05	8.64E-05	grey	0.310691746	9.26E-05				NA
Sapur.0113G13000.2	4.543913668	-0.568334455	0.140318377	-4.05245	5.07E-05	8.67E-05	grey	-0.05251521	0.513623236	GO:0006950		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress protein
Sapur.0050B06900.1	5.853499984	-0.980850481	0.242063191	-4.05185	5.08E-05	8.69E-05	grey	-0.257576296	0.001417776	GO:0043565;GO:0006355;GO:0003700	ATWRKY51,WRKY51	WRKY DNA-binding protein 51	WRKY transcription factor, putative
Sapur.0070G04200.1	1008.100884	0.628455551	0.155129589	-4.05158	5.08E-05	8.69E-05	grey	0.296686875	0.000161414	GO:0006508;GO:0004252		Subtilisin-like serine endopeptidase family protein	subtilisin-like protease
Sapur.0010G02800.2	19.7053085	0.205802564	0.11667514	-4.05056	5.11E-05	8.74E-05	grey	0.31739937	7.03E-05		JB	Chaperone DnaJ-domain superfamily protein	chaperone protein DnaJ
Sapur.0050J76400.1	265.4449308	0.192738829	0.047509944	4.049966	5.12E-05	8.76E-05	grey	0.281326972	0.00032686				complex 1 protein, LYR family protein
Sapur.0110J08700.1	1.782875279	0.795730327	0.196224544	-4.04685	5.18E-05	8.87E-05	grey	-0.312325764	6.82E-05		EPF1	epidermal patterning factor 1	transmembrane protein, putative
Sapur.0120H08300.1	13.10218821	-0.395801033	0.09763033	-4.04663	5.20E-05	8.89E-05	grey	-0.28273957	0.000273884			dentin-sialophosphoprotein-related	hypothetical protein
Sapur.0096G03500.1	1.020847988	-1.145861989	0.28193972	-4.04662	5.20E-05	8.88E-05	grey	-0.283632047	0.000318712	GO:0006813;GO:0055085;GO:0016022;GO:0015299;GO:0006812		K+ efflux antiporter 3	glutathione-regulated potassium-efflux system protein KefB
Sapur.0061J03G00.1	17.38798884	-0.267131318	0.131313664	-4.04661	5.20E-05	8.88E-05	grey	-0.301852023	0.000122065			Ankyrin repeat family protein	ankyrin-like protein
Sapur.0081J14500.1	35.85891412	0.446757966	0.110404446	4.046484	5.20E-05	8.89E-05	grey	0.280210991	0.000378762	GO:0008312		Isopropyl malate isomerase large subunit 1	3-isopropylmalate dehydratase, large subunit
Sapur.0161B18200.2	67.28817294	-0.302238783	0.074629149	-4.04582	5.21E-05	8.91E-05	grey	-0.300498883	0.000131414	GO:0005270;GO:0005515		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING) finger protein
Sapur.0050J05100.4	16.83825156	-0.466093391	0.114934027	-4.0452	5.23E-05	8.93E-05	grey	-0.295132381	0.000175154			Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator RCC1 repeat protein, putative
Sapur.0170G05600.1	1.155057763	0.944806763	0.233418842	4.044775	5.24E-05	8.96E-05	grey	0.319468866	4.54E-05			Helicase/SWI/SNF-related protein	NA
Sapur.0110G01700.1	0.626021502	1.502506021	0.371509304	4.043408	5.27E-05	9.00E-05	grey	0.251369318	0.001495286	GO:0006468;GO:0006672		S-locus lectin protein kinase family protein	NA
Sapur.0130G12200.1	1.437331334	0.904669944	0.223763839	4.04316	5.27E-05	9.01E-05	grey	-0.38343887	7.17E-07			Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.0161J85300.1	3.386416048	0.872272533	0.215991142	4.043094	5.28E-05	9.01E-05	grey	0.251885855	0.001462074	GO:0005515	ATCRAL,CRAL,CRU1	RmlC-like cupins superfamily protein	NA
Sapur.0021G15300.1	0.96462795	-1.118688389	0.276699122	-4.0429	5.28E-05	9.02E-05	grey	-0.037706674	0.439171369		UPA1	tetratricopeptide repeat (TPR)-containing protein	UDP PSI ACCUMULATION protein
Sapur.T060900.1	0.336957561	-1.418270736	0.350920556	-4.041572	5.29E-05	9.04E-05	grey	0.383870215	5.22E-07		ATFIM1,FIM1	fimbrin 1	NA
Sapur.0041G16300.1	121.2158028	-0.108479755	0.026855106	-4.03945	5.34E-05	9.15E-05	grey	-0.305215494	0.000107755	GO:0043209;GO:0016878;GO:0005524	ATGER1,ERS,CNA1	glutamate tRNA synthetase	glutamyl-tRNA synthetase
Sapur.0142J08800.1	1.015720354	0.587602281	0.2446653	4.038864	5.38E-05	9.18E-05	grey	0.284715157	0.000301195				DUF4228 domain protein
Sapur.0092H09400.1	2.027564585	-0.353654143	0.26090594	-4.03849	5.38E-05	9.19E-05	grey	-0.271615665	0.000592261	GO:0005585;GO:0016021		nitrate transporter 2:1	high-affinity nitrate transporter
Sapur.T011200.1	27.63161137	0.365381633	0.094778565	4.036621	5.42E-05	9.24E-05	grey	0.325260237	3.23E-05				NA
Sapur.0170G03900.1	1.53462701	-0.973144208	0.241085732	-4.03651	5.43E-05	9.26E-05	grey	-0.287315674	0.000236713	GO:0016887;GO:0005524;GO:0016020	ABCG11,ATWBC11,COF1,D6	white-brown complex homolog protein 11	ATP-binding cassette protein
Sapur.0050B08000.2	4.900870614	-0.53727497	0.133146622	-4.03575	5.46E-05	9.31E-05	grey	-0.33235008	2.00E-05			Ribosomal protein S5 domain 2-like superfamily protein	ribosomal protein S5 domain protein
Sapur.0115J12500.1	2.391497887	0.675950396	0.167528008	4.034849	5.46E-05	9.33E-05	grey	0.263913139	0.000838354			Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase	regulator of ribonuclease activity protein A
Sapur.0051J13000.1	5.045636671	-0.521139621	0.129438857	-4.03378	5.47E-05	9.37E-05	grey	0.048873005	0.542425129	GO:0004674;GO:0006468;GO:0004672	ATPRK1,PERK1	protein kinase-like receptor kinase 1	protein rich receptor-like kinase PERK1
Sapur.0080G09900.1	1058.868231	0.073862088	0.018311386	4.033479	5.52E-05	9.42E-05	grey	-0.274617794	0.000505331	GO:0016787		Calcineurin-like metallo-phosphoesterase superfamily protein	phytochrome-associated serine/threonine protein phosphatase
Sapur.0161J44400.2	0.623527112	-1.325932248	0.3288412	-4.03214	5.53E-05	9.43E-05	grey	-0.343235434	1.08E-05		MCA2	PLACE family protein	MIDS1-complementing activity protein
Sapur.0086Z06005.5	1.263657607	-1.114889025	0.276313893	-4.03182	5.53E-05	9.45E-05	grey	0.267835236	0.000905554				hypothetical protein
Sapur.T033300.1	64.88968823	-0.826840086	0.205285322	-4.03169	5.54E-05	9.45E-05	grey	-0.411495641	8.62E-08			PLATZ transcription factor family protein	NA
Sapur.0030G02600.1	89.96080034	-0.315927884	0.079275851	-4.03185	5.54E-05	9.48E-05	grey	-0.30775168	8.48E-05				transmembrane protein, putative
Sapur.0105J19300.1	0.593291269	1.57431449	0.390596429	4.030558	5.56E-05	9.50E-05	grey	0.29754343	0.00015402				NA
Sapur.0050J19300.1	492.4434657	0.277077375	0.069174825	-4.02969	5.58E-05	9.51E-05	grey	-0.299122328	0.000141491			Chaperone DnaJ-domain superfamily protein	chaperone protein DnaJ
Sapur.0113G19900.1	58.23788796	0.220554488	0.054573387	4.02958	5.58E-05	9.53E-05	grey	0.31774266	7.04E-05	GO:0005975;GO:0004553		Glycosyl hydrolase superfamily protein	NA
Sapur.0101G08700.1	1.796214694	-0.840668398	0.208601688	-4.02901	5.58E-05	9.56E-05	grey	-0.36937518	1.95E-06			Transcription factor TFIIE, beta subunit-related protein	ETAC subunit
Sapur.0096J04400.2	2.346559581	0.770229838	0.191187056	4.028671	5.61E-05	9.57E-05	grey	0.23088133	0.003623217	GO:0005515		ARM repeat superfamily protein	armadillo/beta-catenin repeat protein
Sapur.0064G12800.1	2.785108836	-0.050315541	0.161446213	-4.02682	5.65E-05	9.64E-05	grey	-0.270732339	0.000605111				NA
Sapur.0080G02600.3	1.778802111	-0.837867705	0.208139736	-4.02603	5.67E-05	9.68E-05	grey	-0.268052045	0.000888537	GO:0008168;GO:0006479		Protein arginine methyltransferase family protein	arginine N-methyltransferase
Sapur.0075G12800.1	539.8231246	-0.180763606	0.044908877	-4.02503	5.70E-05	9.72E-05	grey	-0.32331333	3.62E-05	GO:0005515;GO:0006488;GO:0005524;GO:0004672	HSL1	HAESA-like 1	LRR receptor-like kinase
Sapur.0052B05000.1	2.823861862	-0.394284494	0.18477083	-4.02463	5.72E-05	9.75E-05	grey	-0.291171395	0.000817			HIGH-affinity nitrate transporters superfamily protein	NA
Sapur.0060J00900.1	2.300429604	-0.695076901	0.172738226	-4.02387	5.72E-05	9.76E-05	grey	-0.301761576	0.000122647			Protein of unknown function (DUF594)	NA
Sapur.0130J06300.1	10.08222219	-0.527280695	0.13100504	-4.02356	5.73E-05	9.77E-05	grey	-0.300074176	0.000134604	GO:0005515		C2 calcium/lipid phospholipid phosphotransferase family protein	glutamine peroxidase
Sapur.0070G05100.1	145.7824991	0.275746275	0.068537057	4.023318	5.74E-05	9.79E-05	grey	0.293545561	0.000190479			GRAS family transcription factor	GRAS family transcription factor
Sapur.0110G00700.2	1.990777918	0.451204354	0.112108	4.02268	5.75E-05	9.81E-05	grey	-0.19995927	0.012043331	GO:0005515		adenosylhomocysteinase family protein	adenosylhomocysteinase
Sapur.0161G62200.1	67.96031235	0.391487904	0.097329779	-4.02228	5.76E-05	9.83E-05	grey	-0.344937974	1.00E-05			Protein of unknown function (DUF674)	NA
Sapur.0030B04300.1	11.18544703	0.391279482	0.097410375	4.02166	5.78E-05	9.86E-05	grey	0.297378814	0.000156255	GO:0005887	ATBAG1,BAG1	BCL-2-associated athanogene 1	BAG domain protein 1/regulator of cell death protein, putative
Sapur.0161G61500.1	3.1115866	0.940294892	0.233823614	-4.02138	5.78E-05	9.86E-05	grey	-0.304611928	0.000104943			Protein of unknown function (DUF674)	DUF674 family protein
Sapur.0120B07500.1	3.397662792	0.755003346	0.187781881	4.0208	5.80E-05	9.89E-05	grey	0.304136272	0.000107721	GO:0005515	ARIP12,RLP12	receptor like protein 12	receptor like protein 12
Sapur.0130J08300.1	47.86487968	-0.315906564	0.08531306	-4.02071	5.80E-05	9.89E-05	grey	-0.298254542	0.000184862	GO:0055114;GO:0016491;GO:0006520	GDH2	glutamate dehydrogenase 2	glutamate dehydrogenase
Sapur.0101J15500.1	2.8184968	-0.843499903	0.209607711	-4.02058	5.81E-05	9.90E-05	grey	-0.31869449	6.32E-05			Ca(2)-dependent phospholipid-binding protein (Copine) family	E3 ubiquitin-protein ligase RGLG1
Sapur.0192B04000.1	176.2329263	-0.178424944	0.043796837	-4.02001	5.82E-05	9.92E-05	grey	-0.291171395	7.64E-05			Malate/citrate synthase family	alpha-galactosidase
Sapur.T037100.1	70.02413572	0.235171276	0.058043954	4.019377	5.84E-05	9.95E-05	grey	0.308503718	8.46E-05	GO:0055114;GO:0016491		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.0110H10100.1	8.013191614	0.682039487	0.168401316	4.01929	5.84E-05	9.95E-05	grey	0.347613003	1.97E-06				hypothetical protein
Sapur.0152H15500.2	14.16630498	0.623305771	0.155063709	4.017934	5.87E-05	9.99E-05	grey	0.292628135	0.000109961	GO:0009446;GO:0006468		porphyromonas-type peptidyl-arginine deiminase family protein	NA
Sapur.0170H04500.1	10615.23498	0.166611	0.041665	4.017571	5.87E-05	9.99E-05	grey	0.312636261	5.38E-05	GO:0005737;GO:0016705;GO:0005506	ATCYP96	cyclophilin 96	cyclophilin 96 (CYP96), subfamily A, polypeptide 6
Sapur.0180H05900.2	76.98751313	0.499492538	0.127875254	4.017302	5.88E-05	9.99E-05	grey	0.292464845	0.000201876	GO:0016157;GO:0005985	ATSUS4,SU5A	sucrose synthase 4	sucrose synthase
Sapur.0190J07580.1	98.66648984	0.451372311	0.112378931	-4.01652	5.93E-05	10.08E-05	grey	-0.324631335	3.35E-05	GO:0005515;GO:0006488;GO:0005524;GO:0004672		Leucine-rich receptor-like protein kinase family protein	leucine-rich receptor-like kinase
Sapur.0051H04500.1	471.4460031	0.242544976	0.060389556	4.016166	5.93E-05	10.09E-05	grey	0.262845539	0.000860665			Single hybrid motif superfamily protein	biotin carboxyl carrier of acetyl-CoA carboxylase, putative
Sapur.0010G06400.1	176.9475671	0.383671513	0.095523152	4.016151	5.93E-05	10.09E-05

Sapur.01G0050400.1	8.12298551	1.088060274	0.274879035	3.960308	7.49E-05	0.00012670 5	grey	0.306990332	9.20E-05	GO:0055085,GO:0016020,GO:0006810,GO:0005215	ATLG05510.1	Xanthine/uracil permease family protein	NA
Sapur.003G050400.2	5.537852619	0.486460861	0.122381297	3.960083	7.49E-05	0.00012681 6	grey	0.264985227	0.00080146		ATCG35658.1		transmembrane protein, putative
Sapur.012G047500.1	12.92426949	3.120512041	0.080941612	3.950969	7.58E-05	0.00012682 7	grey	0.305116273	0.000920371	GO:0005524,GO:0003676	ATCG00133.1	nucleic acid binding;ATP-dependent helicase;ATP-binding;helicase;ATP-dependent helicases	NA
Sapur.019G013200.1	69.83262687	0.289968577	0.073243412	-3.95897	7.53E-05	0.00012787 2	grey	-0.297093589	0.000132786	GO:0005515,GO:0043531	AKG27220.1	NB-ARC domain-containing disease resistance protein	NA
Sapur.013G049600.1	3.12838103	0.783087533	0.198078485	3.950803	7.54E-05	0.00012789 1	grey	-0.265472867	0.000778575		AT5G08970.4	HAPSC_NF-YC9	nuclear factor Y, subunit C9
Sapur.019G053600.1	3.571527361	-0.804921074	0.203375296	-3.95781	7.56E-05	0.00012804 6	grey	-0.297370018	0.000105458				transmembrane protein, putative
Sapur.009G068100.1	2.754421338	0.154585704	0.038928874	3.957441	7.58E-05	0.00012816 6	grey	0.262318845	0.000903487		AT4G14320.1	proline-rich family protein	XYPPX repeat protein
Sapur.001G018800.1	370.9381204	0.461808239	0.116682927	3.957371	7.58E-05	0.00012822 7	grey	0.302856115	0.000105543	GO:0007017,GO:0005875	AT5G20110.1	Dynein light chain type 1 family protein	dynein light chain type 1 protein
Sapur.15W0G0053000.1	73.88192952	0.250769932	0.063382119	3.956889	7.60E-05	0.00012856 1	grey	-0.284410317	0.000307261		AT5G15588.1	CPuORF50	conserved peptide upstream open reading frame 50
Sapur.012G062200.1	1.687601199	-0.894881836	0.2262654	-3.95563	7.63E-05	0.00012913 8	grey	-0.318808225	0.360125	GO:0005515	AT5G60690.1	LC8	dynein light chain (LC8)-domain family protein
Sapur.002G413400.2	61.01916608	0.318864581	0.331632216	-3.95524	7.64E-05	0.00012934	grey	-0.308703042	8.37E-05	GO:0006355,GO:0005634,GO:0003677,GO:0009725	AM2 F13.1	auxin response factor 11	auxin response factor
Sapur.002G428300.1	12.07556603	2.917898398	0.737486366	3.954589	7.65E-05	0.00012947 6	grey	-0.311602145	7.06E-05	GO:0016021,GO:0006508,GO:0004252	AT4G01310.1	RHOMBOID-like protein 1	rhomboid protease gluP
Sapur.019G080800.1	0.36020491	1.637946939	0.414163075	3.954841	7.66E-05	0.00012954 5	grey	0.356593317	4.56E-06				hypothetical protein
Sapur.003G071300.1	20.58543435	0.197570207	0.049933291	3.954564	7.67E-05	0.00012976 1	grey	0.312372256	0.000842862	GO:0005515,GO:0006488,GO:0005524,GO:0004672	AT4G08850.1	Leucine-rich repeat receptor-like protein kinase family protein	NA
Sapur.005G006200.1	10.34073092	2.956827897	0.121317189	3.953957	7.68E-05	0.00130005	grey	0.298648576	0.000145147				
Sapur.008G057100.6	1.488985643	-0.596331221	0.150855846	-3.94249	7.85E-05	0.00130251	grey	0.353758662	0.011267	GO:0007264,GO:0005525	AT4G19640.1	ARA-7,ARA7,ATRAB-F2B,ATRAB-F2B,ATRAB-F2B,AT	Ras-related small GTP-binding family protein
Sapur.005G200700.1	5.970179545	0.500576358	0.126648873	3.952478	7.73E-05	0.00130784	grey	0.291571415	0.000211375		AT5G19250.1	FMO1	flavin-dependent monooxygenase 1
Sapur.012G079000.3	1.486894651	-0.868031917	0.219639315	-3.95221	7.74E-05	0.00130923	grey	-0.304825855	0.000105427		AT5G78830.1		hypothetical protein
Sapur.005G147300.1	1.889464493	-0.872431772	0.185602746	-3.95216	7.74E-05	0.00130945	grey	-0.374572172	1.56E-05	GO:0006508,GO:0004185	AT5G42240.1	serine carboxypeptidase-like 42	serine carboxypeptidase
Sapur.016G247900.1	0.618170136	-0.395205557	0.352043269	-3.95351	7.75E-05	0.00131102	grey	-0.284597611	0.000303261		AT4G15480.1		NA
Sapur.006G060900.2	9.311021899	2.396857491	0.101414048	-3.95188	7.76E-05	0.00131081	grey	-0.305051125	0.000108114	GO:0008374,GO:0006629	AT1G03130.1	ATLCAT1,LCAT3	lecithin:cholesterol acyltransferase 3
Sapur.017G011700.1	22.07813514	0.393355811	0.099168447	-3.95057	7.80E-05	0.00131799	grey	-0.304523969	0.000105425		AT5G03320.1		lecithin-binding AGCH domain protein
Sapur.006G097900.1	11.16099669	0.714384382	0.180780268	-3.94952	7.82E-05	0.00132112	grey	0.279848841	0.000465804		AT2G20180.1	Pollen Ole e 1 allergen and extensin family protein	pollen Ole e 1 allergen and extensin family protein
Sapur.014G065500.1	726.8637411	0.164437253	0.041694947	-3.94863	7.88E-05	0.00133113	grey	-0.317092849	6.31E-05		AT4G45980.2		hypothetical protein
Sapur.006G125600.2	2.931021899	0.597570207	0.151282812	3.946856	7.93E-05	0.00133276	grey	0.32232226	0.000843862	GO:0005515,GO:0006488,GO:0005524,GO:0004672	AT4G08550.1	Leucine-rich repeat receptor-like protein kinase family protein	NA
Sapur.T17G000.1	2.426863013	-0.734489329	0.186101669	-3.94671	7.92E-05	0.00133906	grey	-0.283029882	0.000328476				
Sapur.003G020000.1	84.66556887	0.24957481	0.06324043	3.946444	7.93E-05	0.00134048	grey	0.28705482	0.000267326		AT5G16175.1	Thioesterase superfamily protein	acyl-CoA thioesterase, putative
Sapur.016G044700.1	52.11802507	0.363281135	0.092018155	3.946488	7.93E-05	0.00134061	grey	0.279873728	0.000447539		AT2G42280.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH130, putative
Sapur.008G158900.1	0.724933826	1.095354989	0.304145412	3.943387	8.03E-05	0.00135761	grey	0.267916939	0.000692835	GO:0000160	AT4G16110.1	response regulator 2	response regulator 2
Sapur.003G144400.1	251.1072009	0.251496141	0.064538446	3.94249	8.06E-05	0.00136222	grey	0.297020156	0.000377512		AT5G45680.1	TCP family transcription factor	TCP transcription factor, putative
Sapur.015G080900.9	1.428422915	-0.886785872	0.226952825	-3.9421	8.08E-05	0.00136438	grey	-0.305412455	0.000100409	GO:0005085,GO:0016020,GO:0051297,GO:0015238,GO:0006855	AT3G23560.1	ALF5	MATE efflux family protein
Sapur.005G197700.5	1.385621131	-0.591109159	0.133329381	-3.941701	8.08E-05	0.00136627	grey	0.337362647	1.56E-05		AT5G44940.4	tryr/lys-CoR domain of pyglu-superfamily protein	hypothetical protein
Sapur.017G082800.1	168.6251555	0.361600654	0.091744809	3.941375	8.10E-05	0.00136836	grey	-0.255962428	0.002121573		AT5G15740.1		O-fucosyltransferase family protein
Sapur.002G008400.1	1.573816229	0.78329685	0.199232125	3.941222	8.11E-05	0.00136909	grey	0.34812579	1.05E-05	ATCIMS1,ATKPCI-HET2,XPO	AT2G17020.1	CIMS1,ATKPCI-HET2,XPO1 exportin 1A	NA
Sapur.016G050600.1	113.8217627	0.253892666	0.064166807	3.94117	8.11E-05	0.00136932	grey	0.278043129	0.000445933		AT4G45380.1		hypothetical protein
Sapur.003G075400.1	6.313598834	0.662422667	0.168461351	3.940841	8.14E-05	0.00136985	grey	-0.305051125	0.000108114				NA
Sapur.017G004000.1	4.214221506	0.594097847	0.150991622	3.940601	8.15E-05	0.00137243	grey	-0.290215181	0.000226954	GO:0006468,GO:0005524,GO:0004672	AT4G18250.1	receptor serine/threonine kinase, putative	NA
Sapur.004G157500.5	4.612498836	-0.099239306	0.278956234	-3.94054	8.18E-05	0.00137369	grey	-0.302563512	0.000117403		AT5G58140.4	NFL1,PHOT2	phototropin 2 protein
Sapur.014G117100.1	0.587456196	-0.318318992	0.344796584	3.939726	8.21E-05	0.00137773	grey	-0.282143429	0.00034358		AT2G34640.1	Protein of unknown function (DUF3754)	transmembrane protein, putative
Sapur.T18G000.1	15.60932713	0.341964658	0.086882661	3.939451	8.21E-05	0.00137881	grey	0.303404623	0.000113615	GO:0003012,GO:0005086	AT5G60860.1	SEC7-like guanine nucleotide exchange family protein	NA
Sapur.005G141000.2	2.713818994	0.551165437	0.088338062	3.938704	8.16E-05	0.00138304	grey	0.004434149	0.238852385	GO:0008270,GO:0005634	AT5G47420.1	DNWN domain, a CCHC-type zinc finger protein, putative	DNWN domain, a CCHC-type zinc finger protein
Sapur.008G138100.7	6.707776247	-0.469159323	0.119118322	-3.9386	8.20E-05	0.00138354	grey	-0.144904711	0.070185623		AT5G33435.1	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif protein
Sapur.017G049100.1	170.6134541	0.357892759	0.09089191	-3.93767	8.23E-05	0.00138889	grey	-0.284895	0.000147982				hypothetical protein
Sapur.015G027900.1	107.4705246	-0.350803854	0.089100387	-3.93711	8.25E-05	0.00139188	grey	-0.285458503	0.000247482		AT4G21500.1		transmembrane protein, putative
Sapur.003G080600.1	4.102883147	-0.669127478	0.170050794	-3.93621	8.26E-05	0.00139708	grey	-0.296681057	0.000161207				transmembrane protein, putative
Sapur.014G043000.1	12.23862686	2.498087248	0.126545986	3.936097	8.28E-05	0.00139765	grey	0.021914214	0.785296946		AT2G44980.2	SNF2 domain-containing protein / helicase domain-containing protein	SNF2 and helicase domain protein
Sapur.016G088400.4	1.918513628	0.498799329	0.126837812	3.935864	8.29E-05	0.00139883	grey	-0.040503828	0.631935638	GO:0046912	AT2G27080.1	citrate synthase 3	citrate synthase
Sapur.006G000300.1	7.059111117	0.424507157	0.107877308	3.935092	8.32E-05	0.00140336	grey	0.263373042	0.000889876		AT2G01060.1	myb-like HTH transcriptional regulator family protein	Myb family transcription factor, putative
Sapur.005G105000.1	5.518045001	1.641943674	0.417276212	3.934907	8.32E-05	0.00140437	grey	0.249368299	0.001650076	GO:0006468,GO:0006472	AT4G22200.1	Protein kinase superfamily protein	carbohydrate-binding protein of the ER protein
Sapur.008G200000.1	1.716553977	0.951839267	0.237372455	3.934881	8.33E-05	0.00140461	grey	0.224021606	0.004698195		AT2G45618.2		transmembrane protein, putative
Sapur.013G058700.1	729.5948228	-0.20396494	0.051861395	-3.93444	8.34E-05	0.00140605	grey	-0.305170424	0.000101767	GO:0006468,GO:0006672	AT5G07370.2	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.005G041000.1	4.262336443	0.510326845	0.129710704	-3.93404	8.35E-05	0.00140748	grey	-0.310769302	7.45E-05		AT5G17530.1	Chaperone DnaJ-domain superfamily protein	DnaJ heat shock amino-terminal domain protein
Sapur.003G147800.2	1.467912122	-0.925657164	0.235287405	-3.93416	8.35E-05	0.00140849	grey	-0.365854633	2.26E-06		AT4G01150.1	5-locus lectin protein family protein	cyanobacterial aminoacyl-tRNA synthetase CAND domain protein
Sapur.015G022300.2	0.513602201	-0.537185218	0.136626268	-3.93275	8.41E-05	0.00140975	grey	0.292634668	0.000316495	GO:0008544,GO:0006488,GO:0006472	AT2G31140.1	Serine/Threonine kinase	serine/threonine kinase
Sapur.016G043900.3	1.597980376	0.820601593	0.208648229	-3.93301	8.38E-05	0.00141501	grey	-0.130154251	0.104233307	GO:0005515	AT5G37880.1	Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein	anthranilate phosphoribosyltransferase-like protein
Sapur.010G043200.1	2.824219646	-0.165938948	0.197066453	-3.93187	8.41E-05	0.00141688	grey	-0.275568645	0.000608851	GO:0016255,GO:0003700	AT3G23240.1	ethylene response factor 1	ethylene-responsive transcription factor
Sapur.005G154800.1	7.19362675	0.619130687	0.157480494	-3.93145	8.44E-05	0.00142378	grey	-0.295498989	0.000171774	GO:0016866	AT3G04060.1	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	allin lyase-like protein
Sapur.003G147000.1	0.934909275	1.302595085	0.305942588	3.930787	8.47E-05	0.00142779	grey	0.263974045	0.000918485	GO:0016192	AT4G11180.1	Adaptin family protein	NA
Sapur.016G086100.1	68.49316056	0.250161856	0.057650585	-3.9304	8.48E-05	0.00143	grey	-0.290283483	0.000149267	GO:0016020	AT2G07275.1	CAAX amino terminal protease family protein	CAAX amino terminal protease family protein
Sapur.017G128700.1	452.5687225	0.183849443	0.046663399	3.930285	8.48E-05	0.00143063	grey	0.336913237	1.60E-05		AT1G78320.1	Putative integral membrane protein conserved region (DUF2404)	integral membrane protein, putative
Sapur.010G028700.1	43.38707279	0.246000268	0.062447594	3.93035	8.50E-05	0.00143261	grey	0.307758448	8.11E-05	GO:0006468,GO:0006672	AT4G28230.1	Protein kinase superfamily protein	Pto kinase interactor 3
Sapur.006G201700.1	3601.051056	0.306370876	0.077937429	3.92917	8.52E-05	0.00143713	grey	0.260802882	0.000970325		ATRD22,RD22	BURP domain-containing protein	NA
Sapur.005G179200.1	1.117934116	0.988460677	0.251198424	3.92909	8.52E-05	0.00143754	grey	0.331102877	1.25E-05			Ubiquitin carboxyl hydrolase family protein	plant organelle RNA recognition domain protein
Sapur.008G076400.1	3.362186195	-0.626152539	0.159460022	-3.92907	8.53E-05	0.00143376	grey	-0.212900006	0.003313133	GO:0004386	AT5G26370.1	RNA helicase family protein	ATP-dependent RNA helicase DHX8
Sapur.012G088800.2	25.98513602	0.197108882	0.050188287	3.92903	8.53E-05	0.00143886	grey	-0.309063017	7.35E-05		AT2G38700.1	Ribosomal L27 family protein	60S ribosomal protein L27a
Sapur.001G136200.1	1974.997768	-0.13397903	0.034126794	-3.92592	8.64E-05	0.00145638	grey	-0.321059994	4.14E-05	GO:0005515,GO:0006488,GO:0006672	AT5G18680.1	STRUBBELIG-receptor family 6	strubbelig family receptor kinase, putative
Sapur.003G046100.1	43.15464527	0.192166195	0.049127819	-3.92538	8.65E-05	0.00145668	grey	-0.301461615	8.37E-07	GO:0003676	AT3G60000.1	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif, a.k.a. RRM/RNP, RBD protein
Sapur.005G070900.1	17.83827548	-0.370156674	0.094339996	-3.92406	8.71E-05	0.00146794	grey	-0.273543648	0.000527363		AT5G54680.1	SDE3	P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.009G054100.1	2.334545056	-0.806256468	0.205136124	-3.92274	8.75E-05	0.00147538	grey	-0.317790862	5.50E-05		AT2G28010.1	Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.007G058100.1	1.876663388	-0.800480651	0.227972725	-3.921639	8.76E-05	0.00148197	grey	0.275369226	0.000482569		AT5G39180.1	myb domain protein 63	Myb-like DNA-binding domain protein
Sapur.008G129700.1	237.6110023	-0.180154123	0.045941567	-3.92138	8.80E-05	0.00148352	grey	-0.307829418	8.78E-05		AT5G22970.1	Protein of unknown function (DUF506)	DUF506 family protein
Sapur.012G071300.2	0.574131502	-1.405669791	0.366426026	-3.92071	8.81E-05	0.00148757	grey	-0.323451602	1.98E-05	GO:0046872,GO:0003723	AT5G42420.1	RNA-metabolising metallo-beta-lactamase family protein	metallo beta-lactamase, putative
Sapur.014G108600.1	182.8507464	-0.241316018	0.061558845	-3.92054	8.84E-05	0.00148851	grey	-0.295503843	0.000138609		AT4G07940.1	DEGP protease 2	protease Do-like protein
Sapur.019G069900.1	166.0438554	0.133329121	0.034000815	3.92052	8.85E-05	0.00149104	grey	0.277574138	0.000422162	GO:0016787	AT4G19180.1	Histidine phosphatase superfamily protein	GDA1/CD39 (nucleoside phosphatase) family protein
Sapur.012G007400.1	2.338205585	-0.652013106	0.166340562	-3.91974	8.88E-05	0.00149332	grey	-0.334565611	1.85E-05		AT4G34830.1	CAM47	calmodulin 7
Sapur.002G200000.1	0.899616477	-1.165041479	0.297063387	-3.91944	8.89E-05	0.00149504	grey	-0.314863179	3.50E-05		AT1G67310.1	ATEF1,EEF1	elongation factor 1
Sapur.15W0G0110300.2	0.781890015	-1.08397739	0.276928277	-3.91904	8.89E-05	0.00149795	grey	-0.039525255	0.623846196	GO:0055114,GO:0016491,GO:0080167,GO:0016638,GO:0006613	AT5G53480.3	Helicase/SANT-associated, DNA binding protein	glutamate synthase (NADH)
Sapur.012G089500.1	175.4.75949	-0.107382266	0.027398829	-3.91883	8.90E-05	0.00149885	grey	-0.342398686	1.15E-05	GO:0016192,GO:0016021	AT4G04670.2,VAMP726	vesicle-associated membrane protein 726	vesicle-associated membrane protein, synaptobrevin 7R, putative
Sapur.006G185200.1	1.077974157	-0.260720361	0.329417318	-3.918202	8.91E-05	0.00150041	grey	-0.292832332	0.000187744	GO:0005515	AT5G07610.1	F-box family protein	F-box-like protein
Sapur.15W0G0170900.1	81.67538298	0.315039569	0.080495162	3.918151	8.92E-05	0.00150266	grey	0.302121106	0.000981149		AT5G22380.1	PDV1	plastid division1
Sapur.016G097500.1	727.3528737	-0.131287297	0.03355523	-3.9172	8.96E-05	0.00150917	grey	-0.32324691	3.23E-05	GO:0007165	AT5G57750.1		Rho GTPase activating protein with PAK-box/PX1-Rho-binding domain
Sapur.001G136100.2	3.345251847	-0.599461335	0.153049758	-3.91677	8.97E-05	0.00151103	grey	-0.321695571	4.35E-05	GO:0005524	AT5G15750.1	RPT1A	regulatory particle triple-A 1A
Sapur.006G186600.1	886.7358848	0.22602761	0.05771161	3.9164	8.98E-05	0.00151322	grey	0.263944635	0.000837111		AT5G45490.1		phytanoyl-CoA dioxygenase (PhyH) family protein
Sapur.017G011500.1	10.06860027	-0.553883804	0.141950435	-3.91604	9.00E-05	0.00151543	grey	-0.305940077	9.75E-05				
Sapur.003G144700.1	1.194113386	-0.596547088	0.152188226	-3.91507	9.02E-05	0.00151694	grey	-0.339203021	1.38E-05	GO:0043666,GO:0009966,GO:0048364	AT5G22200.2	phosphoprotein phosphatase inhibitors	protein phosphatase inhibitor 2 containing protein
Sapur.004G142900.1	69.42932162	-0.395393788	0.101012868	-3.91429	9.07E-05	0.00152627	grey	-0.313303005	6.46E-05	GO:0005085,GO:0016021	AT2G28120.1	Major facilitator superfamily protein	NA
Sapur.003G028300.1	155.7612168	-0.604329573	0.078198869	-3.91404	9.08E-05	0.00152728	grey	-0.292752209	0.000186653	GO:0005515	AT2G21570.1	Lipase/hydrolase,GLAT,GLAT family protein	A 1-phyl-stress protein
Sapur.014G022100.1	0.380263125	1.856268797	0.47442354	3.912683	9.13E-05	0.00153632	grey	0.388385146	5.00E-07		AT3G44880.1	Helicase/SANT-associated, DNA binding protein	NA
Sapur.001G180500.1	1877.617218	0.385405597	0.098355461	3.911957	9.16E-05	0.00154097	grey	0.288505305	0.000253993	GO:0005975,GO:0004553	AT5G36640.1	HGL1	heteroglycan glucosidase 1
Sapur.019G049500.1	22.01410984	0.386131762	0.098732687	3.910088	9.28E-05	0.00154861	grey	0.319664898	2.35E-05		AT2G01020.1	ATCIMS1,ATKPCI-HET2,XPO	exportin 1A
Sapur.002G199600.1	4801.674433	0.110016267	0.028104433	3.909838	9.29E-05	0.00155413	grey	0.262451102	0.000898148	GO:0016791	AT5G52280.1	PDV1	RNA 2'-terminal phosphate cyclase/enolpyruvate transferase, alpha/beta
Sapur.012G082300.1	25.96223928	0.704671588	0.180234622	3.909075	9.34E-05	0.00155465	grey	-0.267978328	0.000270041	GO:0008468,GO:0005524,GO:0004672	AT5G28280.1	PRSK	PRS-like receptor kinase,Pfam:Protein kinase-like SD2-5, putative
Sapur.006G054800.1	967.8866188	0.168261437	0.043049471	-3.90856	9.38E-05	0.00155214	grey	-0.302186757	0.000118541	GO:0005515,GO:0003677	AT5G15340.1	MBD10	methyl-CPG-binding domain 10
Sapur.006G135300.1	4.026436969	-0.858856151	0.219618815	-3.907945	9.31E-05	0.00156668	grey	-0.282051204	0.000363182	GO:0005515,GO:0006662	AT3G22120.1	Thioredoxin superfamily protein	thioredoxin-like protein
Sapur.013G139800.1	24.92418848	-0.882676274	0.225895846	-3.90745	9.33E-05	0.00156918	grey	-0.299870624	0.000138858	GO:0005975,GO:0004553	AT3G44480.1	BGLU17	beta glucosidase 17
Sapur.002G082200.3	0.373047344	-1.613312386	0.417525309	-3.90714	9.34E-05	0.00157114	grey	-0.081608864	0.309009942	GO:0005515,GO:0006355,GO:0005634,GO:0032502,GO:0006351	AKGRP1,GRP1	growth-regulating factor 1	growth-regulating factor 1, putative
Sapur.013G109500.4	1.402858181	0.993848881	0.254313963	3.906529	9.38E-05	0.00157571	grey	-0.31469107	5.97E-05		AT3G13130.1		hypothetical protein
Sapur.005G185600.3	3.175069037	-0.656808759	0.168157565	-3.906469	9.37E-05	0.00157531	grey	-0.259658549	0.000300013	GO:0055114,GO:0020037,GO:0004096,GO:0006979	AT4G08780.1	CAT1	catalase 1
Sapur.013G025300.1	8.879412265	0.581650467	0.148918975	3.905818	9.38E-05	0.00157948	grey	-0.258806456	0.001064624		AT5G19080.1		RING/U-box superfamily protein
Sapur.012G085700.1	43.21635858	-0.282038896	0.072288554	-3.90525	9.41E-05	0.00158299	grey	-0.285670684	0.000287005	GO:0005524,GO:0006003,GO:0003677	AT5G52120.1	ATSRS2,SRS2	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.005G136300.1	196.3017.5	0.134617191	0.034484976	3.905244	9.43E-05	0.00158284	grey	-0.282237651	0.000341941		AT2G30020.2		Protein of unknown function (DUF1828)
Sapur.015G029700.1	35.29423863	0.318682298	0.081604787	-3.90477	9.43E-05	0.00158589	grey	-0.292202293	0.000204658		AT5G03130.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.012G031100.1	146.180914	-0.263281005	0.066931922	-3.90357	9.48E-05	0.00159383	grey	-0.360406179	1.53E-06	GO:0016758,GO:0008152	AT3G26600.1	DOGT1,UGT73C5	don-glucosyltransferase 1
Sapur.010G042900.1	2.352475867	-0.837812616	0.214664774	-3.90332	9.49E-05	0.00159536	grey	-0.321899694	1.97E-05		AT3G24060.1		Plant self-incompatibility protein S1 family
Sapur.015G022900.1	8.417666143	-0.648203954	0.166114776	-3.90213	9.53E-05	0.00160351	grey	-0.291216619	0.000380462	GO:0005515,GO:0043531	AT5G11810.2	LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.005G090000.4	3.677613871	-0.552260751	0.141569897	-3.90086	9.58E-05	0.00160147	grey	-0.144327134	0.073122788		AT4G38870.2	TLD-containing protein with nucleolar protein	TLD protein
Sapur.005G075500.1	0.468016763	1.262686634	0.324165125	3.899946	9.62E-05	0.00160794	grey	0.317267679	1.55E-05		AT5G55930.1	Nodulin MtN3 family protein	NA
Sapur.013G081300.1	1221.287057	-0.415016642	0.106750638	-3.89768	9.70E-05	0.00163051	grey	-0.259026969	0.001069878		AT5G35970.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	DNA-binding protein smubp-2
Sapur.016G283800.1	27.92161882	-0.408054417	0.104875565	-3.89553	9.80E-05	0.00164685	grey	-0.303274101	0.000112933	GO:0016021,GO:0004252,GO:0006508	AT4W.10,RBL10	RHOMBOID-like protein 10	rhomboid protease gluP
Sapur.013G095800.1	73.31029165	0.016285184	0.007071751	3.894684	9.87E-05	0.00165754	grey	-0.264391058	0.000819617		AT3G08025.1	Cysteine proteinase superfamily protein	OTU-like cysteine protease
Sapur.002G020900.1	170.8356274	0.18270865	0.046921771	3.893899	9.88E-05	0.00165774	grey	-0.282692215	0.000334172	GO:0008270,GO:0005622	AT5T5540.1	STH2	salt tolerance homolog2
Sapur.15W0G0011300.1	275.8129984	0.066401241	0.015835745	3.89329	9.88E-05	0.00166184	grey	-0.317044182	6.68E-06	GO:0005515	AT3G11930.1	ulfm, putative	NA
Sapur.016G209200.1	12.64299779	0.406062503	0.104339408	3.891746	9.95E-05	0.00167236	grey	0.317936632	6.96E-05	GO:0016021,GO:0020037,GO:0016775,GO:0005506	AT3G10670.1	CYP82C2	cytochrome P450 family 82 monooxygenase
Sapur.006G000600.1	26.47506431	0.334653766	0.085846614	3.897127	9.97E-05	0.00167622	grey	0.264391058	0.000819617	GO:0005515	AT5G08020.1	AGAP1,ATSAP2,ATSARA1C,S	secretion-associated RAS family protein
Sapur.017G072500.1	0.31675265	-5.539424282	0.395722483	-3.89016	0.00010178	0.00168315	grey	-0.473473369	3.79E-10		AT4G33700.1	Uncharacterized protein family (UPF0497)	plant integral membrane protein
Sapur.T10S100.1	2.748124619	0.950750207	0.173262229	3.889673	0.00010179	0.00168634	grey	0.281909636	0.000476569		AT4W65.N1DES	N/Hdr-related family	NA
Sapur.T10J000.1	2.022796175	0.825481041	0.212267411	3.888873	0.00010711	0.00169185	grey	0.223877863	0.006822858				
Sapur.T10H000.1	267.7213217	0.265779332	0.06709323	3.888128	0.00010321	0.00169684	grey	0.258319244	0.001008604		AT4G37640.1	PYE	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.018G055300.1	192.5575744	-0.264651285	0.068007701	-3.88862	0.00010324	0.00169694	grey	-0.268281616	0.000270523				NA
Sapur.002G190000.1	9.093776185	-0.423409974	0.108949655	-3.88709	0.00010452	0.00170404	grey	-0.364948974	8.80E-06		AT5G25060.1	Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein, putative
Sapur.007G128800.1	138.5583313	-0.029751194	0.00911281	-3.88601	0.00010507	0.00171159	grey	-0.295268882	0.000175991	GO:0046872	AT4W.G1A,RING1A	RING 1A	RING finger protein
Sapur.016G122200.2	1.720751667	-0.832488425	0.214294674	-3.88483	0.00010324	0.00171079	grey	-0.31810306	9.31E-05	GO:0008168,GO:0008757	AT5G40850.1	UPM5	uroporphyrinogen III C-methyltransferase
Sapur.015G125800.1	2151.112084	0.084200237	0.01667261	3.884167	0.00010461	0.00171994	grey	0.263415452	0.000875681	GO:0005515,GO:0045900	AT4G30220,GO:0006452,GO:0003746,GO:0003723	AT5T5A-1,EIF-5A,EIF5A,EI	eukaryotic translation initiation factor 5A-1
Sapur.009G035000.1	15.61162318	-0.451466671	0.1112245	-3.88444	0.00010258	0.00172243	grey	-0.281638255	0.000312473		AT2G19910.1	ELF4-like 1	ELF4-like protein
Sapur.016G142100.1	3.391658864	0.722329444	0.18857571	3.882724	0.00010721	0.00172724	grey	0.462524564	1.07E-09		AT3G44920.1	Phosphatase-responsive NHX antiporter	BT8/PDQ2 domain protein
Sapur.002G138900.1	1.541461749	-0.874065195	0.225288259	-3.88349	0.00010967	0.00172896	grey	-0.329175598	2.56E-05	GO:0006355,GO:0003677	AT4G26770.1	ANAC042,EMB2301,NST1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
Sapur.015G137200.3	5.719638809	-0.273180264	0.070453268	-3.88346	0.00010967	0.00172908	grey	-0.284947218	0.000331599	GO:0008168,GO:0008168

Sapur.002G181700.1	79.87307688	0.308448677	0.080839889	3.815546	0.000315852	0.00026646	grey	0.27195721	0.00056988	ATSG25400.1	MeG nucleotide pyrophosphohydrolase domain protein
Sapur.010G149600.2	31.97112356	-0.40462669	0.106048884	-3.81547	0.000135927	0.00226709	grey	-0.123401047	3.61E-05	GO:0016833;GO:0009058	ATSG05730.1 AMT1.4;6A1.IDL1.TRPS.WEL anthranilate synthase alpha subunit 1 anthranilate synthase, alpha subunit 1, putative
Sapur.010G150400.7	1.92259212	-0.69589197	0.181580281	-3.81509	0.000136134	0.00227042	grey	-0.135318556	4.88E-06		ATSG18059.4 hypothetical protein hypothetical protein
Sapur.010G192100.1	5.45788768	-0.48676187	0.127582667	-3.81499	0.000136519	0.00227126	grey	-0.133162495	2.01E-05	GO:0008270	ATSG04860.1 ATUBP2;UBP2 ubiquitin-specific protease 2 ubiquitin carboxyl-terminal hydrolase
Sapur.010G208300.1	319.6184667	-0.03078865	0.008050134	-3.81418	0.000136635	0.00227854	grey	-0.131745492	6.67E-05		ATSG24173.1 Exostosin family protein NA
Sapur.010G243400.1	58.15692142	-0.25830283	0.067732929	-3.81351	0.000136984	0.00228427	grey	-0.130187866	0.000113467	GO:0043531	ATSG14482.1 LRR and NB-ARC domains-containing disease resistance protein NBS-LRR type disease resistance protein
Sapur.017G249400.1	5.15507765	-0.51932086	0.136138173	-3.81327	0.000137138	0.00228672	grey	-0.301575509	0.000122922		ATSG43490.1 hypothetical protein hypothetical protein
Sapur.002G287000.1	2.12032273	-0.85152989	0.22028471	-3.8123	0.000137681	0.00229565	grey	-0.369078593	1.86E-06		NA NA NA
Sapur.010G092900.1	0.43864876	1.40763633	0.369255703	3.812091	0.000137796	0.00229746	grey	0.309882855	7.79E-05	GO:0006468;GO:0005524;GO:0004672	ATSG05800.1 ARK2;RK2 receptor kinase 2 NA
Sapur.006G151100.1	1.00315768	0.962167611	0.252485385	3.81063	0.000138615	0.00231084	grey	0.268135	7.18E-05		NA NA NA
Sapur.006G226800.1	0.07118702	-0.96110925	0.252230017	-3.8106	0.000138631	0.00231091	grey	-0.294178034	0.000184327		NA NA NA
Sapur.010G172200.1	0.30137554	1.6442668	0.431607618	3.808839	0.000139621	0.00232734	grey	0.422328607	1.60E-08		ATSG26460.1 NA NA NA
Sapur.018G038400.3	8.52707347	-0.42594899	0.111834952	-3.80873	0.000139683	0.00232881	grey	-0.264990158	0.000796473		ATSG29830.1 ATMAK2;MKL;MKK2 MAP kinase kinase 2 MAP kinase kinase
Sapur.004G208800.1	0.96853419	1.36228688	0.358000924	3.80849	0.000139811	0.00233153	grey	-0.263408376	0.000203649	GO:0008168	ATSG26280.1 NA 5-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.010G103500.2	1.46572815	-0.94915389	0.249368882	-3.80649	0.000140955	0.00234895	grey	-0.267126903	0.000719562	GO:0006468;GO:0005524;GO:0004672	ATSG68680.1 Protein kinase superfamily protein tyrosine kinase domain protein
Sapur.019G215680.1	14.06603931	-0.18375846	0.147568873	-3.80516	0.000141114	0.00235318	grey	-0.369398621	0.000035668	GO:0005992;GO:0008324	ATSG14682.2 Haloacid dehalogenase-like hydrolase (HAD) superfamily protein trehalose-phosphate phosphatase
Sapur.010G865000.6	0.66391019	-1.26417261	0.332162832	-3.80588	0.000141	0.00235466	grey	-0.322590022	3.78E-05	GO:0016021;GO:0006952	ATSG53760.2 ATMLO11;MLO11 Seven transmembrane MLO family protein MLO-like protein
Sapur.014G261200.1	20.29378355	-0.42634851	0.112026233	-3.80574	0.000141137	0.00235555	grey	-0.315900048	5.57E-05		ATSG67070.1 RALFL14 rapid alkalinization factor NA
Sapur.004G287000.1	11.1653755	-0.85285589	0.223933604	-3.80541	0.000141359	0.00235884	grey	-0.277855586	1.05E-05		ATSG27281.1 F-box/RNI-like/FBD-like domains-containing protein NA
Sapur.010G898900.3	2.34102674	0.67393573	0.177124235	3.804876	0.000141875	0.00236368	grey	0.345572995	9.30E-06		ATSG75110.1 transmembrane protein, putative
Sapur.012G056600.1	119.4037626	0.158569327	0.041679153	3.804618	0.000142037	0.00236698	grey	0.293825256	0.000177734	GO:0008270	ATSG10300.1 WLIM1 GATA type zinc finger transcription factor family protein pollen specific LIM domain protein
Sapur.013G029100.1	2.66241465	-0.67479564	0.177411226	-3.80347	0.000142681	0.00237674	grey	-0.314605715	6.07E-05		ATSG13500.1 NA NA NA
Sapur.004G163100.1	4.42885571	-0.56146746	0.148267763	3.802605	0.000143183	0.00238468	grey	-0.277888606	0.000188427	GO:0003824;GO:0006470;GO:0004722	ATSG18520.1 Protein phosphatase 2C family protein protein phosphatase 2C, putative
Sapur.013G076400.1	0.35063185	1.28879724	0.338956007	3.802255	0.000143385	0.00238824	grey	0.369803275	1.87E-06		ATSG26880.1 Helicase/SNF1-associated, DNA binding protein NA
Sapur.010G079300.3	0.47967818	-1.36622688	0.359283896	-3.80042	0.000143543	0.00239092	grey	0.292054929	0.000179725		ATSG04042.1 Major facilitator superfamily protein protein transporter, putative
Sapur.006G180000.1	29.80687854	-0.71802305	0.189445759	-3.79488	0.000147716	0.00245882	grey	-0.308110892	8.65E-05	GO:0050385;GO:0016020;GO:0051297;GO:0015238;GO:0006855	ATSG21440.1 MATE efflux family protein NA
Sapur.010G172600.1	3.79867409	-0.81355669	0.211145664	-3.7948	0.000147762	0.00245884	grey	-0.30624971	9.60E-05		ATSG26121.1 5-adenosyl-L-methionine-dependent methyltransferase superfamily protein trimethylguanosine synthase, putative
Sapur.012G061100.13	1.78818282	-0.73531407	0.19382533	-3.79366	0.000148422	0.00246695	grey	-0.279295772	0.000396562	GO:0005891	ATSG48195.1 Phos (PX) domain-containing protein differentially in FDCP-like protein, putative
Sapur.005G270600.1	1.68380347	-0.70968004	0.187206334	-3.79256	0.000148849	0.00247025	grey	-0.308896896	8.25E-05	GO:0005515	ATSG21281.1 UBP7 ubiquitin-specific protease 7 ubiquitin carboxyl-terminal hydrolase
Sapur.018G086100.2	6.47074093	-0.62913362	0.165892927	-3.79367	0.000148619	0.00247229	grey	-0.310779364	0.000122129	GO:0006468;GO:0006472	ATSG23180.1 CRK10;RLK4 TRICHOME BIREFRINGENCE-LIKE 25 protein kinase family UDP-glucosyl and UDP-glucosyl transferase
Sapur.005G180600.1	448.7918745	-0.20331429	0.053587946	-3.79174	0.000149319	0.00248407	grey	-0.257650355	0.000237907	GO:0016758;GO:0008152	ATSG22180.1 UGT-glucosyltransferase family protein lipase
Sapur.019G042300.1	0.90919401	1.64206692	0.433165559	3.790807	0.000150159	0.00249766	grey	-0.236953306	0.002851435	GO:0006629	ATSG14930.2 SAG101 senescence-associated gene 101 hypothetical protein
Sapur.006G129000.1	14.37608843	-0.62382537	0.174838355	-3.7903	0.000150648	0.00250349	grey	-0.219420339	0.003543311	GO:0004873;GO:0000166	ATSG29393.1 ATRaxo E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein lipase
Sapur.012G082200.1	123.3719367	0.975748882	0.257461268	3.790184	0.000150535	0.00250359	grey	0.261522031	0.000767932	GO:0005515	ATSG47890.1 ARIL;RT_AT4H17 receptor like protein 5 NA
Sapur.008G107900.1	14.70019029	0.829311187	0.218895115	3.7896	0.000150589	0.00250592	grey	0.248763536	0.001680116		ATSG14870.1 PCR2 PLANT CADMIUM RESISTANCE 2 plant cadmium resistance protein
Sapur.010G051000.1	171.7328025	0.105821193	0.027918282	3.788324	0.000151667	0.00252186	grey	0.254609018	0.000218117		ATSG40042.1 Microsomal signal peptidase 12 kDa subunit (SPC12) microsomal signal peptidase 12 kDa subunit
Sapur.013G058800.3	16.64116692	-0.35415208	0.093485926	-3.78788	0.000151936	0.00252622	grey	-0.283075648	0.000344831		ATSG36950.1 hydroxyproline-rich glycoprotein family hypothetical protein
Sapur.T005300.1	1.24012662	-0.67139294	0.202112607	-3.78627	0.000152619	0.00253794	grey	-0.303605975	0.000117132	GO:0008270;GO:0003722;GO:0006235;GO:0005779	ATSG44460.1 APMA;ATPDX12;PDX12 pertein-12 phenylcoumaran benzylic ether reductase-like protein
Sapur.T157000.1	0.28189604	1.48730386	0.392778886	3.786675	0.000153676	0.00253823	grey	0.400597468	2.01E-07		ATSG15130.1 CYP97B3 cytochrome P450, family 97, subfamily B, polypeptide 3 NA
Sapur.005G005200.1	13.68029648	-0.37722887	0.100468455	-3.78576	0.000152703	0.00253845	grey	-0.271302675	0.000388396		ATSG29180.1 NA NA NA
Sapur.008G142800.2	7.23404919	-0.43479543	0.114830643	-3.78643	0.000152825	0.00254028	grey	0.291802868	0.000153706	GO:0005515	ATSG10840.1 Tetratricopeptide repeat (TPR)-like superfamily protein kinesin light chain, putative
Sapur.010G042600.1	7.71374286	-0.56146502	0.149513264	-3.78463	0.000153239	0.00255418	grey	-0.298404564	0.000146955	GO:0003676	ATSG21455.1 RNA-binding (RRM/RBD/RNP motifs) family protein splicing factor U2AF large subunit, putative
Sapur.T150100.1	1.90970497	0.71285349	0.188410347	3.785808	0.000153231	0.00255485	grey	-0.272303378	0.000136228		ATSG12010.1 Disease resistance protein (TIR-NBS-LRR class) family NA
Sapur.002G285000.1	0.76350157	-0.49438385	0.370990174	-3.78495	0.000153738	0.00255515	grey	-0.328617115	4.24E-05		ATSG43980.1 PDLP1;PDLP1A plasmodesmata-located protein 1 salt stress response/antifungal domain protein
Sapur.013G075700.1	0.68307056	-1.27162451	0.336988487	-3.7847	0.000153986	0.00255754	grey	-0.296197815	0.000105507		ATSG48650.2 DE(H/D)-box RNA helicase family protein hypothetical protein
Sapur.15W0G031500.1	3.11327096	-0.56839483	0.15038663	-3.78325	0.000154794	0.00257231	grey	-0.350188202	6.93E-06	GO:0005524;GO:0003676	
Sapur.010G194100.1	121.5030319	0.267495629	0.071000114	3.782669	0.000155069	0.00257674	grey	-0.300872409	0.000128		ATSG26150.1 NA NA NA
Sapur.001G185100.1	8.40264754	0.460334473	0.121670384	3.782527	0.000155244	0.00257952	grey	0.296649635	0.000345311	GO:0006355;GO:0008270;GO:0006355	ATSG10240.1 FRS11 FAR1-related sequence 11 FAR1-related sequence protein
Sapur.012G026200.1	123.3719367	0.975748882	0.257461268	3.782484	0.000155265	0.00258053	grey	0.335272738	7.97E-05	GO:0005515;GO:0006952	ATSG15120.1 ARIL;ATAR17 IBR domain-containing protein E3 ubiquitin protein ligase
Sapur.006T030900.1	22.7525803	-0.46107873	0.121890278	-3.78268	0.000155287	0.00257989	grey	-0.304850876	0.000103578		ATSG27010.1 PCR2 PLANT CADMIUM RESISTANCE 2 NA
Sapur.011G094500.1	77.64139969	-0.62382541	0.165125248	-3.78182	0.000156068	0.00258262	grey	-0.293036668	0.000350961	GO:0030915;GO:0019786;GO:0000724	ATSG15150.1 ATMMZ2;LHP2;MMZ21 RING/U-box superfamily protein RING-U box protein-like NGE2, putative
Sapur.010G047000.1	4.38419029	-0.74249236	0.196430713	-3.77922	0.000156878	0.00260614	grey	-0.374615109	1.36E-06	GO:0008033	ATSG26480.1 ATIPT1;IPT1 isopentenyltransferase 1 cytokinin biosynthetic isopentenyltransferase
Sapur.010G212000.2	1.11687003	-0.66258851	0.175388653	-3.77848	0.000157158	0.00261053	grey	-0.293037372	0.000137674	GO:0016829;GO:0006006	ATSG20667.1 Aspergine synthetase family protein asparagine synthetase, putative
Sapur.013G136500.1	42.62674588	-0.68879263	0.182332782	-3.77786	0.000158183	0.00262718	grey	-0.302652233	0.000130322	GO:0016829;GO:0010334;GO:0008152;GO:0000287	ATSG16730.1 TPS02 terpene synthase 02 NA
Sapur.T036300.1	0.27050481	-1.38423023	0.356912671	-3.77774	0.000158259	0.00262829	grey	-0.383252293	5.81E-07		ATSG29820.1 Magnesium transporter CorA-like family protein NA
Sapur.009G093100.2	10.16807676	-0.44242061	0.117077246	-3.77735	0.000158524	0.00263224	grey	-0.336018525	1.62E-05		ATSG45481.1 hmrA-like nitroreductase family protein family protein phenylcoumaran benzylic ether reductase-like protein
Sapur.010G021400.1	44.95132203	-0.25163415	0.066623435	-3.7771	0.000158665	0.00263477	grey	-0.275288602	0.000472185	GO:0006468;GO:0006672	ATSG34300.1 lectin protein kinase family protein NA
Sapur.T127500.1	0.36192604	-1.37172887	0.364806927	-3.77666	0.000159174	0.00263977	grey	0.41102042	8.32E-08		ATSG15110.1 CYP97B3 cytochrome P450, family 97, subfamily B, polypeptide 3 NA
Sapur.006G160300.1	119.029832	0.144934041	0.038395378	3.774778	0.000160105	0.00265917	grey	0.273635253	0.000349349	GO:0005524;GO:0003676	ATSG42520.1 T-loop containing nucleoside triphosphate hydrolases superfamily protein DEAD-box ATP-dependent RNA helicase
Sapur.006G219500.1	64.66125257	-0.36277092	0.100604886	-3.77386	0.000160674	0.00266774	grey	-0.279278934	0.000466602		ATSG27140.1 HSP20-like chaperones superfamily protein heat shock family protein
Sapur.010G062600.1	332.4549478	-0.24305771	0.064116234	-3.7739	0.000160717	0.00266832	grey	-0.294868304	0.000177636		ATSG11760.1 NA EEIG1/EHBP1 protein amino-terminal domain protein
Sapur.010G150100.1	10.26034997	-0.50536281	0.134058727	-3.77324	0.000161079	0.00266987	grey	-0.32031212	4.32E-05		ATSG22280.1 Protein of unknown function (DUF1218) transmembrane protein, putative
Sapur.010G089900.1	1.79207562	-0.80266153	0.212769033	-3.77201	0.000161936	0.00268851	grey	-0.298812698	0.000347358	GO:0005515;GO:0003700	ATSG30590.1 WRKY DNA-binding protein 21 WRKY transcription factor, putative
Sapur.005G075800.1	292.9219796	-0.18164419	0.048162301	-3.77152	0.000162258	0.00269338	grey	-0.305326469	9.98E-05		ATSG36980.1 NA NA NA
Sapur.010G389800.1	4.79162152	-0.60284972	0.160182181	-3.76755	0.000163183	0.00270431	grey	-0.346312621	8.86E-06	GO:0006355;GO:0005634;GO:0005524;GO:0003250;GO:0006351	ATSG29310.1 DEAD domain-containing / helicase domain-containing protein / HNH endonuclease domain-containing pr NA
Sapur.005G075800.1	245.1944684	-0.12531883	0.033208888	-3.77101	0.000162259	0.00269986	grey	-0.293202082	0.000217556		ATSG44620.1 RNA-processing, 5bn domain protein hypothetical protein
Sapur.006G082900.1	26.87252348	-0.53087832	0.140746687	-3.76631	0.000165679	0.00274792	grey	-0.289552774	0.000235024	GO:0005524;GO:0016491	ATSG05600.1 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein leucoanthocyanidin dioxygenase
Sapur.015G015500.1	1.03428857	1.61747564	0.429479813	3.766127	0.000165799	0.00274988	grey	0.230134911	0.003738841	GO:0006457;GO:0006952	ATSG24020.1 MLP424 MLP-like protein 424 Bet v 1 allergen protein
Sapur.019G041000.1	6.09418767	-0.42502274	0.113696665	-3.76542	0.000166269	0.00275741	grey	-0.296937616	0.000303984		ATSG27020.1 NA ATP binding cassette, acid binding helicases
Sapur.013G094600.1	52.65878537	-0.35382884	0.093916119	-3.76536	0.000166307	0.00275793	grey	-0.328170904	2.61E-05	GO:0020744;GO:0005576;GO:0005618;GO:0005737	ATSG26360.1 SLX2 SLX2G SLX2 transcriptional corepressor SEUSS protein, putative
Sapur.001G170200.1	402.2208269	0.092408111	0.024686328	3.764655	0.000166779	0.00276573	grey	0.260247272	0.000907721	GO:0006015	ATSG20260.1 NRP4 plantacyanin basic blue protein
Sapur.014G106300.1	6.31930743	-0.58485935	0.155313154	-3.76461	0.000166812	0.00276591	grey	-0.27678834	0.000449373		ATSG47830.1 NF-YB5 nuclear factor Y, subunit B5 nuclear transcription factor Y subunit B6
Sapur.015G076300.1	11.88037744	-0.56172429	0.150172639	-3.76427	0.000167033	0.00276943	grey	-0.314489849	6.06E-05	GO:0006412;GO:0005840;GO:0003735	ATSG13730.1 NA Ribosomal protein family protein ribosomal protein
Sapur.006G241000.2	2.58094787	0.72609623	0.191196055	3.763659	0.000167445	0.00277623	grey	0.297268456	0.000156305	GO:0005515;GO:0008236;GO:0006508	ATSG17680.1 Peptidase S41 family protein carboxy-terminal processing peptidase
Sapur.008G067100.1	0.46041508	1.29835686	0.345013395	3.763206	0.000167740	0.00278102	grey	0.263032341	0.000873884	GO:0005515	ATSG19830.2 NTMC2T5.2;NTMC2T9PEG.1 Calcium-dependent lipid-binding (CaLB domain) family protein integral membrane single C2 domain protein
Sapur.005G846400.1	22.24277	-0.61735753	0.164047514	-3.76303	0.000167867	0.00278267	grey	-0.280643532	0.000370622		ATSG48920.1 TED7 trachery element differentiation-related 7 transmembrane protein, putative
Sapur.001G122000.1	107.1441825	-0.14538311	0.038625759	-3.76273	0.000168066	0.00278585	grey	-0.291297312	0.000215193	GO:0005515	ATSG48800.1 Stele-ulpha motif (SAM) domain-containing protein Sos1-fungal family SAM domain protein
Sapur.010G138900.1	50.17937733	-0.62248276	0.165505754	-3.76227	0.000168314	0.00278922	grey	-0.292404976	0.000263187	GO:0005524;GO:0003700	ATSG28140.1 Integrase-type DNA-binding superfamily protein dehydration-responsive element-binding transcription factor 2
Sapur.003G263500.1	1.08333784	-0.88114491	0.234397745	-3.75919	0.000170467	0.00282522	grey	-0.342126138	1.16E-05		ATSG29330.1 NA NA NA
Sapur.010G098700.1	177.4114338	0.214028359	0.056248894	-3.75884	0.000170542	0.00283462	grey	-0.306757268	0.000134622	GO:0006468;GO:0005524;GO:0004672;GO:0030246	ATSG15510.1 Concanavalin A-like lectin protein kinase family protein a-tm-domain receptor kinase
Sapur.017G267700.2	38.87104129	-0.36178703	0.084315217	-3.75744	0.000171665	0.00286479	grey	-0.013775496	0.864038768		ATSG17540.1 RNA-binding (RRM/RBD/RNP motifs) family protein nucleic acid-binding protein
Sapur.003G068000.1	34.41843214	-0.47108257	0.110900423	-3.75503	0.000172583	0.00287905	grey	-0.354542704	1.36E-06	GO:0006412;GO:0005840;GO:0003735	ATSG46950.2 NA breast basic conserved 1 NA
Sapur.016G129900.2	26.52567615	-0.25570638	0.060880513	-3.75561	0.000172678	0.00286129	grey	-0.065295455	0.435156657	GO:0005622;GO:0003779;GO:0030042;GO:0015629	ATSG59890.1 ADF4;ATADF4 actin depolymerizing factor 4 actin-depolymerizing factor
Sapur.004G268700.1	238.1347796	0.090329944	0.050639834	-3.7559	0.000172721	0.00286187	grey	-0.304832344	0.000103394	GO:0005085	ATSG55730.1 YSL7 YELLOW STRIPE like 7 oligopeptide transporter OPT family protein
Sapur.010G150500.1	12.39518027	0.313495524	0.093556741	3.755711	0.000172785	0.00286387	grey	-0.251367351	0.004966571		ATSG19190.1 NA NA NA
Sapur.016G259900.1	0.30631679	1.70248269	0.453406158	3.754873	0.000173429	0.00287317	grey	0.4104947	9.31E-08	GO:0005515	ATSG59190.1 F-box/RNI-like superfamily protein F-box/RNI/LRR plant protein, putative
Sapur.006G241200.1	13.54528888	0.55205174	0.151277	-3.75399	0.000174044	0.00288321	grey	-0.265475734	0.000798511		ATSG29170.1 NA NA hypothetical protein
Sapur.013G058900.1	16.66468866	-0.40493875	0.107878724	-3.75284	0.000174823	0.00288703	grey	-0.268862073	0.000728172	GO:0006468;GO:0005524;GO:0004672	ATSG15230.1 ATLP1;LP1 lipase 1 NA
Sapur.005G058500.1	9.04272366	0.551533884	0.146842368	3.752435	0.000174935	0.00288927	grey	-0.291942251	0.000186492	GO:0005515	ATSG19220.1 RAN GTPase activating protein 2 Ran GTPase activating protein
Sapur.002G062300.3	15.06814663	-0.31884906	0.084953347	-3.75341	0.000174444	0.00288884	grey	-0.284072727	0.000301359	GO:0016491;GO:0006741;GO:0003951	ATSG16640.1 ATNAD(H)2;NAD(H)2 NAD kinase 2 NAD kinase
Sapur.002G231200.1	78.27584718	-0.38980891	0.104000623	-3.75301	0.000174662	0.00289381	grey	-0.253677775	0.001328758	GO:0016491;GO:0051287;GO:0006631	ATSG46630.2 NA 3-oxoacyl-[acyl-carrier-protein] reductase family protein 3-oxoacyl-[acyl-carrier-protein] reductase
Sapur.T064000.1	16.13627348	-0.45889084	0.123315096	-3.7517	0.000175636	0.00290886	grey	-0.419505665	4.68E-08	GO:0051087;GO:0006457;GO:0005783;GO:0005509	ATSG08450.1 AtCRT3;CRT3;BR2;PSL1 calreticulin 3 NA
Sapur.005G129900.1	1.38253835	-0.83179304	0.221968754	-3.75129	0.000175911	0.00290983	grey	-0.336140455	0.000128667		ATSG18490.1 NA NA NA
Sapur.001G178800.1	1.34510086	1.04651622	0.291788994	3.751164	0.000176035	0.00291497	grey	0.2857866	0.000285611	GO:0003677	ATSG68840.1 EDF2;RAP2.8;RAV2;TEM2 related to ABI3/VP1 2 B3 DNA-binding domain protein
Sapur.014G132900.1	13.14030512	-0.45942032	0.122495493	-3.75051	0.000176475	0.00292217	grey	-0.338851196	8.39E-05		ATSG35732.1 NA NA hypothetical protein
Sapur.T086100.1	11.157482	-0.52562176	0.140173842	-3.7488	0.000178147	0.00295028	grey	-0.279908974	0.000388822		ATSG46690.1 G-HOX;GAMMA-HOX;HOX4 gamma histone variant HOX4 NA
Sapur.013G021200.1	191.3116918	0.765778206	0.204236892	3.749681	0.000177156	0.00293156	grey	0.31080119	7.44E-05	GO:0006468;GO:0005524;GO:0004672	ATSG27730.1 Protein kinase superfamily protein Serine/Threonine kinase domain protein
Sapur.006G091100.1	20.74778844	-0.50131171	0.134043415	-3.74867	0.000178507	0.00295717	grey	-0.334994168	1.80E-05	GO:0005515;GO:0045531	ATSG17680.1 NA Disease resistance protein (TIR-NBS-LRR class), putative NA
Sapur.017G062300.1	28.86700498	-0.38546052	0.102812788	-3.74895	0.000177576	0.00293982	grey	-0.271277216	0.005858182		ATSG15780.1 NA Pollen Ole e 1 allergen and extensin family protein pollen protein Ole E 1-like protein
Sapur.006G186600.1	102.0771144	-0.18542887	0.049602418	-3.74866	0.000177697	0.00294144	grey	-0.298719346	0.000244444		ATSG27141.1 NA NA transmembrane protein, putative
Sapur.002G300000.2	11.83997224	-0.30918492	0.082478386	-3.74864	0.000177799	0.00294323	grey	0.001764656	0.982502264		ATSG30390.2 NA NA cytochrome oxidase complex assembly protein
Sapur.004G041000.1	5.90840463	0.833338569	0.222835135	3.74689	0.000178706	0.00295967	grey	-0.308971995	8.24E-05		ATSG48830.1 NA NA NA
Sapur.003G093300.1	2.28293711	-0.73609008	0.197178958	-3.74806	0.000178206	0.00294965	grey	-0.315852117	5.70E-05	GO:0015261	ATSG41330.1 BTR/PO2 domain with WD40/YVTN repeat-like protein family potassium channel tetramerization domain protein, putative
Sapur.005G198000.4	17.03417901	0.295375245	0.078833177	-3.74792	0.000178305	0.00295114	grey	-0.328834074	0.100037055	GO:0006468;GO:0005524;GO:0004672	ATSG29410.1 Protein kinase superfamily protein tyrosine kinase family protein
Sapur.004G082800.1	125.7876048	-0.45162423	0.120819343	-3.74788	0.000178329	0.00295271	grey	-0.277271348	0.000545071	GO:0006526;GO:0004050;GO:0000620;GO:0003723	ATSG26150.1 ARGN adenosine deaminase RNA-specific adenosine deaminase
Sapur.017G045100.1	23.24972015	0.765688941	0.204343245	3.745871	0.000179769	0.00297495	grey	0.252619222	0.001413153	GO:0005515	ATSG23240.1 ATGSTU7;GST25;GSTU7 glutathione S-transferase tau 7 tau class glutathione transferase GSTU27
Sapur.014G213900.1	14796.23842	0.038239527	0.042551563	3.745669	0.000179773	0.00297496	grey	0.269197754	0.000629612	GO:0008234;GO:0006508	ATSG47128.2 Cathepsin B-like cysteine proteinase family protein cysteine protease
Sapur.010G127700.1	16.4605568	-0.49270308	0.398483592	-3.74512	0.000180305	0.00298364	grey	-0.380159661	9.06E-07	GO:0016021	ATSG14040.1 CKS(RDL1/RPK1/SYG1) family protein serotonin and polytropic murine leukemia virus receptor PHO1, putative
Sapur.002G201700.1	392.7520384	0.167705155	0.045611131	3.679649	0.000181131	0.00299746	grey	0.27969975	0.000447746		ATSG18180.1 ARM repeat superfamily protein dexdy/helicase superfamily protein
Sapur.014G074400.1	79.09623893	-0.31912896	0.085238814	-3.74384	0.000181157	0.00299795	grey	-0.300325898	0.000132586		ATSG05100.1 TBL25 TRICHOME BIREFRINGENCE-LIKE 25 Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.006G162600.1	3080.82235	0.255818638	0.068200179	-3.74305	0.000181802	0.00300781	grey	-0.301450169	0.000124	GO:0016491;GO:0006469;GO:0008270	ATSG37980.1 ATCAD7;AD7;CAD7;LI1;ELI3-1 elicitor-activated gene 3-1 cinnamyl alcohol dehydrogenase-like protein
Sapur.017G002200.1	143.112164	0.603963743	0.161451077	3.741795	0.000182711	0.00303227	grey	-0.267059365	0.000727189	GO:0016758;GO:0008152	ATSG05680.1 UGT74E2 Uridine diphosphate glycosyltransferase 74E2 NA
Sapur.010G146500.1	1.78467003	0.812214365	0.218729884	3.741669	0.000182867	0.00303491	grey	-0.287079968	0.000304011		ATSG27660.1 NA SPT2 chromatin protein chromatin binding protein
Sapur.010G055900.1	33.12275669	-0.49403925	0.132042211	-3.74152	0.000183097	0.00303548	grey	-0.252517276	0.001416131	GO:0005515;GO:0016491;GO:0050664;GO:0004601	ATSG47910.1 ATBGH10;BGH10 oxidoreductase, FAD-binding protein, NAD(P)-binding domain-containing protein respiratory burst oxidase-like protein
Sapur.013G094400.1	77.22164774	-0.29706287	0.079636273	-3.74109	0.000183226	0.00303663	grey	-0.282633	0.000335163		ATSG26840.1 AGD6;UL-EA6 AGAMOUS-like 61 MADS box protein, putative
Sapur.005G111701.1	16.03857473	-0.35665716	0.095342903	-3.74077	0.000183459	0.00303451	grey	-0.305879759	0.000300453		ATSG26110.1 NA NA PsbW domain protein
Sapur.011G094000.1	8.17921868	-0.58723109	0.182658522	-3.74068	0.000183511	0.00305503	grey	-0.284275086	0.000308297	GO:0005515	ATSG46190.1 ARIL;PB;RL;PB receptor like protein 6 receptor like protein 6
Sapur.016G269300.1	939.9953243	0.143363681	0.038606795	3.740196	0.000184196	0.00306542	grey	-0.292429272	0.000202059		ATSG17600.1 NA microRNA-associated protein-related microtiffelin-associated protein-related
Sapur.003G059100.10	1.12555518	-0.95080073	0.254388466	-3.73922	0.000184593	0.00305247	grey	-0.293828091	0.001089691	GO:0000160	ATSG18020.1 APRR2;PRR2 Chell-like two-component response regulator family protein two-component response regulator-like APRR2 protein
Sapur.007G100300.1	15.58606293	-0.37972494	0.101594194	-3.73809	0.000185448	0.00305924	grey	-0.247748386	0.001075833	GO:0005515;GO:0005634;GO:0003700;GO:0046983;GO:0003677	ATSG25140.1 AGL21;SVP K-box region and MADS-box transcription factor family protein NA
Sapur.018G073400.1	2.81513966	-0.89947341	0.240616886	-3.73816	0.000185171	0.00305033	grey	-0.269302328	0.000615335		ATSG47231.1 aminoacyl-tRNA ligases;ATP binding;nucleotide binding NA
Sapur.003G052900.1	1.80988934	-0.55082611	0.147331833	-3.73769	0.000185752	0.00307053	grey	-0.267251161	0.000721519		ATSG28120.1 NA abaptin thioesterase otubain-like protein
Sapur.015G077700.1	1.8614119	-0.91738044	0.245453107	-3.73569	0.000185808	0.00307193	grey	0.303815364	0.000113679	GO:0005515	ATSG26480.1 RNI-like superfamily protein F-box protein SKIP19
Sapur.010G186800.1	107.4315561	-0.38305452	0.102582492	-3.73547	0.000186183	0.00307609	grey	0.315648718	5.65E-05		ATSG26170.1 ACT7 actin 7 actin 1
Sapur.013G185000

Sapur.15WG100700.1	41.86680434	0.30755549	0.083238145	-1.694884	0.00220024	0.00036181	gw	-9.29720853E-20	0.00015687	ATMYB86,MYB86	myb domain protein 86
Sapur.003G121300.B	2.65591936	-0.738603783	0.199693678	-3.69464	0.00022032	0.00036285	gw	-0.008214151	0.91867546		
Sapur.006G196600.1	750.4391149	0.14484934	0.039207786	3.694413	0.00022036	0.00036286	gw	-0.28752499	0.00302658	GO:0005085,GO:0046873,GO:0030001,GO:0016020	magnesium transporter protein
Sapur.005G133800.1	236.8264299	-0.160573381	0.04347269	-3.69375	0.00022097	0.00036315	gw	-0.16731486	0.03633567	GO:0016747,GO:0006355	MYST histone acetyltransferase, putative
Sapur.006G136600.1	8.63827346	0.750326633	0.20310057	3.69324	0.00022145	0.00036424	gw	-0.13475876	0.00930801		NA
Sapur.010G137900.2	0.48937638	1.378338941	0.373259581	3.692709	0.00022178	0.00036479	gw	0.251767612	0.0016856	GO:0005975,GO:0004553	endo-1%2C4-beta-glucanase
Sapur.T034400.1	91.49326601	0.507425581	0.137439371	3.691986	0.00022251	0.00036752	gw	0.29421871	0.000183859		NA
Sapur.15WG014300.1	0.419905011	0.157585545	0.42189391	-3.69391	0.00022577	0.00036589	gw	-0.343812206	9.18E-06		Plant protein of unknown function (DUF247)
Sapur.002G017100.1	33.53914545	0.393627986	0.106619104	-3.6919	0.00022585	0.00036589	gw	-0.27621918	0.000459077	GO:0004468,GO:0004672	calcium-dependent protein kinase 29
Sapur.008G075200.4	1.038513879	-0.296657424	0.080227117	-3.68679	0.00023117	0.00037457	gw	-0.24221693	0.02237312		Protein of unknown function (DUF315)
Sapur.014G124500.1	1103.10389	0.277541861	0.048102175	-3.69093	0.00023434	0.00036718	gw	-0.325105563	3.26E-05	GO:0019843,GO:0006412,GO:0005840,GO:0003735	ribosomal protein L6 family
Sapur.006G126400.1	1549.481396	0.154874076	0.042432564	-3.68677	0.00023557	0.00036744	gw	-0.278757166	0.004073937	GO:0017190,GO:0006633	acyl-ACP thioesterase
Sapur.007G012200.1	25.30052903	0.263891554	0.071246712	3.690008	0.00023247	0.00036841	gw	0.278881133	0.000447308	GO:0033177,GO:0015991,GO:0015078	vacuolar H+-pumping ATPase 16 kDa proteolipid subunit 4
Sapur.005G156700.1	4.867492201	-0.61378681	0.196404228	-3.68665	0.00023347	0.00036801	gw	-0.247329124	0.038235271	GO:0051016,GO:0008290	Subunit 3 of heterotrimeric actin-capping protein Capz superfamily
Sapur.012G074000.1	17839.41033	0.367876567	0.09971498	3.685281	0.00023689	0.00036479	gw	0.28823969	0.000251452	GO:0030976,GO:0000287,GO:0003824	AHAS,ALS,CSR1,IMR1,TIP5 chlorsulfuron/imidazolinone resistant 1
Sapur.006G033700.1	6.069709279	0.777259682	0.164763149	3.68603	0.00023562	0.00036754	gw	0.366858879	0.00372367		NA
Sapur.T130500.1	9.620802143	0.937515665	0.254195561	3.688239	0.00023581	0.00037057	gw	0.31984579	4.46E-05		Exostosin family protein
Sapur.010G051100.2	0.792629916	0.750827968	0.204496472	3.688066	0.00023938	0.00037148	gw	0.024747985	0.758340658	GO:0005515	Galectose-oxidase/kelch repeat superfamily protein
Sapur.005G031800.2	0.793935563	0.185812176	0.05029825	3.6875	0.00024075	0.00037251	gw	-0.254123927	0.053193702	GO:0045905,GO:0006412	Signal recognition particle 9 kDa protein
Sapur.013G069900.1	6.12821848	-0.674115068	0.18209113	-3.68548	0.00023873	0.00037497	gw	-0.3964342	0.000163433		Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase
Sapur.006G188300.1	600.6197344	0.252188736	0.068294686	3.68469	0.00024009	0.00038182	gw	0.243151569	0.002205258		NA
Sapur.002G030900.1	0.010568181	1.325201384	0.35963388	3.684882	0.00022836	0.00375779	gw	0.242384735	0.00221415	GO:0016021,GO:0016020,GO:0022857	WAT1 Walls Are Thin 1
Sapur.T005800.1	0.805022203	0.185291917	0.275623112	3.68425	0.00023975	0.00037606	gw	-0.28121976	0.00206		NA
Sapur.013G098400.1	0.896568756	1.360035567	0.342015515	3.68413	0.00023985	0.00037678	gw	0.250843953	0.00153602		hypothetical protein
Sapur.006G196200.1	0.404227906	-0.611378687	0.175234765	-3.68334	0.00024107	0.00037767	gw	-0.42518341	2.77E-08		NA
Sapur.017G016700.1	3.968799636	0.500195043	0.135181051	3.683041	0.00023048	0.00378345	gw	-0.230048889	0.00375969		Protein of unknown function (DUF1336)
Sapur.004G099700.1	0.670818324	-0.412372533	0.180588023	-3.68208	0.00023138	0.00379754	gw	-0.32784412	2.77E-05		Protein of unknown function (DUF295)
Sapur.003G049100.1	0.484661121	-0.128957827	0.36614385	-3.68201	0.00023402	0.00380784	gw	-0.251914143	0.054562248	GO:0009882,GO:0009451,GO:0003723,GO:0005122	Pseudouridine synthase family protein
Sapur.006G093000.1	66.23631721	-0.290444189	0.078908884	-3.68076	0.00023543	0.00381694	gw	-0.297600386	0.00015351		
Sapur.011G075200.1	1000.115469	0.185141795	0.050296055	3.6805	0.00022774	0.00382054	gw	-0.296494335	0.000162609		pathogenesis-related family protein
Sapur.016G239500.1	5.310645099	0.654497715	0.177862123	3.67974	0.00023472	0.00383161	gw	-0.27080976	0.006341387	GO:0016020,GO:0006970	glutamate-gated kainate-type ion channel receptor subunit glurS protein
Sapur.004G242300.1	22.34433505	0.256501084	0.069726524	3.679448	0.00023178	0.00383582	gw	-0.10032937	0.113183869	GO:0009506,GO:0005524,GO:0009396,GO:0004326	thylakoidal/plastidic protein 9
Sapur.002G239000.1	0.36615616	1.729282341	0.470110257	3.678461	0.00023645	0.00385503	gw	0.370693854	1.76E-06		NA
Sapur.006G121900.1	1.654177764	0.945093938	0.25587268	3.67691	0.00023806	0.00387364	gw	0.315328851	5.76E-05		bidirectional sugar transporter
Sapur.017G025400.1	2.077224473	0.677942594	0.184388806	3.676861	0.00023612	0.00387414	gw	0.318912799	4.68E-05	GO:0004468,GO:0005524,GO:0004672	receptor serine/threonine kinase, putative
Sapur.003G061300.2	1.304443375	-0.354664269	0.096575166	-3.67605	0.00023686	0.00388663	gw	-0.23611763	0.000183763		SNARE associated Golgi protein family
Sapur.012G289600.1	2.00421804	0.817895657	0.22500968	3.67592	0.00023694	0.00388807	gw	0.301609645	0.000123665		UDP-Glycosyltransferase superfamily protein
Sapur.T029700.2	0.997919881	0.876118785	0.365182386	3.67539	0.00023487	0.00389596	gw	0.303452952	0.000111833		SNF2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing pr
Sapur.009G030600.1	0.6642264	-1.015352673	0.29693543	-3.67452	0.00023831	0.00390912	gw	-0.242646935	0.002198184		Thioesterase superfamily protein
Sapur.017G058800.1	0.770887679	0.996827071	0.271272243	-3.67407	0.00023871	0.00391562	gw	-0.32765389	2.85E-05		Major facilitator superfamily protein
Sapur.T013020700.1	4.482997247	0.111183662	0.032306522	3.67396	0.00023878	0.00391954	gw	0.268845056	0.000677717	GO:0006355,GO:0003677	NAC domain transcription factor
Sapur.019G027500.1	291.2066887	0.190404673	0.051844377	-3.6737	0.00023967	0.00392091	gw	-0.30007629	0.000134364		cell division cycle-like protein, putative
Sapur.T015500.1	1.825646937	0.268453111	0.073015707	-3.67269	0.00024008	0.00393512	gw	-0.347543313	8.91E-06		RNA pseudouridine synthase
Sapur.003G139900.1	1.867159795	-0.84478296	0.257305488	-3.67183	0.00024036	0.00394921	gw	-0.25476429	0.002819986		
Sapur.006G192300.1	1.69615445	0.961488444	0.261886522	3.671674	0.00024067	0.00395129	gw	0.293045621	0.000207366	GO:0031683,GO:0019001,GO:0007186,GO:0004871,GO:0003924	guanine nucleotide-binding protein alpha-2 subunit
Sapur.009G139500.1	1442.685246	-0.122601172	0.033391686	-3.67161	0.00024029	0.00395211	gw	-0.283005185	0.000363917	GO:0003676	Splicing factor, CCL-like
Sapur.T006000.1	0.363671203	-0.307554459	0.083842009	-3.67115	0.00024307	0.00396451	gw	-0.388941499	8.57E-07		Protein 1A
Sapur.010G121000.1	1758.70326	0.207644693	0.056564585	3.670931	0.00024569	0.00396622	gw	0.243583641	0.00232274		SPIRAL1-like1
Sapur.004G096200.1	22.21737931	0.262783849	0.071587159	3.670846	0.00024746	0.00396332	gw	0.270654179	0.000613055		NA
Sapur.016G094500.1	1121.18284	-0.135883276	0.037020739	-3.67055	0.00024202	0.00396774	gw	-0.312168041	6.86E-05	GO:0043758,GO:0042132,GO:0005975	high-cyclic electron flow 1
Sapur.012G040600.1	4.46873169	0.499026039	0.136119395	3.670459	0.00024215	0.00396894	gw	0.285100471	0.000235561		
Sapur.T013020300.1	22.14603386	-0.658165519	0.124142081	-3.66872	0.00024273	0.00397769	gw	-0.01578631	0.885632881		plectotrin homology (PH) domain-containing protein
Sapur.015G099800.1	1.504821191	-0.367038677	0.291001724	-3.66867	0.00024273	0.00397789	gw	-0.24936737	0.00163334		Ankyrin repeat family protein
Sapur.016G183900.1	41.48625204	-0.200684184	0.0850329	-3.66862	0.00024275	0.00397853	gw	-0.27842217	0.000383843	GO:0005515	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.010G162500.3	9.303663228	0.485443565	0.132303949	3.669182	0.00243128	0.00398802	gw	-0.23661503	0.000573397		ubiquitin-conjugating enzyme E2
Sapur.003G082200.3	4.932451183	0.095008376	0.136206181	3.668653	0.00243423	0.00399593	gw	0.030345235	0.672602972	GO:0030150,GO:0005744	Translocase of outer membrane subunit tim16
Sapur.15WG1134001.1	1650.145788	0.139441314	0.03802913	3.666697	0.00245703	0.00402575	gw	0.2457524	0.001921997	GO:0019773,GO:0006511,GO:0004175,GO:0051603,GO:0005839,GO:0004298	proteasome subunit alpha type-2 protein
Sapur.T186900.1	9.460663444	-1.320575852	0.360178474	-3.66645	0.00245944	0.00402953	gw	-0.285413754	0.002298357		NA
Sapur.009G192300.1	11.96243365	-0.365168882	0.099329659	-3.66619	0.00246119	0.00403194	gw	-0.246413493	0.003846468	AMKIP0X0 MAPK/KRK kinase 1	
Sapur.006G186200.1	1.892391691	0.671506108	0.18317418	3.665943	0.00246429	0.00403704	gw	0.29372886	0.000153801		Putative lysine decarboxylase family protein
Sapur.15WG121900.2	0.538716122	0.305564249	0.086410088	-3.66419	0.00246957	0.00404551	gw	-0.32239242	2.11E-05		Protein of unknown function (DUF1295)
Sapur.016G190100.1	2.018878899	-0.776434086	0.211330702	-3.66508	0.00242764	0.00405031	gw	-0.272781612	0.005467766	GO:0008289	Polyketide cyclase/dehydrase and lipid transport superfamily protein
Sapur.009G126700.1	154.9033334	-0.142221541	0.038885495	-3.66507	0.00242775	0.00405031	gw	-0.33275325	7.46E-05		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.010G187400.1	22.08619421	0.331781554	0.090515779	3.665051	0.00243729	0.00405034	gw	0.235492813	0.002987621		
Sapur.010G184300.1	91.59512063	0.180238435	0.049237181	3.664797	0.00243744	0.00406081	gw	0.28562756	0.000287685		
Sapur.019G081500.1	0.787942252	1.144653924	0.313200068	3.664362	0.00244955	0.00406085	gw	0.322463843	3.81E-05	GO:0005515	ubiquitin-conjugating enzyme 30
Sapur.015G088800.1	1.202638869	-0.615537037	0.173435518	-3.66442	0.00244798	0.00406134	gw	-0.28698968	0.003082223		NA
Sapur.017G039300.1	1.279540849	-1.126188209	0.307368004	-3.66397	0.00244833	0.00406642	gw	-0.268947371	0.002688811	GO:0006468,GO:0005524,GO:0004672	BIR1 BAK1-interacting receptor-like kinase 1
Sapur.003G203300.1	4.46873169	0.499026039	0.136119395	3.670459	0.00242115	0.00396894	gw	0.285100471	0.000235561	GO:0005515	ALG ubiquitin-like 6
Sapur.007G080400.4	0.249417288	-0.607934362	0.192928284	-3.66037	0.00248562	0.00408077	gw	0.604913175	6.01291537E-08	GO:0005886,GO:0005215	Major facilitator superfamily protein
Sapur.006G230600.1	16.1420191	0.418570082	0.114270477	3.662977	0.00249301	0.00408168	gw	0.242741178	0.00218997	GO:0006468,GO:0004672	Protein kinase superfamily protein
Sapur.010G152100.1	70.62563895	-0.200684184	0.05708184	-3.66182	0.00250426	0.00409088	gw	-0.298341881	0.00014756		ATSPIRIL4,TUFEL,SPIRIL LIF1 synthesis of pseudo-U
Sapur.010G075300.1	1.30693009	-0.110615609	0.303303752	-3.66179	0.00250456	0.00410037	gw	-0.236615203	0.002846029		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.006G197500.1	196.4023766	-0.212852766	0.05831366	-3.66162	0.00250601	0.00410126	gw	-0.268412428	0.000676318		cassin kinase-like protein, putative
Sapur.002G139400.2	9.885629952	-0.475785785	0.129943162	-3.661492	0.00250751	0.00410146	gw	-0.23307804	0.002275009	GO:0005515,GO:0007165,GO:0000155	ethylene response
Sapur.007G042000.1	207.6043104	-0.163831257	0.044756149	-3.66093	0.00252283	0.00412947	gw	-0.283196274	0.000350347		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.004G153800.2	12.88833537	0.387969735	0.10601767	3.659482	0.00252726	0.00413651	gw	-0.28490735	0.002097987		calcium dependent protein kinase 1
Sapur.016G194200.1	22.27662661	-0.302061781	0.088045944	-3.65803	0.00253176	0.00414388	gw	-0.287506434	0.000261168	GO:0005886,GO:0005975,GO:1901137,GO:0004360	Plant protein of unknown function (DUF827)
Sapur.006G184100.1	0.528482904	-0.672606582	0.204436459	-3.6565	0.00253926	0.00416157	gw	-0.28503316	0.002965589		Disease resistance-response gibberellin-like protein family protein
Sapur.012G032300.2	1.539573693	0.926614541	0.252388432	-3.65834	0.00253857	0.00416542	gw	-0.28048706	0.000375525		exostosin family protein
Sapur.015G207700.1	0.380653777	1.407356266	0.384763269	3.657185	0.00254281	0.00418094	gw	0.327134926	7.86E-05	GO:0006468,GO:0005524,GO:0004672	cdc2cAt CDC2C Thioredoxin activity protein
Sapur.T181100.1	0.4296429	-1.417661249	0.387600566	-3.61754	0.00255651	0.00416679	gw	-0.395814595	2.88E-07		Heavy metal transport/detoxification superfamily protein
Sapur.003G095600.1	348.2941836	0.248822893	0.06809115	3.657249	0.00254936	0.00417125	gw	0.228416629	0.004011771		Pectin lyase-like superfamily protein
Sapur.010G019300.1	1.931379236	-0.778818861	0.212997651	-3.65703	0.00255155	0.00417462	gw	-0.31628168	5.42E-05	GO:0043531	NB-ARC domain-containing disease resistance protein
Sapur.T013028800.1	174.6210153	0.187856788	0.052736349	3.656977	0.00255287	0.00417588	gw	-0.277389652	2.59E-10	GO:0055234,GO:0003676,GO:0006486	DEAD/H box RNA helicase family protein
Sapur.013G061600.1	0.463638827	1.650407068	0.451407589	3.656179	0.00256002	0.00418786	gw	0.273571525	0.000226655	GO:0055114,GO:0016614,GO:0050660	Glucose-methanol-choline (GMC) oxidoreductase family protein
Sapur.013G060500.1	8.766418372	0.373164605	0.185754211	3.656157	0.00256024	0.00418882	gw	0.352510055	0.014204115	GO:0006429,GO:0006508,GO:0004190	aspartic protease
Sapur.T062300.1	0.556640924	1.087613673	0.297527946	3.655587	0.00256574	0.00419984	gw	0.310088885	7.75E-05		
Sapur.019G053000.3	0.548115379	1.383188766	0.374308781	3.654733	0.00257445	0.00421091	gw	0.265142337	0.000796789	GO:0006096,GO:0005975,GO:1901137,GO:0004360	glutamine-fructose-6-phosphate transaminase (isomerizing),sugar binding,transaminases
Sapur.018G026300.1	189.6026346	0.072606582	0.019436459	-3.65455	0.00257636	0.00421375	gw	-0.31003518	7.78E-05		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.019G062000.2	10.14625606	0.472614213	0.129341375	3.654006	0.00258518	0.00422244	gw	0.23157229	0.007237177		exostosin family protein
Sapur.T032700.1	268.1877544	0.232761393	0.063719286	3.653925	0.00259593	0.00424514	gw	0.243457002	0.002032049		Thioredoxin superfamily protein
Sapur.017G121600.1	28.60686116	0.902379413	0.247072081	-3.65229	0.00259591	0.00425013	gw	-0.247138653	0.001805787	GO:0046872,GO:0030001	Heavy metal transport/detoxification superfamily protein
Sapur.016G137500.2	0.688006684	-0.181178791	0.123416565	-3.65166	0.00260248	0.00426543	gw	-0.2072946	0.009192007	GO:0004601,GO:0005515	Protein kinase superfamily with tetratricopeptide repeat domain
Sapur.004G045700.1	26.18694568	-0.768414566	0.206944122	-3.6518	0.00260411	0.00425787	gw	-0.272054668	0.001587165	GO:0005515	Leucine-rich receptor-like protein kinase family protein
Sapur.T013021200.1	37.53413234	0.364808424	0.098404628	3.651177	0.00260436	0.00425887	gw	-0.297886166	0.000315264		homolog of yeast suppressor of sup35
Sapur.014G132300.1	7.996608461	-0.460821542	0.126202249	-3.65147	0.00260745	0.00426292	gw	0.08819855	0.272061299	GO:0008080	AcpL Coa N-acyltransferases (NAT) superfamily protein
Sapur.016G195300.2	15.02918983	0.319352429	0.087508363	-3.65125	0.00260868	0.00426626	gw	-0.256436677	0.001875563		Homeodomain-like superfamily protein
Sapur.008G043000.2	11.33602502	0.345192191	0.094566487	3.650259	0.00261976	0.00428262	gw	0.28098136	0.000364355		DNA/RNA-binding protein Kin17, conserved region
Sapur.006G194600.1	0.664520938	1.062080687	0.290977329	3.650046	0.00262193	0.00428596	gw	0.323058022	4.14E-05		
Sapur.018G056300.1	0.574183432	1.643836015	0.449898433	3.649483	0.00262769	0.00429516	gw	0.268813972	0.007206598	GO:0007165,GO:0005515,GO:0043531	Disease resistance protein (TIR-NBS-LRR class) family
Sapur.013G105600.1	0.381919295	1.734562981	0.475035109	3.649398	0.00262855	0.00429636	gw	0.31800179	4.66E-06	GO:0006468,GO:0005524,GO:0004672	cyclin-dependent kinase C-1
Sapur.T029100.1	1.815769165	0.553731818	0.151777658	3.64829	0.00263991	0.00431471	gw	0.273157723	0.003802564	GO:0016887,GO:0005524,GO:0016020	ABC-2 type transporter family protein
Sapur.016G169900.1	127.5650617	0.195966685	0.053719493	3.64759	0.00264712	0.00432627	gw	0.253155615	0.001354664		hypothetical protein
Sapur.007G122200.1	260.1682213	0.542511049	0.149110028	3.646742	0.00265265	0.00434013	gw	0.245862842	0.003933891		Dnaj heat shock family protein
Sapur.016G183800.1	4.053887869	-0.520792886	0.142814156	-3.64672	0.00265613	0.00434035	gw	-0.27206487	0.001546416		
Sapur.003G161300.1	189.2475133	0.146888829	0.040389654	3.646346	0.00265996	0.00434597	gw	0.273604095	0.000535795		TBL23 TBOXHOME B/IRER/INGER/CLE-LE 23
Sapur.004G042700.3	0.949423837	-0.926483879	0.254171362	-3.64494	0.00267459	0.00436966	gw	-0.278603837	0.000410572	GO:0003887	AAA-type ATPase family protein
Sapur.016G195400.1	2.086089826	-0.602330124	0.18175031	-3.64414	0.00268289	0.00438258	gw	-0.272921798	0.000545524		acclimation of photosynthesis to environment
Sapur.003G001705.1	260.4799023	-0.418613176	0.114768899	-3.64392	0.00268515	0.00438611	gw	-0.283935131	0.000312913	GO:0008234,GO:0006508	aylem cysteine proteinase 2
Sapur.001G058400.1	0.507573822	-0.433807863	0.393488945	-3.64385	0.00268589	0.00438703	gw	-0.33212503	2.14E-05		Plant protein of unknown function (DUF247)
Sapur.006G200700.1	68.00870087	-0.477437461	0.075564386	-3.64285	0.00269691	0.00440171	gw	-0.274672408	0.004988072	GO:0005622,GO:0003776,GO:0030042,GO:0015629	actin depolymerizing factor 4
Sapur.009G126400.1	133.4347688	0.160010364	0.043936596	3.641847	0.00270589	0.00442025	gw	0.257191939	0.001115753		ovate transcriptional repressor
Sapur.T034000.1	0.276866177	0.125367146	0.034438962	-3.64113	0.00271235	0.00442989	gw	0.319186262	7.51E-05		hypothetical protein
Sapur.003G142900.1	308.598822	0.163493079	0.044899661	-3.64127	0.00271292	0.00442965	gw	-0.28463404	0.000302607		hypothetical protein
Sapur.006G135700.1	0.373561633	0.940327312	0.258174331	3.640381	0.00272725	0.00444627	gw	-0.31128336	3.78E-06		RmlC-like cupins superfamily protein
Sapur.002G032200.2	4.113031988	0.49621082	0.136183836	3.639554	0.00273111	0.00445869	gw	0.277368992	0.000431885		synteksin-52 protein
Sapur.002G050900.1	2.645464243	0.598371362	0.16443156	3.639367	0.00273667	0.00446706	gw	-0.253133239	0.010498663		Translation elongation factor GTP-binding
Sapur.014G063300.1	19.2511825	0.385214168	0.10580317	3.638422	0.00274303	0.00447772	gw	-0.290807038	0.000218854	GO:0005515	2 calcium/lipid-binding plant phosphoribosyltransferase family protein
Sapur.017G075100.1	5.896279012	-0.474076304	0.130164051	-3.63788	0.00274892	0.00448711	gw	-0.257720797	0.001139421		glutathione peroxidase
Sapur.001G081800.1	2.497843244	-0.941161619	0.258777738	-3.63575	0.00275988	0.00450269	gw	-0.20718088	0.009404561	GO:0055114,GO:0070180,GO:0070275	guanylate-binding family protein
Sapur.005G141100.1	4.292399224	0.551513693	0.151627487	3.637284	0.00277518	0.00496988	gw	-0.37629206	1.18E-06	GO:0005515	cytochrome P450, family 74, subfamily A, polypeptide 1
Sapur.013G051000.1	0.819331316	0.283583794	0.4569908	-3.63581	0.00277113	0.00456227	gw	0.329517108	2.51E-05	GO:0003677	Glutathione S-transferase family protein
Sapur.008G061100.1	0.350707048	1.954838629	0.537820169	3.63493	0.00278056	0.00457786	gw	0.343225205	1.24E-05	GO:0006355,GO:0003700,GO:0007275	AP2/B3-like transcriptional factor family protein
Sapur.T008300.1	0.508833648	1.362507161	0.347402166	3.63399	0.00279073	0.00459423	gw	-0.317272798	5.68E-05		Integrase-type DNA-binding superfamily protein
Sapur.016G093200.1	3.334013368	0.562888948	0.154343779	3.6339	0.00279169	0.00459558	gw	0.273881919	0.000546729		NA
Sapur.015G287700.1	1515.123008	0.190174861	0.052353461	-3.63297	0.00279727	0.00460749	gw	0.242270508	0.003008664	GO:0005085,GO:0016020,GO:0008811,GO:0005216	cyclic nucleotide-gated ion channel protein, putative
Sapur.016G275200.3	0.630940059	2.058851275	0.332716118	-3.6333	0.00279816	0.00456546	gw	-0.24897265	0.016659782		SET domain-containing protein
Sapur.015G220400.1	0.411149778	1.2106588	0.33322728	3.633312	0.00280005	0.00456825	gw	0.268402287	0.000746807	GO:0004568,GO:0006047	S-locus lectin protein kinase family protein
Sapur.006G037500.1	117.1128468	-0.218311443	0.060045112	-3.63297	0.00280244	0.00457697	gw	-0.262826164	0.000870967	GO:0005524,GO:0016887,GO:0016021,GO:0008810,GO:0005215	ABC transport family protein
Sapur.006G073200.2	7.862776204	-0.430201502	0.118426398	-3.6266	0.00280517	0.00467621	gw	-0.283887351	0.000314454		alpha-L-fucosidase
Sapur.015G082600.1	1.073855341	-0.216025201	0.167629195	-3.63241	0.00280879	0.00458064	gw	-0.29064809	0.002218889		NA
Sapur.012G059400.1	80.25857787	0.174189482	0.047975494	-3.6308	0.00282543	0.00460881	gw	-0.301892246	0.000121752		PPR protein, putative
Sapur.001G121000.1	1.597794466	0.551513693	0.151627487	3.63264	0.00281337	0.00459621	gw	-0.292345058	0.000172661		NA
Sapur.009G061800.1	53.76813078	-0.228043883	0.062916812	-3.63025	0.00283142	0.00461813	gw	-0.307195572	9.09E-05		Protein of unknown function, DUF593
Sapur.T013023900.1	12.92700281	0.904531898	0.249159707	3.629841	0.00283298	0.00462122	gw	-0.311371033	7.01E-06	GO:0043531	NB-ARC domain-containing disease resistance protein
Sapur.015G030800.1	5.726368099	-0.401300939	0.110509479	-3.62848	0.00285093	0.00464926	gw	-0.30733202	9.03E-05		Emsy N Terminus (ENT)/ plant Tudor-like domains-containing protein
Sapur.T014000.1	4.735737542	0.905984725	0.250000723	3.626978	0.00286132	0.00466526	gw	-0.319763624	1.80E-05		
Sapur.018G052700.1	870.6538263	-0.121574479	0.033514551	-3.62751	0.00286175	0.00466641	gw	0.364730464	2.65E-06		gdsl nucleotide sugar transporter 4
Sapur.008G061300.1	1102.901689	0.104670725	0.028834896	3.627486	0.00286194	0.00466646	gw	0.232825909	0.003941669		
Sapur.011G088200.1	8.025642118	1.064651194	0.293468357	3.627019	0.00286753	0.00467452	gw	0.297978935	0.000152606		
Sapur.15WG1149400.2	1.082661132	0.189172143	0.298236212	0.626319	0.00028740	0.00468674	gw	0.015548707	0.846740031		
Sapur.013G075500.1	28.15496923	0.362732572	0.100004881	3.626487	0.00287768	0.00469106	gw	0.268929465	0.00026005		
Sapur.009G017000.15	2.070525052	0.691070765	0.190558571	3.625843	0.00288802	0.00469468	gw	0.274294131	0.000508288	GO:0015336,GO:0003824,GO:0055139,GO:0019008,GO:0006777	molybdenum cofactor biosynthesis protein A
Sapur.019G044000.1	1.860895215	0.337104779	0.093000769	3.625125	0.00289365	0.00470623	gw	0.289394606	0.000172015	GO:0005515	Disease resistance protein (TIR-NBS-LRR class) family
Sapur.013G049200.1	0.27488878	1.475135525	0.407008845	3.62387	0.00290228	0.00471802	gw	0.37475001	1.33E-06		
Sapur.008G084200.1	218.6142459	0.105166602	0.029248131	-3.6215	0.00290819	0.00473683	gw	-0.28167838	0.002023386		cytochrome P450, family 71, subfamily A, polypeptide 1
Sapur.001G026600.1	6.247614653	0.825267513	0.227794951	3.623171	0.00290104	0.00474254	gw	0.247181009	0.001802238	GO:0016021,GO:0016020,GO:0022857	wound-induced protein W112
Sapur.003G167600.2	40.84952283	0.473583794	0.131000377	3.61659	0.00291395	0.00476327	gw	-0.047839134	0.167188665		nodulin MtN21 /EamA-like transporter family protein
Sapur.016G244400.1	180.6192223	-0.125360493	0.034617389	-3.62131	0.00291111	0.00477624	gw	-0.290690727	0.000223671		transmembrane protein, putative
Sapur.004G208900.1	118.139728	0.199713621	0.055150092	3.621274	0.00292155	0.00479574	gw	0.249916665	0.001991513		Uncharacterized conserved protein UCP022280
Sapur.005G130500.1	48.7567774	-0.219292886	0.060504732	-3.62077	0.00292727	0.00480592	gw	-0.275490888	0.000582949	GO:0008270	transmembrane protein, putative
Sapur.007G089400.3	2.050350885	-0.695933429	0.192082256	-3.62031	0.00292974	0.00479751	gw	0.010608745	0.989436208	GO:0055114,GO:0016491	RING-type E3/U box family protein
Sapur.013G046500.1	0.420113442

Sapur.05G0153400.6	14.4447178	-8.32288624	0.080747864	-3.5591	0.000373129	0.00002733	grey	0.153548448	0.054859942	GO:0030244;GO:0016760;GO:0016810	cellulose synthase A, catalytic subunit
Sapur.05G0216800.1	14.3705861	-0.39252884	0.110321618	-3.15808	0.000373579	0.00005053	grey	-0.26326846	0.100749734		NA
Sapur.05G0232600.1	43.47515803	-0.25119192	0.070608384	-3.55793	0.000373786	0.00005357	grey	-0.25729655	0.091414689	GO:0005515	NB-ARC domain-containing disease resistance protein
Sapur.05G0152000.1	159.0845108	-0.36348892	0.102163969	-3.55721	0.000374812	0.00006988	grey	-0.27228879	0.095604078	GO:0007165	CBL-interacting Serine/Threonine-kinase
Sapur.05G0253300.1	172.9524627	0.16331552	0.045913388	3.55703	0.000375027	0.00007377	grey	0.26219311	0.093723719	GO:0006488;GO:0006672	Protein kinase superfamily protein
Sapur.05G0128100.1	6.15635384	0.76086939	0.219397428	3.56504	0.000375823	0.00008568	grey	0.275735444	0.100473428	GO:0005975;GO:0004553	Glycosyl hydrolase superfamily protein
Sapur.05G0295200.1	1.61164608	0.88347538	0.248424078	3.55638	0.000376103	0.00008899	grey	0.242755299	0.102188635		NA
Sapur.01TG119005.1	4.49851005	0.52962881	0.148924828	3.55292	0.000378126	0.00008997	grey	0.267604019	0.09573173		ARM repeat superfamily protein
Sapur.15WG0105000.1	21.67698222	-0.35267275	0.099176061	-3.55615	0.000378336	0.00009088	grey	-0.28892588	0.00024943		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.05G0255900.11	1.14741367	-0.93118782	0.261988852	-3.55395	0.000378519	0.00009724	grey	-0.27605649	0.09466593	GO:0051861;GO:0046836;GO:0017089;GO:0005737	Glycosyl transfer protein (GLTP) family protein
Sapur.09G0611100.1	0.48675214	-1.52531755	0.428995263	-3.55554	0.000379197	0.00010642	grey	-0.34394627	1.038E-05	GO:0016787	Calcineurin-like metallo-phosphoesterase superfamily protein
Sapur.01TG0100.1	1949.163627	0.01377164	0.045606484	3.55437	0.000378881	0.00011338	grey	-0.2817547	0.09066887	GO:0008234;GO:0008508	vacuolar processing enzyme 1
Sapur.7G0680.1	0.35282788	1.99060746	0.560102427	3.554167	0.000379179	0.00011379	grey	0.410243834	9.50E-08		NA
Sapur.01TG0297700.1	1.45443877	0.55662425	0.156625521	3.55058	0.000379363	0.00011764	grey	0.262608508	0.09792587		NA
Sapur.01TG0041000.1	0.47802344	1.55642522	0.438045881	3.55311	0.000380705	0.00012631	grey	0.266630684	0.09773831		DNA-ligase-like superfamily protein
Sapur.01TG0413400.2	2.51453294	0.68355719	0.186057263	3.52707	0.000381288	0.00013116	grey	0.280388864	0.098391389	GO:0016020;GO:0005234;GO:0004970	glutamate receptor 1
Sapur.07G0695300.1	2.03511226	0.78094867	0.21984025	3.55246	0.000381813	0.00011703	grey	0.261846736	0.09393786		NA
Sapur.09G0230500.1	228.5196919	0.48763822	0.137346119	3.55047	0.000384432	0.00022111	grey	0.33301589	7.77E-05		F-box family protein
Sapur.05G0251200.1	305.1458464	0.30231229	0.085198064	3.55028	0.000384611	0.00022133	grey	0.284439119	0.092603213	GO:0055544;GO:0005509	annexin 3
Sapur.03G0121900.1	0.94259136	-0.06234234	0.29923209	-3.55023	0.000384898	0.00022773	grey	-0.33857468	1.44E-05	GO:0046983	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.01G0250700.2	15.16696602	-0.72747532	0.205128969	-3.54965	0.000385034	0.00017224	grey	-0.26352376	0.09194953		DHHC type zinc finger family protein
Sapur.01BG118300.1	420.2529018	-0.13822187	0.038949759	-3.54873	0.000387093	0.00026173	grey	-0.27372815	0.09348698	GO:0005515	evolutionarily conserved C-terminal region 10
Sapur.05G0298145.1	197.5166646	0.05570205	0.020669595	-3.54854	0.000387278	0.00026602	grey	-0.2946056	0.09409231		ubiquitin-conjugating enzyme E2
Sapur.01G0868400.1	1.86763162	0.82936273	0.233770399	-3.54851	0.000387419	0.00026639	grey	-0.22381028	0.09835982		NA
Sapur.01TG0279000.1	1443.606031	0.13911277	0.039205162	-3.54846	0.000387441	0.00026721	grey	-0.28883843	0.09243758	GO:0003723	RNA-binding KH domain-containing protein
Sapur.05G0251100.1	31.76577877	0.38200845	0.107668013	-3.54826	0.000387778	0.00026716	grey	-0.26363527	0.09085129	GO:0055114;GO:0016491;GO:0008152	aldehyde dehydrogenase 3I1
Sapur.7G0620.1	0.35164024	1.21336459	0.341960167	3.548247	0.000387805	0.00026717	grey	0.30983494	7.87E-05		NA
Sapur.09G0881200.1	15.13680092	-0.36348223	0.1061467	-3.54772	0.000388588	0.00028496	grey	-0.26346597	0.09049317	GO:0006468;GO:0005234;GO:0004672	Protein kinase superfamily protein
Sapur.03G0147100.3	4.97613812	0.47368785	0.13352313	3.547608	0.000388746	0.00028863	grey	-0.04624771	0.52031255	GO:0005515	Ubiquitin-conjugating enzyme family protein
Sapur.01J0202700.1	101.6326491	0.21279952	0.07068857	3.54573	0.000389	0.00030385	grey	-0.26398078	0.09093702	GO:0016758;GO:0008152	dcn-glycosylase/lyase
Sapur.03G0127900.1	133.2974655	0.37471605	0.105731733	-3.54388	0.000394129	0.00063721	grey	-0.25601567	0.09219011	GO:0016887;GO:0005524;GO:0016020	ABC-2 type transporter family protein
Sapur.04G0260700.1	1.08101587	0.84183319	0.192388794	3.54066	0.000395	0.00017224	grey	-0.26352476	0.09194953		NA
Sapur.04G0237400.1	8.25005823	0.69264958	0.195455132	3.54375	0.000394442	0.00037655	grey	0.25089846	0.091058864	GO:0003674;GO:0003824	PDC2
Sapur.05G0251600.1	25.84734663	0.67496842	0.19026128	3.54646	0.000394667	0.00036796	grey	-0.26497826	0.09297197	GO:0007165;GO:0005515;GO:0004231	disease resistance protein (TIR-NBS-LRR class), putative
Sapur.7I5J200.1	0.37014138	1.34333207	0.379161686	3.542898	0.000395756	0.00039686	grey	0.36898779	1.41E-06		NA
Sapur.09G0620500.2	11.60602331	-0.64043175	0.181008	-3.54257	0.000396249	0.00039849	grey	-0.27983666	0.09380071	GO:0006813;GO:0055085;GO:0016021;GO:0015299;GO:0006812	4 calthiohine-regulated potassium-efflux system protein KefB
Sapur.15WG0101200.1	0.38074614	1.55926216	0.44017659	3.542348	0.000396582	0.00040927	grey	0.328196023	2.71E-05		NA
Sapur.05G0291200.1	139.2668829	0.21717304	0.061322399	3.541466	0.000397865	0.00042968	grey	0.26899548	0.09967362	GO:0005515;GO:0006468;GO:0005524;GO:0004672	Leucine-rich repeat receptor-like protein kinase family protein
Sapur.09G0179000.3	0.64453884	0.74788229	0.2128262	3.5409	0.000398764	0.00044439	grey	0.312851961	0.05604172	GO:0005515;GO:0006468;GO:0004672	Leucine-rich repeat protein kinase family protein
Sapur.03G0159300.1	135.8105964	-0.40883782	0.115496895	-3.54053	0.000399924	0.00046201	grey	-0.27491605	0.09510861	GO:0006355;GO:0003700	Integrase-type DNA-binding superfamily protein
Sapur.01G0211800.1	227.3852374	0.36270277	0.079857395	3.54007	0.000400015	0.00046314	grey	-0.26114969	0.09094768	GO:0005506;GO:0003700	cytokinin response factor 4
Sapur.15WG0103000.7	0.37517873	-1.47643515	0.417171434	-3.53918	0.000401377	0.00046485	grey	-0.24138004	1.08E-05		IQ calmodulin-binding motif protein, putative
Sapur.07G0288600.1	1.11372364	0.97109884	0.275000496	3.532357	0.000401411	0.00060188	grey	-0.24692873	0.09165275		transmembrane protein, putative
Sapur.05G0641800.2	1.45417735	-0.76600378	0.21670424	-3.53754	0.000403387	0.00052417	grey	-0.24308531	0.09215722		PPR containing plant protein
Sapur.01G0154500.1	141.8654319	0.16761884	0.0508164	3.53725	0.000404997	0.00052429	grey	0.228809155	0.09466589		thioredoxin domain-containing protein (TRX) domain protein
Sapur.09G0190600.1	664.571522	0.09557402	0.028149525	3.537125	0.000404201	0.00052889	grey	0.261587543	0.09093273		Zinc finger C-x8-C-x5-C-x3-H type family protein
Sapur.01G0188000.1	2.50050962	0.77028117	0.217769151	3.527377	0.000404428	0.00053223	grey	0.262192562	0.09091934	GO:0005515	phosphosulfokinase receptor 1
Sapur.01G0281900.1	194.3754157	0.26701691	0.075562264	3.536806	0.000406997	0.00056411	grey	0.255824923	0.092232942		NA
Sapur.01G0041300.1	152.6172743	0.37202783	0.105346326	3.530576	0.000405135	0.00056469	grey	-0.045434533	0.572049481	GO:0005515	stomatal cytokinesis defective / SCD1 protein (SCD1)
Sapur.02G0294600.1	2.52025589	0.68407904	0.2348022392	3.530519	0.000406884	0.00057094	grey	0.277458511	0.09434655	GO:0032542	sulfiredoxin
Sapur.07G0122100.1	91.1696794	-0.41439191	0.116974045	-3.53489	0.000409795	0.00060782	grey	-0.23819187	0.09267876		DNA heat shock family protein
Sapur.01G0597100.1	58.64667969	0.38182333	0.109284858	-3.53449	0.000408563	0.00060574	grey	-0.28624003	0.09439018	GO:0016491	12-oxophytodienoate reductase 1
Sapur.01G0125500.1	118.0648858	0.35659121	0.100947311	3.532468	0.000411	0.00064742	grey	0.254385017	0.091304345	GO:0008152;GO:0003824	5'-adenylylsulfate reductase, putative
Sapur.03G0288500.1	14.78093777	0.56209453	0.161152042	3.52449	0.000411729	0.00064754	grey	0.225237234	0.094386673		NA
Sapur.01G0152000.1	318.0759043	-0.24360248	0.069914971	-3.53192	0.000412547	0.00066031	grey	-0.27300614	0.09054575	GO:0005975;GO:0004553	Glycosyl hydrolase family protein
Sapur.03G0330600.1	0.30442624	1.56388326	0.442888319	3.531395	0.000413174	0.00067314	grey	0.3681703	1.09E-05		NA
Sapur.01G0491600.1	61.6733056	0.29508807	0.083533885	3.53124	0.000413617	0.00067673	grey	0.254108987	0.091328834		DUF1685 Protein
Sapur.01G0138200.1	970.6619177	0.05580579	0.015805579	3.530921	0.000416116	0.00068447	grey	0.263152114	0.091032106	GO:0003676	RNA-binding (RRM/RBD/RNP motifs) superfamily protein
Sapur.01G0154500.1	12.49667576	0.36168866	0.098394606	3.529413	0.000416429	0.00068594	grey	0.324233177	3.41E-05		structure-specific endonuclease subfamily protein
Sapur.01G0284800.10	14.13667363	0.30087351	0.085208551	3.530366	0.000419496	0.00069785	grey	0.31244083	6.78E-05	GO:0005515;GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain
Sapur.07G0690300.2	4.80056142	0.44164639	0.125077202	3.529413	0.000419429	0.00070287	grey	0.004944008	0.97187924	GO:0006351;GO:0006288;GO:0003677	BED domain (BTF2-like transcription factors, Transposase-associated proteins and DOZ2-like proteins)
Sapur.01T0264600.2	0.46474886	-1.20678827	0.341595035	-3.52602	0.000417109	0.00073147	grey	-0.34910131	7.43E-06	GO:0055085;GO:0016021	Auxin efflux carrier family protein
Sapur.01G0251300.1	3.51757532	0.56211446	0.162164127	3.52387	0.000417973	0.00074026	grey	-0.28332024	0.09232667		short-chain dehydrogenase reductase
Sapur.03G0159500.1	296.755122	0.27164287	0.076869225	3.527959	0.000418777	0.00075772	grey	0.232514148	0.093376762	GO:0045454;GO:0015035;GO:0006662	thioredoxin
Sapur.01G0233000.2	2.03583814	0.60872589	0.173849	3.503187	0.000419	0.00077187	grey	0.32408012	2.52E-05	GO:0016758;GO:0008152	UDP-glucuronosyltransferase 73C1
Sapur.15WG0126900.1	0.16165496	1.06983481	0.318862391	3.527127	0.000420096	0.00077934	grey	0.329182653	7.91392137	GO:0016884	Amidase family protein
Sapur.01G0277300.1	1937.123904	0.07637301	0.021754579	3.510422	0.000421124	0.00078673	grey	-0.32426044	0.000846979	GO:0005515;GO:0005488;GO:0003180	SRF72 RNA-binding protein
Sapur.01G0133100.1	238.2582169	0.15910724	0.045122937	-3.52609	0.000421748	0.00080411	grey	-0.27302152	0.00545926	GO:0006468;GO:0006672	signal recognition particle subunit SRP72
Sapur.7D5J800.1	124.2476944	0.15168071	0.043008522	3.526083	0.000421755	0.00080411	grey	0.257506675	0.091108423		kinase APK1B
Sapur.09G0136000.1	253.3737305	0.05780054	0.04476975	-3.52551	0.000422664	0.00081884	grey	0.3009055	7.89E-05		PPR containing plant protein
Sapur.01G0201400.1	10.89565511	0.61681826	0.175003445	3.524615	0.000424098	0.00084125	grey	0.274178027	0.09511197	GO:0008544;GO:0006468;GO:0004672	transmembrane protein, putative
Sapur.09G0202100.1	24.46268077	0.31537431	0.089499676	3.523805	0.000425397	0.00086187	grey	0.2107126	0.09807655		S-lectin protein kinase family protein
Sapur.01G0162700.1	13.04106431	0.54720175	0.155782695	3.522932	0.000428	0.00088417	grey	0.256185383	0.091601617	GO:0007165;GO:0005515;GO:0043531	Cytokinesis-deficient protein 5 (CYD5)
Sapur.01G0132700.1	7.71817514	0.61188071	0.173745581	3.522118	0.000427685	0.00088981	grey	-0.26487792	0.09008855	GO:0005515;GO:0005515	Disease resistance protein (TIR-NBS-LRR class) family
Sapur.03G0130500.1	53.84514135	0.45234091	0.128433373	3.522363	0.000427879	0.00090089	grey	0.28192188	0.09264612	GO:0009607;GO:0006952	NBS-LRR disease resistance protein
Sapur.09G0134600.1	52.50566645	0.47504617	0.135027217	3.521218	0.000428	0.00090269	grey	0.271016817	0.09058106	GO:0005515	HYP-rich protein family
Sapur.03G0130700.5	1.02002855	-0.94197059	0.268042383	-3.5151	0.000429581	0.00090857	grey	-0.24131571	0.09232581	GO:0004857	ARM repeat superfamily protein
Sapur.15WG0966600.1	0.85096349	1.31639341	0.374548168	3.514617	0.000430388	0.00090715	grey	0.28042942	0.09037429	GO:0015937;GO:0005524;GO:0004594	Import/export protein 1
Sapur.03G0144000.1	150.5789882	0.24836836	0.070727952	3.514403	0.000430504	0.00090726	grey	0.268147736	0.09109726		pantothenate kinase 2
Sapur.05G0581000.1	78.9165607	0.16143066	0.045945407	-3.51313	0.000432854	0.00091546	grey	-0.28317768	0.09203029	GO:0007021	Protein of unknown function (DUF581)
Sapur.03G0207600.1	11.87764252	0.34507541	0.098282311	3.511314	0.000432888	0.00091565	grey	0.244617764	0.09201829	GO:0015154;GO:0016021;GO:0015375	C-X(4)-cysteine C-X-cysteine-containing protein
Sapur.01G0289800.1	1.77713705	0.91308668	0.260196241	3.512498	0.000434916	0.00075187	grey	0.246209326	0.09188065	GO:0016887;GO:0005524;GO:0055085;GO:0043626;GO:0016021;GO:0006810	Cu+ copper transporter family
Sapur.05G0291100.1	4.33337104	-0.46734386	0.133045734	-3.51166	0.000434131	0.00075788	grey	-0.25760365	0.09132651		PGP11
Sapur.09G0072200.2	1.32254076	-0.83846115	0.238777185	-3.51158	0.000434545	0.00071758	grey	-0.28114276	0.09034101	GO:0006412;GO:0005840;GO:0005622;GO:0003735	Ribosomal protein S7e family protein
Sapur.01G0122200.1	0.47278393	1.99282551	0.567789	3.511007	0.000434622	0.00071882	grey	0.23632564	0.09280417		NA
Sapur.03G0182900.3	2.96563887	0.56832227	0.161885575	3.51062	0.000437063	0.00720117	grey	0.147972761	0.06438187	GO:0008270;GO:0005515	RING/U-box superfamily protein
Sapur.09G0284800.1	4851.560944	-0.08087902	0.023031173	-3.51044	0.000437172	0.00720579	grey	0.378889669	1.02E-06		low-molecular-weight cysteine-rich 68
Sapur.05G0812000.2	0.54862709	-0.27345764	0.363484115	-3.50868	0.000439345	0.00073527	grey	0.094538089	0.23868667		
Sapur.03G0427700.6	4.79777466	-0.48683522	0.139631148	-3.50756	0.000439381	0.00729588	grey	-0.13806952	0.08463479	GO:0070569;GO:0008152	Gln:Nle:Lsi:IpLT2
Sapur.01TG147004.2	0.86680113	-0.05842487	0.301854063	-3.50644	0.000441547	0.00731279	grey	-0.2715194	0.09089491		N-acetylglucosamine-1-phosphate uridylyltransferase 2
Sapur.15WG0948800.1	3.16370218	0.53445856	0.152427445	3.502362	0.000443576	0.00731451	grey	0.263050209	0.09091509		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01G0268800.2	2.42027118	0.68036367	0.194026397	3.50621	0.000443635	0.00731832	grey	0.225242816	0.09287807	GO:0005515	26S proteasome non-ATPase regulatory subunit
Sapur.01G0136800.3	1.08290218	-0.87533203	0.249654072	-3.50618	0.000445481	0.00071187	grey	-0.13153873	0.10561554		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.09G0245400.1	957.3544458	-0.17008161	0.050865425	-3.50579	0.000445526	0.00072927	grey	-0.28834443	0.09203111	GO:0005524;GO:0006260;GO:0005663;GO:0003689	replication factor C subunit 1
Sapur.07G0614000.1	225.9841902	0.33946053	0.096839865	3.50338	0.000449393	0.00739546	grey	0.310765193	7.45E-05		Ribosomal L29 family protein
Sapur.01G0364700.2	19.37553187	0.61404313	0.175224559	3.503162	0.000449	0.00740423	grey	-0.30809004	0.09088888		phloem protein 2-A13
Sapur.01G0270500.1	375.3447991	-0.12559104	0.035876233	-3.5009	0.000446369	0.00074629	grey	-0.24127643	0.09928986		tubulin folding cofactor E / PFifferling (PFI)
Sapur.01TG281100.1	70.81877599	-0.40420427	0.115402377	-3.50075	0.000446958	0.00746786	grey	-0.25373568	0.09341748	GO:0005468;GO:0009672	receptor serine/threonine kinase, putative
Sapur.01G0280800.1	36.42715141	0.35649139	0.101864779	3.499653	0.000448679	0.00749805	grey	0.215192605	0.097304003	GO:0016788	GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.09G0291100.1	902.9130751	-0.38147283	0.108418822	-3.49964	0.000450879	0.00756805	grey	-0.27355788	0.00426143		HSP20-like chaperones superfamily protein
Sapur.01G0404100.1	336.0844317	-0.57268239	0.163688525	-3.49966	0.000450655	0.00755854	grey	0.258151027	0.092974064		carotenoid cleavage dioxygenase 7
Sapur.01G0875000.1	1.26365702	0.92988782	0.26865505	3.498513	0.000451786	0.00757959	grey	0.24828105	0.09204719		NA
Sapur.01G0188000.1	0.18622553	2.25362877	0.6755302	3.497	0.000453988	0.00765287	grey	0.277239966	0.09054005		NA
Sapur.03G0351300.3	4.12003019	-0.49524865	0.141732447	-3.49669	0.000457064	0.00757965	grey	0.10363568	0.17618348		Kinase-related protein of unknown function (DUF1296)
Sapur.01G0122500.1	0.67696924	1.12154264	0.32386	3.49571	0.000458	0.00760731	grey	-0.28050809	0.09207235		ATP binding microtubule motor family protein
Sapur.03G0130700.1	4.78424756	-0.68780231	0.196782897	-3.49569	0.000458236	0.00760721	grey	-0.24627006	0.09187417	GO:0008168	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.03G0730100.2	0.29000000	1.85410233	0.534025363	3.469656	0.000467366	0.00809643	grey	0.307968266	0.08908642		SNF2 domain-containing protein/ helicase domain-containing protein / HNH endonuclease domain-containing protein
Sapur.01G0643000.3	28.79921266	-0.28154882	0.080536273	-3.4955	0.000473167	0.00761201	grey	-0.26813625	0.09096784	GO:0005085;GO:0016021	Major facilitator superfamily protein
Sapur.01G0284700.1	35.92809223	-0.30194712	0.103008096	-3.495	0.000474067	0.00762583	grey	-0.27281237	0.09054546	GO:0006508;GO:0004197	metacaspase 1
Sapur.01G0273200.2	22.83862792	-0.21778613	0.060594841	-3.49489	0.000476072	0.00765192	grey	-0.22813678	0.09978559		Transcription factor jumonji (jmj)/C domain-containing protein
Sapur.01G0250000.1	0.49247236	1.08876594	0.31157086	3.494756	0.000476424	0.00763112	grey	0.30728287	9.28E-05		ATCHML1,ATXPO1,HET2,XPO1 exportin 1a
Sapur.05G0251800.1	2.81416379	0.70250754	0.201000424	3.493402	0.000476908	0.00765707	grey	0.264648778	0.09074033		sinaR-2
Sapur.09G0188000.1	798.7563671	0.14084935	0.04020585	3.49297	0.000479048	0.00768274	grey	0.228847845	0.09268111	GO:0004413;GO:0003743	Translation initiation factor SUI1 family protein
Sapur.01G0251100.1	7.36001224	0.36131589	0.104536095	3.48287	0.000479662	0.00769534	grey	0.24862027	0.09009887	GO:0016491;GO:0016020	GroES-like zinc dehydrogenase family protein
Sapur.01G0697300.1	21.66023939	0.76461356	0.218929671	3.4925	0.000478521	0.00769552	grey	0.24874158	0.09018373	GO:0055114;GO:0016491;GO:0016491	12-oxophytodienoate reductase 2
Sapur.01G0317000.4	10.49905669	0.07408262	0.021888293	3.491667	0.000479068	0.00769287	grey	0.260317612	0.09025258	GO:0005515	tetratricopeptide repeat (TPR)-containing protein
Sapur.05G0101000.1	212.38704	0.15695148	0.04605975	3.490455	0.000482199	0.00775353	grey	0.215010772	0.09757058		NA
Sapur.01G0185800.1	17786.7298	0.86608434	0.24258605	-3.49026	0.000482546	0.00775587	grey	-0.26381327	0.09978618	GO:0005515;GO:0006468;GO:0004672	Leucine-rich repeat transmembrane protein kinase
Sapur.01G0117000.4	1.05029154	0.90805788	0.251258076	-3.49022	0.000482615	0.00775572	grey	-0.30100524	0.09107716		NA
Sapur.05G0181400.1	139.6515544	0.11767955	0.033668513	-3.48981	0.000483272	0.00777127	grey	-0.28952158	0.09023266		serine/threonine protein phosphatase 2A regulatory subunit B' protein
Sapur.01G0281200.1	122.6443992	0.32886437	0.18197576	-3.48953	0.000483871	0.00777789	grey	0.40009308	2.28E-07		ankyrin-like protein
Sapur.05G0845000.1	5.36398127	0.76415531	0.219016193	3.488854	0.000485096	0.00779784	grey	0.23093812	0.0036147		NA
Sapur.03G0139700.1	0.58979266	0.97188446	0.278364274	-3.48871	0.000484791	0.00779232	grey	-0.3605978	1.52E-06		cysteine-rich repeat secretory protein
Sapur.01G0128800.1	123.18022	0.36541197	0.104803451	3.486641	0.000489128	0.00786151	grey	0.215027246	0.09684366		hypothetical protein
Sapur.01G0622300.1	765.7410063	0.17207702	0.053879309	3.479167	0.000492012	0.00797853	grey	0.271181877	0.09091578	GO:0055114;GO:0016616;GO:0016020;GO:0004450	isocitrate/isopropylmalate dehydrogenase family protein
Sapur.09G0680800.2	6.76167683	0.51755778	0.15994616	3.486021	0.000490262	0.00798788	grey	0.257178836	0.09119471	GO:0008270	Cytidine/deoxycytidylate deaminase family protein
Sapur.03G0148000.1	9.76463134	0.74111494	0.229064258	3.4853	0.000490785	0.00799885	grey	0.309698262	0.08843026		Uncharacterized protein family (UPF0487)
Sapur.01G0282900.1	0.54723629	-1.26228332	0.363100479	-3.48462	0.000492843	0.00791968	grey	0.338834304	1.41E-05		Subtilase family protein
Sapur.09G0270400.2	15.95888007	0.31138363	0.08935872	-3.48445	0.000493315	0.00792423	grey	-0.23053716	0.09367334	GO:0003723	KH domain-containing protein
Sapur.09G0265400.2	23.99487984	0.52187383	0.160157482	3.482971	0.000495883	0.00796737	grey	0.119182051	0.13603504		RING/U-box superfamily protein
Sapur.03G0147300.1	0.27105823	1.58385898	0.454901307	3.482922	0.000495972	0.00796803	grey	0.419127216	4.67E-08		AP2/B3-like transcriptional factor family protein
Sapur.03G0147000.1	0.27105823	1.58385898	0.454901307	3.482922	0.000495972	0.00796803	grey	0.419127216	4.67E-08		AP2/B3-like transcriptional factor family protein
Sapur.15WG0915100.1	572.995267	0.22316883	0.064196727	-3.48266	0.000496451	0.00797533	grey	-0.25403437	0.09132323	GO:0005515	Transducin/WD40 repeat-like superfamily protein
Sapur.05G0190500.1	0.77927347	0.73727209	0.211721308	3.481577	0.000497	0.00798352	grey	-0.48859996	1.81E-10	GO:0007275;GO:0006355;GO:0003700	Integrase-type DNA-binding superfamily protein
Sapur.05G1310000.4	21.33574442	0.76131883	0.220015214	3.481193	0.000497128	0.00798827	grey	-0.27130793	0.09056078	GO:0016868;GO:0006096;GO:0004619	Phosphoglycerate mutase family protein
Sapur.01G0237400.1	93.53273671	-0.59082429	0.172087461	-3.48188	0.000499412	0.00799442	grey	-0.27263254	0.09043164	GO:0006355;GO:0005634;GO:0003700;GO:0005575	transcription factor NAC3/ANAC073/ANAC075 family
Sapur.01G0237900.1	16.27564818	0.38964148	0.113914499	-3.48154	0.000498545	0.00800704	grey	-0.48407095	1.34E-10	GO:0055114;GO:0016020;GO:0003885;GO:0050660;GO:0016491	L-galactono-1,4-lactone dehydrogenase
Sapur.05G0280800.1	1.48724760	0.42168232	0.123345079	3.481464	0.000498675	0.00800753	grey	0.237329229	0.09481663	GO:0055114;GO:0016021;GO:0016705;GO:0050506	cytochrome P450 family 81, subfamily A, polypeptide 2
Sapur.05G0573300.2	0.35118051	-1.65267272	0.474825786	-3.48059	0.000500315	0.00803468	grey	0.401108274	1.81E-07		calcium sensing receptor
Sapur.7D7I500.1	0.78843984	1.03758707	0.28238368	3.47882	0.000503827	0.00808748	grey	0.239875535	0.09247918		NA
Sapur.03G0288000.1	200.4253263	0.24461858	0.07075571	3.479485	0.000504256	0.00808793	grey	0.251717277	0.09158896		AT-hook motif nuclear-localized protein 20
Sapur.09G0145000.4	18.37576877	0.36923443	0.106269084	3.476623	0.000507771	0.00815243	grey	0.137166642	0.08616929	GO:0005515;GO:0016021	zinc induced facilitator-like 2
Sapur.15WG0104000.1	1.30517303	0.17427165	0.5139853	3.476541	0.000507926	0.00815453	grey	0.32215285	0.08090546		NA
Sapur.07G0661000.1	0.47315274	-1.70040801	0.51504293	-3.47623	0.000508588	0.00816348	grey	0.166251632	0.07319409		photosystem II stability/assembly factor, chloroplast (HCF136)
Sapur.7I3I700.1	0.34470533	1.48183209	0.426279472	3.475194	0.000508584	0.00816429	grey	0.46171526	1.01E-08		NA
Sapur.04G0417000.2	0.46090794	-1.6471561	0.416338476	-3.47591	0.000509118	0.00817248	grey	-0.28952158	0.09023266		Expressed protein
Sapur.01G0181300.1	0.00002964	0.85275163	0.245336696	3.475638	0.000509639	0.00818049	grey	0.282604038	0.09037878		cycloartenol synthase 1
Sapur.01BG117200.1	3.28217512	0.89448345	0.257496663	3.474413	0.000511973	0.00821751	grey	0.253630948	0.09141207	GO:0005515	receptor-like protein 45
Sapur.15WG0491800.1	0.63261244	0.37908857	0.397208296	-3.47422	0.000512341	0.00822382	grey	-0.32920032	2.56E-05		MYB transcription factor
Sapur.01G0182000.1	550.8020969	0.17036766	0.049004144	3.473945	0.000512866	0.00823155	gr

Sapur.010G065400.1	4.34631025E-4	-0.49349296	0.14368269	-3.43415	0.00059442	0.00346982	grey	-0.25748849	0.00113875	GO:0005515	ATAG14750.1	IQD19	IQ-domain 19	IQ calmodulin-binding motif protein
Sapur.017G049800.1	2525.904583	0.20378437	0.05935555	3.433382	0.00056101	0.00052483	grey	0.24796664	0.01740732	GO:0005114;GO:0016616;GO:0006694;GO:0003854	ATAG22820.1	GAE6	UDP-D-glucuronate 4-epimerase 6	UDP-D-glucuronate 4-epimerase
Sapur.009G281000.1	1.5807633	0.58769381	0.17116329	3.432485	0.00056976	0.00063831	grey	0.24031261	0.00243518	GO:0003700;GO:0006357	ATAG20410.2	anac034,ANAC035,LOV1,NV	NAC domain containing protein 35	NAC transcription factor
Sapur.018G051800.3	5.70128868	0.43129628	0.12565141	3.432356	0.00058381	0.00056002	grey	0.09933269	0.21579148		ATAG20060.2		alpha/beta-Hydrolases superfamily protein	acyl-protein thioesterase
Sapur.005G071300.1	189.9527344	0.22164673	0.06498603	3.429328	0.00060532	0.00066088	grey	0.16387528	0.00843837	GO:0016810;GO:0006807	ATAG50090.1		carbon-nitrogen hydrolase family protein	glutamine-dependent NAD(+) synthetase, putative
Sapur.001G192300.2	3.85425401	-0.53080906	0.15478808	-3.42921	0.00060539	0.0006701	grey	-0.24160725	0.00229416		ATAG19390.1		Uncharacterized protein family (UPF0114)	plant/TSK130-170 protein, putative
Sapur.008G157400.12	2.34067258	0.59803387	0.17673292	3.428558	0.00060796	0.00060592	grey	0.01523632	0.84463047					hypothetical protein
Sapur.007G087700.2	19.25265076	0.31970253	0.09318135	3.43024	0.00060732	0.00070281	grey	-0.25990005	0.0015192					NA
Sapur.011G078000.1	1.46862975	-0.98768887	0.28814579	-3.42774	0.00060831	0.00072081	grey	-0.2847005	0.0003006					NA
Sapur.001G168800.2	2.34866736	0.35189787	0.4151327	3.426603	0.00060939	0.00074022	grey	0.31450236	1.84E-05		ATAG11870.1	RHD3	Root hair defective 3 GTP-binding protein (RHD3)	RAD3/HAR defective-like protein
Sapur.009G089900.1	1.71126052	-0.62549361	0.18255827	-3.42688	0.00060565	0.00075076	grey	-0.30526004	0.00101233		ATAG18840.2		Tetratricopeptide repeat (TPR)-like superfamily protein	Tetratricopeptide repeat
Sapur.013G097200.1	3.38441496	0.37133056	0.10833475	-3.42672	0.00060913	0.00075584	grey	-0.26120212	0.00948284		ATAG25651.1		Copper transport protein family	hypothetical protein
Sapur.002G183900.4	0.71066587	-0.07376945	0.31337256	-3.42651	0.00061193	0.00076305	grey	-0.09683465	0.22778174	GO:0004648;GO:0006672	ATAG26700.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.010G047700.2	54.86603844	0.24427188	0.07128936	3.426473	0.00061374	0.00076387	grey	0.24603804	0.01837169		ATAG26300.1		TLD-domain containing protein	TLD protein
Sapur.004G046700.1	0.41494074	1.97609147	0.46323441	-3.42596	0.00062629	0.00079184	grey	-0.05127044	0.94918223		ATAG73150.2			hypothetical protein
Sapur.013G000.1	8.51569938	0.49362731	0.13809785	3.424033	0.00063893	0.00085451	grey	0.26458533	0.00770849		ATAG48550.1		Vacuolar protein sorting-associated protein 26	NA
Sapur.001G184300.1	795.0749316	0.15261465	0.04457926	3.423966	0.00061076	0.00085189	grey	0.21611541	0.00659208	GO:0005525	ATAG06630.1	ATRAB-A2A,ATRAB11C,ATR	RAB GTPase 11C	small GTPase family Rab protein
Sapur.012G294700.1	38.89351396	0.24381041	0.07129102	3.423393	0.00061846	0.00087328	grey	0.3023822	0.00119219					lectin-domain receptor kinase A4.2, putative
Sapur.005G303200.1	4.08795417	0.77974991	0.22778584	3.423024	0.00062187	0.00088737	grey	0.21449619	0.00869171	GO:0006355;GO:0003700	ATAG23261.1		Integrase-type DNA-binding superfamily protein	ethylene-responsive transcription factor ERF088
Sapur.016G244200.1	1003.785713	0.24386423	0.07128367	-3.42331	0.00061826	0.00087473	grey	-0.24027899	0.02436271	GO:0008299;GO:0016765;GO:0015979	ATAG17050.1	SPS2	solanesyl diphosphate synthase 2	solanesyl diphosphate synthase
Sapur.015G251400.1	-1.12419317	0.26398736	0.3071844	-3.42319	0.00062639	0.00088761	grey	0.29372202	0.00104552		ATAG47820.1		DNAse I-like superfamily protein	NA
Sapur.008G144300.1	217.4804709	0.15307251	0.04478497	3.422153	0.00061893	0.00087963	grey	0.25803521	0.00353381	GO:0071949	ATAG24340.1	EMB2421,EMB2600	FAD/NAD(P)-binding oxidoreductase family protein	FAD/NAD(P)-binding oxidoreductase family protein
Sapur.009G126100.1	3.59852917	0.16817494	0.15723352	3.422667	0.00059416	0.00088854	grey	0.22464221	0.02667274	GO:0004544;GO:0006488;GO:0006427	ATAG11340.1		S-locus lectin protein kinase family protein	Serine/Threonine-kinase
Sapur.015W0154200.1	8.15085902	0.77870588	0.22750767	-3.42143	0.00062207	0.00094114	grey	-0.27868917	0.00408784	GO:0005524	ATG18820.1	EMB3007	Tcp-1/cpn60 chaperonin family protein	NA
Sapur.001G011800.1	390.6613132	0.89386165	0.26607216	3.420637	0.00064646	0.00103537	grey	0.28024301	0.00377792	GO:0005515;GO:0055114;GO:0046872;GO:0016702	ATAG45140.1	ATLIP2,LOX2	lipoxygenase 2	NA
Sapur.152G044700.1	0.61719126	1.65407124	0.48363109	-3.42084	0.00062788	0.00986871	grey	-2.72288732	0.00560742	GO:0005634	ATAG17680.1	NDF1		NA
Sapur.006G173800.1	4.77324701	-0.49158892	0.14373028	-3.41985	0.00062638	0.00996397	grey	-0.28813028	0.00024631		ATAG03000.2		RING/U-box superfamily protein	E3 ubiquitin ligase RFA, putative
Sapur.005G307000.2	11.31789808	0.01355165	0.10282319	3.419372	0.00067658	0.00101964	grey	0.27875765	0.00040738	GO:0016301	ATAG46090.1		Diacylglycerol kinase family lipid kinase	Yeg1/Ypk2/Sc2/Bnr1 family lipid kinase
Sapur.016G178800.3	5.67978336	0.35235633	0.12846122	3.418429	0.00062938	0.00100788	grey	0.25238372	0.01428014	GO:0005524;GO:0004020;GO:0000103	ATAG14750.1	AKN1,APK,APK1,ATAKN1	APS kinase	adenylylsulfate kinase
Sapur.T041300.1	1.42978096	0.44255465	0.20127254	3.418025	0.00063241	0.01005381	grey	-0.25201968	0.00157454		ATAG29100.1			NA
Sapur.013G014000.1	0.62068529	-1.05768289	0.32385467	-3.4144	0.00063234	0.01019581	grey	-0.33186248	1.93E-05	GO:0016788	ATAG28650.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-like lipase/acylhydrolase
Sapur.006G047300.1	0.47127171	1.76018781	0.51553615	3.414182	0.00063958	0.01019961	grey	-0.28850297	0.00254552					hypothetical protein
Sapur.013G138200.2	3.17604039	-0.60012949	0.17589396	-3.41135	0.00064116	0.01022457	grey	-0.16121582	0.24368769		ATAG3400.1	DFL2,GH3.10	Auxin-responsive GH3 family protein	indole-3-acetic acid-amido synthetase GH3.5 protein, putative
Sapur.002G242300.1	20.27564593	0.66217876	0.19429875	3.408266443	-3.41359	0.00064117	grey	-0.25025544	0.00181883		ATAG27362.1		Chloroplast nucleoid DNA binding superfamily protein	heavy metal-associated isoprenylated plant protein
Sapur.003G091400.2	0.98356377	-0.96683358	0.28324356	-3.41343	0.00064501	0.0103	grey	-0.3082514	8.57E-05	GO:0003682	ATAG64300.1	HEN4	RNA-binding KH domain-containing protein	K-like RNA-binding domain protein
Sapur.013G138300.1	135.0653568	0.61618388	0.19374211	-3.41149	0.00064608	0.01030201	grey	-0.25377087	0.01348894	GO:0055114;GO:0050661;GO:0006006;GO:0004345	ATAG45190.1	GGPD4	glucono-6-phosphodehydrogenase 4	glucono-6-phosphono-D-glucono-lactone dehydrogenase 4
Sapur.003G034300.1	86.82825686	0.36106032	0.10648368	3.41	0.00064703	0.01031641	grey	-0.26136035	0.00055343		ATAG19780.1		Protein kinase superfamily protein	pfkB-type carbohydrate kinase family protein
Sapur.012G077800.1	42.78794998	0.49802987	0.14604509	-3.41082	0.00064675	0.01032646	grey	-0.27528369	0.00484113	GO:0005975;GO:0004553	ATAG40435.1			transcription factor bHLH93
Sapur.019G045105.1	334.6265507	0.15374676	0.04673216	3.410307	0.00064946	0.01033537	grey	0.27149781	0.00583848		ATAG17520.1	MEX1,BCP1	root cap 1 (RCP1)	maltose excess-like protein, putative
Sapur.003G095500.1	1170.832099	0.71941211	0.21096613	3.410032	0.00064952	0.01035488	grey	0.24008411	0.02646665		ATAG29230.1	SPI12	SPIRAL1-like2	hypothetical protein
Sapur.011G089300.1	20.07238146	1.36545133	0.10716568	3.409852	0.00065027	0.01036077	grey	-0.26814634	0.00682254					NA
Sapur.005G129200.1	194.3159448	0.25101709	0.07337867	3.409844	0.00065001	0.01036105	grey	0.25140406	0.00126164		ATG78170.1			WW domain protein, putative
Sapur.005G135600.1	9896.162757	0.11703181	0.10268882	3.40976	0.00065002	0.01036374	grey	-0.31850007	4.91E-05		ATHSL;HS1	ATHSL;HS1	heat stable protein 1	stress responsive NAC barrel domain protein
Sapur.005G091500.1	4.93018716	0.42718152	0.12531527	3.409746	0.00065224	0.01036376	grey	0.25863258	0.00372218	GO:0005515	ATAG66240.2		Transducin/WD40 repeat-like superfamily protein	Sec1-complex component SWD2
Sapur.003G082300.1	181.4417322	0.29268143	0.08604429	3.408318	0.00065447	0.01041751	grey	0.25513613	0.01260627	GO:0005515	ATAG40170.1		receptor like protein	NA
Sapur.007G103800.1	93.60002554	0.18433544	0.05409321	-3.40786	0.00065751	0.01043425	grey	-0.27304399	0.00062351	GO:0003723	ATAG64300.1	HEN4	RNA-binding KH domain-containing protein	K-like RNA-binding domain protein
Sapur.003G084800.1	1725.033958	0.16187897	0.04758873	3.407658	0.00065825	0.01044209	grey	-0.25377087	0.01348894	GO:0055114;GO:0050661;GO:0006006;GO:0004345	ATAG45190.1	GGPD4	glucono-6-phosphodehydrogenase 4	glucono-6-phosphono-D-glucono-lactone dehydrogenase 4
Sapur.T091600.2	13.6332872	0.32192435	0.09456724	3.40702	0.00066754	0.01046531	grey	-0.26101882	0.00075425		ATAG59480.1		pfkB-like carbohydrate kinase family protein	pfkB-type carbohydrate kinase family protein
Sapur.019G199000.2	0.37472621	-1.31840143	0.38704578	-3.40637	0.00065824	0.01048968	grey	-0.26103493	3.16E-06		ATAG40435.1			transcription factor bHLH93
Sapur.014G144400.1	1346.12753	-0.05421493	0.01653714	-3.40576	0.00066946	0.01050537	grey	-0.25928007	0.01232666	GO:0003924	ATAG17520.1	MEX1,BCP1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	GPN-loop GTPase
Sapur.007G207700.3	5.41070478	-0.42589558	0.12509893	-3.40546	0.00066519	0.01052362	grey	0.20302666	0.01118583	GO:0005515	ATAG21180.2	ATLIP2,TLP2	tubby like protein 2	tubby like 5 box protein
Sapur.008G147900.4	0.76112877	-0.41270504	0.2400807	-3.40537	0.00066107	0.01054029	grey	-0.24219739	0.02245073	GO:0016491;GO:0016117	ATAG10440.1		Lycopene beta/epsilon cyclase family	lycopene beta/epsilon cyclase
Sapur.008G139300.1	14.51950052	-0.34529429	0.10149808	-3.40461	0.00066529	0.01055536	grey	-0.24772047	0.01179426	GO:0008168;GO:0008152	ATAG63410.1	APG1,E37,JGP37,VTE3	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	2-methyl-6-phytyl-1%2C4-benzoquinone methyltransferase
Sapur.013G052400.2	7.56209065	-0.18892004	0.06648297	-3.40448	0.00066709	0.01056412	grey	-0.19850204	0.01963615	GO:0016020;GO:0008376;GO:0006486;GO:0030246	ATAG26120.1		Galactosyltransferase family protein	galactosyltransferase
Sapur.002G019500.1	3.70023487	0.91137874	0.26765142	-3.40417	0.00066344	0.01057138	grey	-0.29679951	0.00160443	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATRA-CYP450.1;RED1;BNT1;	cytochrome P450, family 81, subfamily B, polypeptide 1	cytochrome P450, family 81, subfamily B, polypeptide 1	NA
Sapur.003G060600.1	19.13663325	0.61968166	0.17510756	3.404004	0.00066386	0.01057583	grey	-0.31518705	0.00007718	GO:0006629	ATAG10955.2		alpha/beta-Hydrolases superfamily protein	triacylglycerol lipase
Sapur.010G067000.1	0.66451233	1.41076017	0.41459514	3.402755	0.00066710	0.01062491	grey	-0.24528805	0.01951327					hypothetical protein
Sapur.003G052600.7	16.67924875	0.31951988	0.09388564	-3.40248	0.00066773	0.01063511	grey	-0.31425253	6.39E-06		ATG17615.1	ATCBL1,CBL1,SCABP5	calcineurin B-like protein 1	calcineurin B-like protein
Sapur.007G088400.1	1161.16747	0.46329413	0.10148397	-3.40232	0.00066847	0.01063629	grey	-0.23167745	0.03509795		ATG23970.1	SDL6-1	SDL6 heme-binding family protein	SDL6 heme-binding family protein, putative
Sapur.001G076300.1	9.60362962	0.92968872	0.14979882	3.402353	0.00068082	0.0106039	grey	0.22395364	0.00257331	GO:0043565;GO:0006355;GO:0003700	ATG15070.1	AtWRKY41,WRKY41	WRKY family transcription factor	WRKY transcription factor
Sapur.006G112000.1	489.2131137	0.20968008	0.06126548	3.402085	0.00068251	0.01064094	grey	-0.26957802	0.00268455	GO:0005525;GO:0005875	ATG45590.1		GTP-binding protein of unknown function (DUF526) family protein	zinc knuckle protein
Sapur.001G124400.1	234.0060425	0.28730388	0.08430391	-3.4021	0.00068692	0.0106477	grey	-0.25166811	0.00178355		ATAG37260.1	ATMFB73,MFB73	myb domain protein 73	R2R3-MYB transcription factor, putative
Sapur.003G138500.1	13.08673984	0.25273627	0.07707945	-3.40153	0.00067036	0.01066969	grey	-0.3115111	4.58E-05	GO:0016020	ATAG27585.1		SPFH/Band 7/PHB domain-containing membrane-associated protein family	SPFH domain/Band 7 family protein
Sapur.001G150500.1	10.82518408	0.56345623	0.16378827	3.400953	0.00067154	0.01069159	grey	-0.24947097	0.01626762		ATAG31890.2	ATMYB26,MS35,MYB26	myb domain protein 26	R2R3-Myb transcription factor, putative
Sapur.001G139500.1	2.37840268	-0.66075459	0.18332566	-3.40075	0.00067316	0.01069854	grey	Bas-BP2/NDP kinase-like superfamily protein			ATG27125.1			RanBP2-type zinc finger protein
Sapur.004G061400.1	239.6144076	0.16079548	0.04728692	-3.40056	0.00067281	0.01070545	grey	-0.27330112	0.01348071	GO:0005662;GO:0008324	ATAG60540.1		NAD(P)-binding Rossmann-fold superfamily protein	dTDP-4-dehydrorhamnose reductase
Sapur.014G046300.1	7.14229319	0.15956265	0.04695153	-3.40015	0.00067509	0.01071463	grey	-0.23246651	0.03193112	GO:0008017;GO:0070510;GO:0005524;GO:0003777;GO:0005871	ATG63465.1		P-loop nucleotide triphosphate hydrolases family protein with CH (Calponin Homology) domain	NA
Sapur.014G079100.10	7.13476861	-0.35763869	0.10524753	-3.3983	0.00067851	0.01079289	grey	-0.28964822	0.00233733	GO:0055114;GO:0008615;GO:0004733	ATG46580.1		Pyridoxamine 5'-phosphate oxidase family protein	pyridoxamine 5'-phosphate oxidase-related FMN-binding protein
Sapur.004G169800.1	91.79699895	0.27501728	0.08095234	3.397126	0.00068976	0.01083912	grey	0.24607797	0.02100166	GO:0005975;GO:0004553	ATG11820.1		D-Glycosyl hydrolases family 17 protein	NA
Sapur.017G068500.1	386.9579609	0.22223889	0.06518179	3.397033	0.00069119	0.01085156	grey	0.25688043	0.01161717		ATAM9B6;MFB6;MFB6CRV;	myb domain protein 6	MYB transcription factor	NA
Sapur.019G074200.1	0.29178242	1.25070561	0.36827598	3.396562	0.00068232	0.01086044	grey	0.33818413	1.61E-05		ATG27410.1		Domain of unknown function (DUF313)	DUF313 domain protein
Sapur.017G111000.1	7.38482483	-0.56283084	0.16548193	-3.39629	0.00068049	0.01087053	grey	0.30713897	9.11E-05	GO:0008168	ATAG21240.1		S-adenosyl-L-methionine-dependent methyltransferase superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.008G089600.1	62.58582816	-0.41074396	0.12096704	3.395423	0.00068526	0.01090014	grey	0.26479018	0.00806983	GO:0016021	ATAG37480.1	PHOL1,H1	phosphotyrosine protein family protein	phosphate transporter 1, putative
Sapur.019G127500.1	144.1031113	0.26098085	0.30164663	3.395203	0.00068896	0.01096324	grey	0.33821021	1.64E-05		ATG37180.1			NA
Sapur.006G041200.1	5.11024883	0.57446374	0.16924069	3.39389	0.00069073	0.01096643	grey	0.23669198	0.02839859		ATG20898.1			NA
Sapur.010G120600.1	1179.777562	0.01621016	0.24764731	3.393446	0.00069166	0.01098103	grey	0.24208063	0.02215511	GO:0046981;GO:0003677;GO:0006355;GO:0005634;GO:0003700	ATAG29190.1	AGL7,AP1	K-box region and MADS-box transcription factor family protein	ARITA1A-like MADS-box PTAF1 protein
Sapur.005G205400.1	15.04468839	0.71297828	0.21010785	3.393391	0.00069033	0.01098372	grey	0.26562717	0.00773925	GO:0007165;GO:0005515;GO:0005515	ATAG12010.1		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.001G049900.1	0.95554883	0.95731684	0.28213739	-3.39328	0.00069108	0.01099456	grey	-0.28517915	0.00238383		ATAG31980.1			NA
Sapur.008G086200.1	12.68870942	-0.76007836	0.22401638	-3.39305	0.00069165	0.01099556	grey	-0.26286553	0.00090872		ATAG20610.1	ALPHA-DOX1,DOX1,DOX1,P	Peroxidase superfamily protein	NA
Sapur.010G136700.1	372.7698256	0.16086308	0.04744132	-3.39276	0.00069313	0.01100631	grey	-0.25257102	0.00149474		ATAG2685.1		Acid phosphatase/vanadium-dependent haloperoxidase-related protein	acid phosphatase/vanadium-dependent haloperoxidase-like protein, putative
Sapur.T014580.1	1.26364849	0.81869496	0.24141799	3.392266	0.00069186	0.01100898	grey	0.24724239	0.01798164		ATAG25120.1		disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.011G060800.1	0.46325169	1.98427923	0.58478845	3.392651	0.00069299	0.01100998	grey	0.28367426	0.00317915		ATAG20880.1	RHS14	root hair specific 14	NA
Sapur.005G189700.1	780.7347576	0.11936293	0.03484857	-3.3924	0.00069326	0.01101594	grey	-0.31853806	1.46E-05	GO:0008168	ATAG27230.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ATXA03
Sapur.003G076400.2	4.57066769	0.53624987	0.15813257	3.392269	0.00069164	0.01101041	grey	0.25481628	0.01278945		ATAG16530.1		tRNA/pseudouridine synthase-associated domain	Rho guanine nucleotide exchange factor, putative
Sapur.013G131300.1	60.08223133	0.56340248	0.16802183	-3.39145	0.00069247	0.01105614	grey	-0.28692274	0.00303543		ATAG2680.1	ZIFP4	zinc finger protein 4	zinc finger protein, putative
Sapur.005G118300.1	1.25611144	0.84916076	0.25048631	-3.39005	0.00069887	0.01111177	grey	-0.26729329	0.00071864		ATAG10940.2	AGI1,SARK2-4,SNRK2.4,SRK	Protein kinase superfamily protein	NA
Sapur.008G069500.1	7.80439561	0.51601241	0.15237176	-3.38958	0.00070001	0.01113051	grey	-0.26169875	0.00390443		ATAG4810.1	CAM7	calmodulin 7	NA
Sapur.T087500.1	5.62208763	-0.46956297	0.14601965	-3.38882	0.00070312	0.01118013	grey	-0.28492846	0.00298228					NA
Sapur.016G276200.1	40.09952579	0.23781795	0.07050594	-3.38757	0.00070514	0.01121046	grey	0.14089824	0.07871122	GO:0016192	ATG54750.1		Transport protein particle (TRAPP) component	trafficking protein particle complex subunit
Sapur.006G163600.1	13.36056622	0.45448816	0.13410716	3.386403	0.00070875	0.01126557	grey	0.20805035	0.08930404		ATG3245.1	AtI7.1		DUF4228 domain protein
Sapur.008G142800.1	2.16295609	0.65067269	0.19214711	3.386086	0.00070892	0.01127008	grey	0.29386956	0.00189167		ATG30860.1			hypothetical protein
Sapur.004G170700.1	563.3694335	0.08156822	0.04892818	3.38562	0.00070918	0.01128854	grey	0.25338466	0.00245564	GO:0005085;GO:0016020;GO:0008021;GO:0005247	ATG5464.1	ATCLC-E,CLC-E,CLCE	chloride channel E	chloride channel, CIC protein
Sapur.006G121000.5	1.87607223	0.72615428	0.21454028	3.384557	0.00071932	0.01133185	grey	0.25124089	0.01503233	GO:0005085;GO:0016020;GO:0015297;GO:0015238;GO:0006855	ATG21340.1		MATE efflux family protein	MATE efflux family protein
Sapur.005G208300.1	31.56548886	0.30346258	0.10627445	3.383831	0.00071402	0.01136141	grey	0.27025407	0.00016461	GO:0007165;GO:0005515;GO:0004351	ATG2510.1		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.015G327700.1	2.19715495	-0.56760881	0.30966851	-3.38347	0.00071548	0.01137561	grey	-0.27660879	0.00452341	GO:0008146	ATAG7610.1	ATSOT16,ATSTA,CDR-7-SC	sulfotransferase 16	flavonol 4'-sulfotransferase, putative
Sapur.003G039700.2	6.65484473	0.67498561	0.14024547	-3.3344	0.00071631	0.01137639	grey	-0.21451441	0.03576469					hypothetical protein
Sapur.T081800.1	9.06916524	0.60316722	0.17830535	-3.38279	0.00071725	0.01140221	grey	-0.26141158	0.00932919					NA
Sapur.002G063600.1	18.10757984	0.61884623	0.19421273	3.382731	0.00071716	0.01140469	grey	0.24897963	0.01664016	GO:0008270;GO:0005515	ATAG13228.1		RING/U-box superfamily protein	RING/U-box superfamily protein
Sapur.005G202500.4	2.19319282	0.95328615	0.17588655	-3.38251	0.00071878	0.01141308	grey	-0.13038811	0.03497769		ATAG27240.1		DNA/ RNA helicase N-terminal domain-containing protein	chaperone protein DnaJ, putative
Sapur.003G071000.2	11.90382868	0.36818183	0.10887736	-3.38167	0.00072059	0.01144719	grey	-0.26414206	0.00829332		ATG3440.1		SKI domain-containing protein	Rho guanine nucleotide exchange factor
Sapur.010G082800.1	591.6173259	0.18722599	0.05537639	3.380927	0.00072417	0.01149154	grey	0.22816154	0.09450227		ATG4870.1	PCR2	PLANT CADMIUM RESISTANCE 2	plant cadmium resistance protein
Sapur.003G045000.1	155.2033996	0.29026864	0.08583615	3.380557	0.00072339	0.01149021	grey	0.24460856	0.02018724	GO:0006508;GO:0004190	ATG16563.1		Eukaryotic aspartyl protease family protein	aspartyl protease
Sapur.001G046900.1	1722.266334	0.67658245	0.04376261	3.380377	0.00072570	0.01149755	grey	0.23138202	0.02152322	GO:0006355;GO:0005622	ATG7930.1	NTL2B	nuclear transport factor 2	nuclear transport factor 2
Sapur.010G080400.3	2.34653606	-0.69620483	0.20566361	-3.38022	0.00072427	0.01150697	grey	-0.24920232	0.01609063	GO:0055114;GO:0016491	ATG60560.1	ATRBOH F,ATRBOHF,RBOH	respiratory burst oxidase protein F	respiratory burst oxidase-like protein
Sapur.003G300300.1	790.8340823	0.18540383	0.05456754	-3.38006	0.00073471	0.01151122	grey	-0.26950448	0.00064013		ATG8000.1		CAX2/Sodium/proton antiporter family protein	CAX2/Sodium/proton antiporter
Sapur.010G231300.1	1.30234578	0.73706241	0.21805815	3.380045	0.00073739	0.01151132	grey	0.23107865	0.03193672					NA
Sapur.016G269300.1	153.2026265	0.30100151	0.10109151	3.380037	0.00073757	0.01151548	grey	0.28368149	0.00282439		ATG48200.1			transmembrane protein, putative
Sapur.008G095600.1	468.2476594	0.12087537	0.03576298	3.379493	0.00073198	0.01153338	grey	0.24881806	0.00167585	GO:0006412;GO:0005840;GO:0003735	ATG68590.1		Ribosomal protein PSRP-3/Tc70S	plastid-specific 30S ribosomal protein, putative
Sapur.016G097400.1	23.22346575	-0.49349075	0.14609384	-3.3782	0.00072631	0.01158736	grey	-0.26329724	0.00077281		ATG03670.1		ankyrin repeat family protein	ankyrin repeat protein
Sapur.010G120400.5	0.38949254	1.28460771	0.38060742	3.378257	0.00072973	0.01159061	grey	0.26417416	0.00184294	GO:0007275	ATG69180.1	CRC	Plant-specific transcription factor YABBY family protein	YABBY-like transcription factor CRABS CLAW-like protein, putative
Sapur.004G061000.1	356.5763004	0.14764270	0.04370582	3.378024	0.00073086	0.01159346	grey	0.23609063	0.02849772	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATG48480.1	RKI1	receptor-like kinase 1	inactive receptor kinase, putative
Sapur.011G058800.1	219.2873188	0.62294325	0.18439662	3.377969	0.00073139	0.01161061	grey	0.27008626	0.00262444		ATG5990.1		Leucine-rich repeat (LRR) family protein	receptor-like kinase
Sapur.005G080600.1	0.51228811	2.35015066	0.70332145	3.376837	0.00073245	0.01164251	grey	0.25692711	0.01021726					NA
Sapur.005G055100.1	17.82174684	0.37460446	0.11103166	3.375848	0.00073594	0.01165267	grey	0.02868928	0.76694551	GO:0005515	ATG05630.1		RING/U-box protein	splicing factor, arginine/serine-rich 2-like, 2 mpu interacting protein%3C
Sapur.008G053800.1	45.82437572	0.23443185	0.06949316	3.375154	0.00073746	0.01171284	grey	0.29328848	0.00191119	GO:0005267;GO:0032777;GO:0006357	ATG04670.1		Enhancer of polycomb-like transcription factor protein	enhancer of polycomb-like protein
Sapur.001G117700.1	37.49443470	0.17588684	0.05213939	3.374967	0.00073747	0.01171884	grey	0.26316183	0.00092525	GO:0005267;GO:0006357	ATG4244.2		Transcription factor IIA gamma chain / TFIIA-gamma (TFIIA-γ)	transcription initiation factor IIA subunit 2
Sapur.016G169200.2	11.62287565	0.31450674	0.09233159	-3.37328	0.00074278	0.01179108	grey	-0.26319986	0.00869501		ATG3160.1			hypothetical protein
Sapur.016G077700.1	5.70300548	0.68178738	0.2025162	3.372918	0.00074762	0.01180824	grey	0.24964054	0.01848215	GO:0008324;GO:0006370;GO:0004722	ATG2680.1		Protein phosphatase 2C, putative	protein phosphatase 2C, putative
Sapur.006G117200.5	0.48788865	-1.23737666	0.36698411	-3.37264	0.00074652	0.01181176	grey	0.07848531	0.32814687	GO:0016157;GO:0005985	ATG3190.1	ATSUS4,SUS4	sucrose synthase 4	sucrose synthase
Sapur.010G082300.1	199.7849684	0.30440556	0.09027928	3.372208	0.00074568	0.01183543	grey	0.25187858	0.00257463		ATG10660.1		CDC68-related	CDC68-related
Sapur.010G027300.1	133.4904969	0.30511191	0.09094157	3.372069	0.00074877	0.01188331	grey	0.22363256	0.04869958		ATG23190.1		Kelch repeat-containing F-box family protein	F-box/kelch-repeat F-box family protein
Sapur.010G053900.1	11.57849994	-0.97208207	0.17860384	-3.37016	0.00075149	0.01192208	grey	-0.28127481	0.00335062		ATG37850.1			hypothetical protein
Sapur.003G092800.1	0.53952884	0.91018247	0.27129397	3.371659994	-3.37011	0.01193054	grey	-0.23973897	0.02487176	GO:0008790	ATG25620.1		Late embryogenesis abundant protein, group 1 protein	se

Sapur.005G009500.1	1.11492599	-0.9978776	0.30040128	-3.12121	0.00896289	-0.01414037	grey	-0.27230677	0.00506306	GO:0055114;GO:0016491	AT4G10580.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.003G098700.1	13.72749166	0.66514625214	0.20027674	3.321137	0.00886515	0.01414326	grey	-0.19869351	0.01260722		AT5G64160.1	Disease resistance-responsive (dirigent-like protein) family protein	disease resistance response protein
Sapur.002G169200.1	10.24043929	0.26135375	0.07664950	3.11887	0.00909351	0.01425292	grey	-0.26108139	0.00269672	GO:0046872;GO:0016020;GO:0006621	AT5G58170.1	ER lumen protein retaining receptor family protein	ER lumen protein retaining receptor family protein
Sapur.007G124800.1	284.4108159	0.09244035	0.02765283	-3.31859	0.00904723	0.01427071	grey	-0.25588381	0.01218244		AT5G59800.1		hypothetical protein
Sapur.005G078100.1	0.57547149	-0.19138932	0.10610386	-3.31772	0.00907556	0.01431401	grey	-0.34984025	0.01459308	GO:0044302;GO:0042256	AT5G55420.1	Translation initiation factor IF6	NA
Sapur.016G294300.1	850.4945537	-0.12311679	0.03711827	-3.31736	0.00908708	0.01433152	grey	-0.26270701	0.00887392	GO:0005856;GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005875	AT5G55930.2	KCBP/MICKP,NW	kinesin-like calmodulin-binding protein (ZWICHEL)
Sapur.017G123400.1	13.13905396	0.41668547	0.12560829	3.317385	0.00908903	0.01433391	grey	0.24113637	0.00234977		AT5G14470.1	NB-ARC domain-containing disease resistance protein	NA
Sapur.003G096200.1	346.6118864	0.25696127	0.07747557	3.317386	0.00909029	0.01433931	grey	0.24088955	0.00237559	GO:0009955	AT2G27220.1	Cupredoxin superfamily protein	plastocyanin-like domain protein
Sapur.013G045600.1	8.10854601	0.80632426	0.24316524	-3.31703	0.00909792	0.01434655	grey	-0.29819708	0.00148852	GO:0016853;GO:0005975	AT5G04880.1	DRT102	DNA-damage-repair/toleration protein (DRT102)
Sapur.009G075100.1	2484.649578	0.08706381	0.02670613	-3.31703	0.00910964	0.01434665	grey	-0.29819251	0.00296383	GO:0016614;GO:0046872;GO:0051536;GO:0051539;GO:0016491;GO:0008270	AT1G64510.1	ATC4/AC4C,CAD,CAD-C,CAD4	cinnamyl alcohol dehydrogenase family protein
Sapur.015G078700.1	0.66903883	-3.35478372	0.40860789	-3.31567	0.00916421	0.01441434	grey	-0.12953632	0.5[illegible]		AT4G23720.1	Protein of unknown function (DUF1191)	Atg8ol, putative
Sapur.003G151300.1	12.18955134	0.53152625	0.16052705	-3.31528	0.00915508	0.01441394	grey	-0.2626958	0.0028763		AT4G28481.1	mitogen-activated protein kinase kinase kinase	MAP kinase kinase kinase
Sapur.009G131000.1	488.0349451	-0.47132697	0.14219507	-3.31464	0.00917621	0.01446516	grey	-0.25814377	0.01088149		AT2G17230.1	EXL5	EXORDIUM like 5
Sapur.003G077400.1	103.3224267	-0.18962628	0.05719178	-3.31462	0.00918671	0.01448613	grey	-0.27230918	0.1638356	GO:0008152	AT4G24060.1	3-isopropylmalate dehydratase, small subunit	3-isopropylmalate dehydratase, small subunit
Sapur.007G065300.1	517.6346721	-0.18432628	0.05558746	-3.31375	0.00930545	0.01450851	grey	-0.24802929	0.01735833	GO:0045454	AT3G19780.1		NA
Sapur.004G284900.1	39.72316456	0.26135337	0.07580176	3.31364	0.00930906	0.01454135	grey	-0.26181453	0.00736265	GO:0006468;GO:0004672	AT5G18910.1	Integrin-linked protein kinase family	tyrosine kinase family protein
Sapur.014G308500.1	402.2973147	-0.27174257	0.08200492	-3.31355	0.00932195	0.01456178	grey	-0.26779088	0.00257261		AT4G27930.1	AGP26,AT4GP26	transmembrane protein, putative
Sapur.008G143000.1	8.854693884	0.30607265	0.09230072	3.311121	0.00932211	0.0145429	grey	0.25282751	0.00151183				hypothetical protein
Sapur.009G075300.1	2.941684502	0.28489246	0.08601948	3.28104659	0.00939193	0.01464835	grey	0.24073232	0.0021897		AT5G10340.1		hypothetical protein
Sapur.T170800.1	0.26031645	1.54890461	-0.46792882	-3.31015	0.00939246	0.01466907	grey	0.40293017	1.68E-07				NA
Sapur.005G100400.1	4352.008312	-0.07908793	0.02388111	-3.30991	0.00939367	0.01467262	grey	0.26128839	0.00480803		AT2G11140.1	ATPRP2,PRP2	proline-rich protein 2
Sapur.006G132100.1	15.41108689	-0.29352755	0.11984129	-3.30937	0.00939562	0.01473029	grey	-0.27627268	0.00459622	GO:0055085;GO:0022857;GO:0016021	AT1G18830.1	ATPTS,ATPMTS,PMTS	polyol/monosaccharide transporter 5
Sapur.017G097800.1	5.812667773	1.01562561	0.30606417	3.30662	0.00944324	0.01475024	grey	0.28267129	0.00317932	GO:0006468;GO:0005524;GO:0004672	AT4G16820.1	Protein kinase superfamily protein	Protein kinase superfamily protein
Sapur.015W0109100.1	1.89515543	0.67659074	0.20458318	3.307181	0.0094924	0.01484376	grey	0.23871476	0.03935201		AT5G48640.1	Transmembrane amino acid transporter family protein	NA
Sapur.016G283200.1	1.46882258	0.89896016	0.27211755	3.307162	0.00950464	0.01484606	grey	0.22938041	0.04832266	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT4G08680.1	CYP98A3	3-coumaroyl shikimate 3'-hydroxylase
Sapur.009G124700.1	73.90615937	-0.43891221	0.13273934	-3.30668	0.00944082	0.01486814	grey	-0.29751191	0.00172895	GO:0055114;GO:0051539;GO:0016491	AT5G21105.2		Plant L-ascorbate oxidase
Sapur.006G089500.2	0.49319871	1.22703861	0.37108941	-3.30656	0.00944448	0.01487732	grey	-0.3472217	8.38E-06	GO:0006096;GO:0004332	AT4G21230.1	FBA1	fructose-bisphosphate aldolase 1
Sapur.014G023500.1	11.69602887	0.60257856	0.18306916	3.3065	0.00946693	0.01487924	grey	0.22357716	0.04884357				fructose-bisphosphate aldolase
Sapur.008G117500.1	2345.518123	-0.10874226	0.03289772	-3.30547	0.00948187	0.01493065	grey	-0.26879056	0.00566421	GO:0043039;GO:0016876;GO:0005524;GO:0006418;GO:0004812;GO:0000166	AT5G26830.1		threonyl-tRNA synthetase
Sapur.003G150600.1	10.12460473	0.26135337	0.07980574	3.304839	0.00950	0.01494957	grey	-0.27452684	0.00502668		AT4G31980.1		NA
Sapur.003G131100.1	315.1128763	0.14939547	0.04528669	3.301514	0.00955851	0.01503209	grey	-0.24884659	0.00237052	GO:0016568;GO:0005634	AT4G24550.1	ATING1,ING1	RING/FYVE/PHD zinc finger superfamily protein
Sapur.008G143500.1	4.42814464	0.36153169	0.12707457	3.30373	0.00957	0.01505677	grey	0.2126327	0.01033022	GO:0005515	AT2G37880.1	Calcium-dependent lipid-binding (CaLB domain) plant phosphoribohydrolase family protein	Calcium-dependent lipid-binding (CaLB domain) plant phosphoribohydrolase family protein
Sapur.008G032300.1	55.3120264	0.21881526	0.06631545	-3.30163	0.00961262	0.01513149	grey	-0.26519806	0.00788849	GO:0016820;GO:0016471;GO:0015992	AT1G19300.1	AVMA10,VMA10	vacuolar membrane ATPase 10
Sapur.003G098700.1	1.21273844	0.85266325	0.27827954	3.30159	0.00962205	0.01516136	grey	0.25747119	0.00476611		AT5G17460.1		Galactose-binding protein
Sapur.015G045500.1	5.513643332	-0.47375926	0.14294024	-3.3004	0.00965486	0.01519654	grey	-0.25486249	0.01008525	GO:0005515;GO:0006488;GO:0005524;GO:0004672	AT5G28440.1	HSL1	HASEA-like 1
Sapur.003G075300.1	0.53952394	0.83261282	0.27194551	3.300	0.00966609	0.01520533	grey	0.30932404	0.1[illegible]				
Sapur.L52G42000.2	64.58995864	0.89842488	0.27100646	3.29966	0.00968367	0.0152397	grey	0.29786622	0.00151	GO:0005886;GO:0006468	AT3G08170.1	AT3GH,EMB1873	porphyromonas-type peptidyl-arginine deiminase family protein
Sapur.006G140000.4	24.6017986	0.26978242	0.08178816	3.299495	0.00968859	0.01524289	grey	0.24837836	0.01709176	GO:0072364;GO:0005525	AT4G24765.1	ARF1,ARL1,ATARL1	ADP-ribosylation factor 3
Sapur.014G052000.1	581.3865743	0.09379232	0.03023768	3.29927	0.00969412	0.01525475	grey	0.29998458	0.00135612	GO:0005515	AT4G40030.1	ARA8/ORL1D-1	ubiquitin-protein ligase, putative
Sapur.001G058700.1	0.36105383	1.37397346	0.41458196	3.298999	0.00970303	0.01532675	grey	0.30642431	9.50E-05				NA
Sapur.005G048600.1	7.093166153	0.36780734	0.11848945	3.29802	0.00973	0.01539179	grey	-0.20907936	0.03930192	GO:0016624;GO:0008152	AT5G09330.1	Thiamin diphosphate-binding fold (THDP-binding) superfamily protein	2-oxoisovalerate dehydrogenase alpha subunit, putative
Sapur.002G159800.2	0.82625838	-0.95361215	0.28972151	-3.29751	0.00975468	0.01534488	grey	-0.18506285	0.03102665	GO:0055114;GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005875	AT4G27500.1	F-box/ nucleotide triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain	kinesin heavy chain, putative
Sapur.014G060300.1	1.40779473	0.75164793	0.22809188	3.29701	0.00977	0.01537034	grey	0.23157975	0.05883726		AT5G15160.1	AT8S-A,ATC8S-E,J8S	cytochrome b5-like heme/steroid-binding domain protein
Sapur.T006300.1	164.2110395	-0.43903849	0.13343475	-3.29689	0.00977623	0.01537659	grey	-0.25192724	0.01132976	GO:0005634;GO:0009575;GO:0005513	AT5G18230.2	transcription regulator NOT2/NOT3/NOT5 family protein	vacuolar (H+)-ATPase G subunit
Sapur.014G051500.1	1.49470684	1.16424209	0.35322975	3.295991	0.00980751	0.01542433	grey	0.26105413	0.00894628		AT2G07461.1	Leucine-rich repeat transmembrane protein kinase	receptor-like Serine/Threonine kinase, putative
Sapur.015W0119300.1	296.1593934	0.26233472	0.07958836	3.295711	0.00981728	0.01543886	grey	0.2350999	0.03038315		AT1G31200.1	ATPP2-A9,PP2-A9	phloem protein 2-A9
Sapur.009G093000.1	5.29444212	-0.47009416	0.14266645	-3.29566	0.00988194	0.01554062	grey	-0.26831174	0.00557592	GO:0016020	AT5G07160.1	ATSYP112,SYP112	syntaxin of plants 112
Sapur.T014G086600.1	577.6273197	-0.05192226	0.01667689	-3.29426	0.00998806	0.01570188	grey	-0.28072889	0.00245166	GO:0016787	AT4G14140.1	ATPAP26,PAP29	purple acid phosphatase 29
Sapur.006G117300.1	1111.334133	-0.29514293	0.08965372	-3.29381	0.00998404	0.01554099	grey	-0.29533644	0.00107565	GO:0004857	AT5G07460.1		Plant invertase/pectin methylesterase inhibitor superfamily protein
Sapur.009G124900.1	47.20729353	0.89969016	0.27311687	3.293	0.00998133	0.01555486	grey	0.23813608	0.03267784	GO:0016758;GO:0008152	AT5G42620.1	UGT72B3	UDP-glucosyltransferase 72B3
Sapur.014G000900.1	1.39125648	1.15957101	0.34608281	3.292773	0.00992044	0.01559674	grey	0.25135283	0.01135881	GO:0003824	AT5G78955.1	CAMS1	camellosil C synthase 1
Sapur.015G042500.1	0.56869022	0.37374865	0.11924873	3.29182	0.00993679	0.01564874	grey	-0.24241002	0.02216766		AT1G27520.1		ATP binding cassette A1 binding helicases
Sapur.007G067800.1	0.49725802	1.17388219	0.35788587	3.291236	0.00995742	0.01568074	grey	0.26851009	0.00664071				NA
Sapur.016G268700.4	1.53871555	0.77536793	0.23509188	3.29076	0.00997	0.01570861	grey	0.26660607	0.00737789	GO:0005515	AT5G07330.1	Calcium-dependent lipid-binding (CaLB domain) family protein	Calcium-dependent lipid-binding (CaLB domain) family protein
Sapur.009G090400.1	2.34804861	0.62988575	0.19148792	3.289406	0.00999993	0.01578159	grey	-0.22168405	0.05294448		AT1G55P1,LISPL1	unknown seed protein like 1	dehydration-responsive protein RD22, putative
Sapur.003G061500.1	4.68876963	0.66106504	0.20142888	3.289	0.01001	0.01580033	grey	-0.25088031	0.01018363	GO:0006497;GO:0006952	AT4G19310.1	Polyketide cyclase/dehydrase and lipid transport superfamily protein	pathogenesis-related protein Bet V I family protein
Sapur.009G036400.1	68.25465571	0.28096469	0.08542112	3.28905	0.01002561	0.01580003	grey	-0.23872726	0.02598884		AT4G18180.2	F-box family protein	F-box plant protein
Sapur.016G297700.1	449.6891161	0.39118323	0.12043845	-3.28897	0.01003541	0.01580368	grey	-0.28350801	0.00382668	GO:0008266	AT5G57040.1	BIGYN,PIS1A	Tetratricopeptide repeat (TPR)-like superfamily protein	fission 1 protein
Sapur.003G161800.2	136.6818418	0.24807999	0.08624795	3.288483	0.01007287	0.01583037	grey	0.21862892	0.03802591		AT5G25180.1	Late embryogenesis abundant protein (LEA) family protein	late embryogenesis abundant protein (LEA) family protein
Sapur.013G020000.1	724.2628881	-0.38027234	0.11546144	-3.28824	0.01008816	0.01586333	grey	-0.2467551	0.01183664	GO:0008146	AT5G07180.1	ATSGT1B,ATSTA,CORI-73,SGT	sulfotransferase 16	flavonol 3-sulfotransferase, putative
Sapur.010G040900.1	1350.656663	-0.07127748	0.02168427	-3.28769	0.01009238	0.01585952	grey	-0.25183876	0.0[illegible]27		AT1G66410.2	AT-AHA9,ATCRY2,CRY2	cryptochrome protein 28	cryptochrome protein 28
Sapur.018G024400.1	348.2022661	-0.11071782	0.03368172	-3.28674	0.01010353	0.01592545	grey	-0.24519014	0.01937805		AT4G24970.1		alpha/beta-Hydrolases superfamily protein	NA
Sapur.T014G061700.1	14.31767663	0.37358788	0.11362871	3.28551	0.01018554	0.01600364	grey	-0.22208184	0.05181649		AT4G20230.1		hypothetical protein
Sapur.003G103300.1	329.2638112	0.11842764	0.03606593	3.283856	0.01021973	0.01608801	grey	-0.22442272	0.00476223	GO:0005085;GO:0016021;GO:0008643;GO:0005515;GO:0000139	AT5G41760.1	Nucleotide-sugar transporter family protein	UDP-galactose transporter
Sapur.T170800.1	0.26031645	1.54890461	-0.47126944	-3.28364	0.01024	0.01609947	grey	0.28980602	0.02236483		AT4G23810.1		cryptochrome protein 28
Sapur.016G043400.2	1.66822798	-0.76118327	0.23182615	-3.28367	0.01023516	0.01610288	grey	-0.13672231	0.0888079	GO:0008152;GO:0003824	AT5G60510.1	ATP-dependent caseinolytic (Clp) protease/cocitonase family protein	enoyl-CoA hydratase
Sapur.T003C154G0.1	7.820172544	0.66183532	0.19907479	3.283368	0.01025702	0.01611689	grey	-0.26793014	0.00906353	GO:0016491;GO:0016649	AT5G62180.1	Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.001G007800.1	162.7162627	0.30776425	0.09375675	3.282339	0.01029498	0.01617175	grey	-0.24313423	0.02117549		AT2G20480.1		hypothetical protein
Sapur.004G060500.1	3.79561979	0.34389843	0.10667682	-3.28161	0.01032152	0.01621268	grey	-0.27815159	0.00421929		AT3G62960.1		NA
Sapur.010G080300.1	240.3630092	0.22388994	0.06787952	3.28073	0.01036119	0.01624298	grey	0.24138112	0.01213104	GO:0016021	AT2G14140.1	CPuORF29	conserved peptide upstream open reading frame 29	hypothetical protein
Sapur.011G028800.2	3.55387746	-0.49161889	0.14966771	-3.28101	0.01039435	0.01624565	grey	-0.26157977	0.00752989	GO:0016301	AT4G21540.1	SPHK1	sphingosine kinase 1	D-erythro-sphingosine kinase/diacylglycerol kinase
Sapur.001G162300.1	0.38571615	0.94188579	0.41006959	3.27924	0.01041309	0.01631418	grey	0.29177762	0.00214652	GO:0004871;GO:0000160	AT4G16160.2	AHP4	HPT phosphotransfer 4	NA
Sapur.003G070500.1	1.06329293	-0.93365609	0.28453485	-3.27903	0.01041632	0.01635984	grey	-0.29480096	0.00179304	GO:0042626;GO:0008896	AT4G01880.1	PDLA1,PDLA4	DNA primase;DNA primases	DNA primase small subunit
Sapur.006G177500.1	1.24262164	1.01618386	0.30861875	3.27775	0.01044381	0.01640149	grey	0.26542689	0.00290322		AT5G47760.1		DNAse I like protein 3	NA
Sapur.016G272900.1	42.23047858	0.69580789	0.21230302	3.277413	0.01047613	0.01645332	grey	0.30593529	9.76E-05	GO:0003676	AT5G25680.1	RNA-binding (RRM/RBD/RNP motifs) family protein		eukaryotic translation initiation factor 3 subunit B
Sapur.008G143800.1	120.3583097	0.19829449	0.06051322	3.27704	0.01048	0.01647318	grey	0.23423871	0.00318301	GO:0006468;GO:0004672	AT3G18810.1	STRUBBELIG-receptor family 8	strubbelig receptor kinase, putative
Sapur.006G090800.3	3.62176435	-0.52558796	0.15885395	-3.27703	0.01049056	0.01647116	grey	-0.12680382	0.12587275	GO:0005085;GO:0046873;GO:0030001;GO:0016020	AT5G66510.2	ZIP metal ion transporter family	ZIP family transporter
Sapur.008G140400.1	1.22764542	-0.76313168	0.22935656	-3.27616	0.01052272	0.01652087	grey	-0.20372295	0.01128658	GO:0016567;GO:0006464	AT4G24330.1	ARM repeat superfamily protein	U-box protein	U-box protein
Sapur.013G120300.1	1.30662474	0.61605064	0.19734826	3.275459	0.01053	0.01653	grey	-0.20080655	0.01199882	GO:0046872;GO:0016491	AT5G06330.1	Heavy metal transport/detoxification superfamily protein	copper transporter atox1 protein, putative
Sapur.013G117200.1	19.61730876	-0.36301789	0.08022254	-3.27544	0.01055469	0.01656085	grey	-0.2341637	0.00557592	GO:0006412;GO:0005840;GO:0003735	AT5G47320.1	RPS19	ribosomal protein S19	ribosomal protein S19
Sapur.G023800.1	5.62388173	0.32582231	0.09952636	-3.27463	0.01057993	0.01660752	grey	0.25345851	0.01360477		AT4G21250.1		Histone2 dehydrogenase-like hydrolase (HAD) superfamily protein	histone2 dehydrogenase-like hydrolase domain protein
Sapur.008G261500.1	540.2408876	0.12006780	0.03667675	3.274129	0.01059881	0.01663637	grey	0.28487261	0.00311265		AT5G55540.1	LETM1-like protein	LETM1 and EF-hand protein
Sapur.014G194900.1	2.6155584	0.54758394	0.16729334	3.274069	0.01060103	0.01664251	grey	0.26276167	0.00771117	GO:0009378;GO:0006310;GO:0006281;GO:0005515	AT4G31550.1	AAA-type ATPase family protein	AAA-type ATPase family protein
Sapur.013G102600.1	10.76839563	0.74788192	0.22845564	3.273583	0.01061933	0.01666621	grey	0.2289763	0.00739429	GO:0046872;GO:0000001	AT5G06330.1	Heavy metal transport/detoxification superfamily protein	copper transporter atox1 protein, putative
Sapur.T014G139900.1	1.67461055	0.52180884	0.16000834	3.273	0.01063137	0.01671804	grey	-0.28387924	0.00187204		AT5G07210.1	NADP(+)-linked oxidoreductase family protein	aldo/keto reductase family protein
Sapur.013G022100.1	28.66525055	0.32327199	0.09879718	3.272648	0.01065453	0.01671907	grey	0.27185752	0.00157648		AT5G05345.1	Chaperone DnaJ-domain superfamily protein	chaperone protein DnaJ
Sapur.016G258000.1	210.1238845	0.18385388	0.05623149	3.272	0.01066834	0.01673426	grey	0.23121751	0.01127453		AT1G32351.1		transmembrane protein, putative
Sapur.018G041500.1	7.56245262	0.77496729	0.23658895	3.272329	0.01066655	0.01673635	grey	-0.29324798	0.00176166				NA
Sapur.001G176900.2	8.51686359	0.33215466	0.10153837	-3.27208	0.01067608	0.01675925	grey	-0.24138735	0.00232254	GO:0016021	AT7MN1,TMN1	transmembrane nine 1	transmembrane 9 superfamily protein
Sapur.013G087700.1	790.7955421	-0.16878355	0.05157853	-3.27187	0.01069388	0.01676195	grey	-0.22164648	0.01231564	GO:0005515	AT1G66480.1	HIT zinc finger (PARA-like conserved region	HIT zinc finger and PARA-like domain-containing protein, putative	HIT zinc finger and PARA-like domain-containing protein, putative
Sapur.002G078600.4	1.51675163	0.70161855	0.21449056	3.271071	0.01070411	0.01680857	grey	0.23227164	0.00419938	GO:0008168	AT5G24140.1	OSU1,QJ/JA2,TQ2	5-adenosyl-L-methionine-dependent methyltransferases superfamily protein	5-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.005G144300.2	7.757944	0.52408161	0.16277647	3.270793	0.01070483	0.01682429	grey	0.24974411	0.01608185	GO:0005515	AT4G38650.1	RTBP(CC domain-containing protein)	C2-RTBs1- -Ero1- -N-terminal-to-kinase-complex-4/TH-domain-with-Ca2+-binding-protein-1	ubiquitin-conjugating enzyme E2
Sapur.003G091600.2	7.16448295	0.52958876	0.16200747	-3.26861	0.01076643	0.01693611	grey	-0.23121602	0.01023158		AT5G63800.1	UBC5	ubiquitin-conjugating enzyme 5	ubiquitin-conjugating enzyme E2
Sapur.015G084000.3	0.90343741	0.36770314	0.29304561	3.268766	0.01078175	0.01694384	grey	0.05696176	0.47631869	GO:0016021;GO:0006605;GO:0004348	AT5G49920.1	Beta-glucosidase, GBA2 type family protein	beta-glucosidase, GBA2 type family protein
Sapur.008G137600.2	0.32462214	2.00485198	0.61468676	3.268054	0.01082897	0.01698556	grey	0.26384773	0.00839479	GO:0016021	AT3G24430.1	ATMDH3,PHD1	phosphate 1	phosphate transporter Pho1
Sapur.015G167000.1	0.42137369	0.81374621	0.55006811	-3.2676	0.01086648	0.01705114	grey	-0.25006426	0.01585432		AT5G44160.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	lipid transfer protein, putative
Sapur.004G204300.1	81.54444662	0.34632374	0.10608515	-3.26698	0.01087026	0.01704789	grey	-0.24324668	0.02223316	GO:0005515	AT5G61150.1	Lish and RanBPM domains containing protein	Ran-binding protein in the microtubule-organizing centre protein
Sapur.013G135200.1	19.70045004	0.60229932	0.21189470	3.26676	0.01087855	0.01706059	grey	-0.26323701	0.00863376		AT5G11510.1	TBL37	Plant protein of unknown function (DUF828)	beclin-like AGP protein
Sapur.010G161600.1	3486.978617	0.195782	0.05994843	3.26674	0.01088736	0.01706055	grey	-0.23965509	0.03819348		AT4G02580.1	AT-HSC70-1,HSC70-HSC70-1	heat shock cognate protein 70-1	Non-cell-autonomous heat shock cognate protein
Sapur.T004000.1	0.32002164	1.05448877	0.33153356	-3.26565	0.01092138	0.01712481	grey	-0.42218026	3.64E-08		AT5G60470.1	Plant protein of unknown function (DUF247)	NA	NA
Sapur.015W0140400.1	0.72377824	1.03910809	0.31823556	3.26533	0.01093936	0.01714324	grey	-0.23393223	0.03197796				NA
Sapur.007G072200.1	2.56937713	0.57834970	0.17713040	3.265291	0.01093516	0.01714079	grey	0.22458165	0.04648851				NA
Sapur.004G302700.1	0.61656464	1.02075288	0.3183476	-3.26389	0.01098537	0.01722227	grey	0.27459551	0.00510757		AT5G26850.1	Uncharacterized protein	cyclin, putative
Sapur.003G081200.1	0.36191222	1.42012128	0.43518339	3.263376	0.01100933	0.01725882	grey	0.30953617	7.07E-05				NA
Sapur.006G089600.2	4.6506402	0.40152207	0.12304247	3.263363	0.01100991	0.01725871	grey	0.26540000	0.00771218		AT5G69030.1	BSD domain-containing protein	BSD domain protein
Sapur.001G091000.1	1.59054136	0.66248174	0.20304905	3.26368	0.01100640	0.01725863	grey	0.23779703	0.00271563	GO:0004689;GO:0005524;GO:0004672	AT4W40,WNK8	ATWNK8,WNK8	with no lysine (K) kinase 8	Serine/Threonine kinase domain protein
Sapur.005G087000.1	1.60521888	0.53673263	0.17040572	3.26248	0.01103	0.01730074	grey	-0.31343052	2.23E-05	GO:0005515	AT5G38180.1	GTG1/GTG2,GTB,GTU19	gibberellin receptor 1	NA
Sapur.001G118200.1	113.15707	-0.16708859	0.05174837	-3.26229	0.01105155	0.01732073	grey	-0.24861743	0.01687748		AT5G26310.1		hydroxyproline-rich glycoprotein family protein	LRX2, putative
Sapur.016G183700.2	-13.08126376	-0.33547346	0.10287793	-3.26107	0.01109913	0.01739281	grey	-0.27928042	0.00246115	GO:0016810;GO:0006807	AT5G22040.1	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein	carbon-nitrogen family hydrolase	carbon-nitrogen family hydrolase
Sapur.T014G000900.1	1.77440364	-0.76276426	0.23416602	-3.26081	0.01110124	0.01742581	grey	-0.27281816	0.00674584		AT2G40520.1	Disease resistance-responsive (dirigent-like protein) family protein	disease resistance-responsive (dirigent-like protein) family protein	disease resistance-responsive (dirigent-like protein) family protein
Sapur.006G207900.1	153.2550866	-0.21829552	0.06696071	-3.25965	0.01115511	0.01747804	grey	-0.26315574	0.00868867		AT3G01750.1	TESTIS/TLTS01	Testis/TSG1-like CXC domain-containing protein	cysteine-rich polycomb-like protein, putative
Sapur.010G039300.1	67.49893664	0.51528168	0.16196099	-3.25859	0.01118348	0.01752184	grey	-0.15350847	0.05493961		AT5G19220.1	ATGA1,FLA11	FASCICLIN-like arabinogalactan protein 11	1-aminocyclopropane-1-carboxylate oxidase-like protein
Sapur.019G074100.1	2.79557415	1.19825816	0.36773774	3.258547	0.01123845	0.01758425	grey	0.34863082	1.27E-05		AT4G27430.1	Domain of unknown function (DUF313)	NA	NA
Sapur.006G135400.1	96.77374264	0.20735887	0.09129015	-3.25759	0.01125	0.01762766	grey	-0.2546275	0.01185215		AT5G04910.1	FrzT pre-rRNA processing protein	FrzT pre-rRNA processing protein	FrzT pre-rRNA processing protein
Sapur.008G082000.1	349.8452163	0.17647045	0.05419639	-3.25626	0.01128916	0.01768473	grey	-0.28517337	0.00238316	GO:0016272;GO:0006457	AT5G49510.2	PFD3	prefoldin 3	prefoldin subunit 3
Sapur.006G111500.1	43.81846268	0.76568	0.23535	3.25	0.01130	0.01774324	grey	0.22368844	0.00556341	GO:0016020;GO:0008643	AT5G46290.1		proton transporter 5e561 subunit gamma	proton transporter 5e561 subunit gamma
Sapur.013G129500.3	17.64458114	0.34016664	0.10459636	-3.25488	0.01134139	0.01777688	grey	-0.24291604	0.02294254	GO:0007264;GO:0005525	AT5G59840.1	Ras-related small GTP-binding family protein	small GTP-binding protein	small GTP-binding protein
Sapur.003G179000.1	0.61656464	1.02075288	0.3183476	3.254433	0.01136	0.01780173	grey	-0.25153362	0.00229898		AT5G05760.1	Spase class 1 family protein	NA	NA
Sapur.006G601000.2	10.46053664	0.38264579	0.11763659	3.252795	0.01144759	0.01789735	grey	0.2932865	0.00193121	GO:0005085;GO:0042626;GO:0016021;GO:0006810;GO:0005524;GO:0016887	AT3G28345.1	ABC transporter family protein	multidrug/pheromone exporter, MDR family, ABC transporter family protein, putative	multidrug/pheromone exporter, MDR family, ABC transporter family protein, putative
Sapur.016G089600.1	1.57255005	0.77480193	0.23703846	-3.2527	0.01143667	0.01791072	grey	-0.23816232	0.00266754	GO:0008168;GO:0006479	AT3W9T4A,PRMT4A	protein arginine methyltransferase 4A	Histone-arginine N-methyltransferase	Histone-arginine N-methyltransferase
Sapur.004G051300.1	10.36819454	0.32503177	0.10125853	3.25146	0.01148599	0.01798571	grey	0.23054628	0.03567983		AT4G27861.1		hypothetical protein	NA
Sapur.003G021400.1	0.51097311	2.41785336	0.74376602	3.250884	0.01151237	0.01802755	grey	0.22873657	0.03398931		AT3G26190.1

Sapur.008G151700.1	1.651493041	-0.66606462	0.209745389	-3.19246	0.00141066	0.022595377	grey	-0.235427806	0.002995882	AT3G32340.1	MENG	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.001G036900.1	3.770272166	0.676017318	0.211957816	3.191943	0.00141191	0.001295213	grey	0.233417023	0.003260083	GO:0016020;GO:0006810;GO:0005215	AT5G08830.1	ATRAMP1;NRAMP1;PMIT1
Sapur.002G284800.2	40.04566014	0.216879095	0.267636869	3.189137	0.00141199	0.002301729	grey	0.275236864	0.00047574		AT1T8310.1	Protein kinase superfamily protein
Sapur.008G094400.1	0.582653276	0.071908941	0.335645808	3.190714	0.00141918	0.002308384	grey	0.246113573	0.001889409	GO:0016758;GO:0008152	UGT73B5	UDP-glucosyl transferase 73B5
Sapur.010G144500.1	3.87556682	0.527398857	0.165267547	3.190579	0.00141983	0.002309331	grey	0.260780673	0.000971233	GO:0016157		INV/AS domain-containing protein
Sapur.002G171300.1	15.9415892	0.310535375	0.097273722	3.190518	0.00141019	0.002309672	grey	0.260136809	0.001000831	GO:0043565;GO:0006355;GO:0003700	AT2G04880.2	ATWRKY1;WRKY1;ZAP1
Sapur.012G095200.1	2.860963697	0.548836018	0.17209071	3.189998	0.00142738	0.002312548	grey	0.24094801	0.00241391		AT2G7975.1	Yos1-like protein
Sapur.005G091100.1	0.354557553	1.816451058	0.569060757	3.188501	0.00143123	0.002324935	grey	-0.30612685	8.17E-05		AT5G18190.2	AtRLP9;RLP9
Sapur.019G073900.1	28.62617224	-0.276181833	0.086645563	-3.18764	0.00143406	0.002331493	grey	-0.09987442	0.213302032	GO:0008016;GO:0008470;GO:0006400		
Sapur.005G071200.1	58.94862112	-0.183602569	0.057629451	-3.18759	0.00143409	0.002331764	grey	-0.266166344	0.002848886			
Sapur.003G131400.1	12.00326427	-0.385596771	0.11941027	-3.1873	0.00143606	0.002333854	grey	-0.26249453	0.007085125	GO:0009228;GO:0004417	AT3G24030.1	hydroxyethylthiazole kinase family protein
Sapur.008G179000.2	2.248180137	-0.275238423	0.18322888	-3.18723	0.00143649	0.002334286	grey	-0.238916712	0.002582866		AT3G15451.1	Protein kinase family protein
Sapur.001G088100.1	160.5728077	-0.342657819	0.107532275	3.186825	0.00143844	0.002337347	grey	0.245065607	0.002488055	GO:0004857	AT4G47670.1	Plant invertase/pectin methylesterase inhibitor superfamily protein
Sapur.002G262600.1	0.834406285	-0.230682813	0.072308232	-3.18682	0.00143907	0.002338576	grey	-0.242670327	0.002081181			
Sapur.001G050900.1	161.1826354	-0.165728832	0.052017748	-3.18601	0.00144519	0.002343375	grey	-0.252118876	0.001464665	GO:0005515	AT4G48800.1	Sterile alpha motif (SAM) domain-containing protein
Sapur.010G288400.1	28.14743859	-0.268008403	0.102337308	-3.18401	0.00145255	0.002358691	grey	-0.255486104	0.077162385	GO:0005739;GO:0004129	AT5G48050.2	Cytochrome c oxidase, subunit VIb family protein
Sapur.005G177200.2	1.062276813	0.852496058	0.267787833	3.183476	0.00145183	0.002362752	grey	0.178487706	0.025318854		AT3G31260.1	APG8;ATAPG8
Sapur.004G208100.1	843.6893304	-0.147222145	0.046256488	-3.18274	0.00145891	0.002368461	grey	-0.248410804	0.001706244		AT3G11720.2	AtMYB30;RL3
Sapur.002G170501.700.1	0.615454983	-0.192461528	0.060486529	-3.18246156	0.00146056	0.00237267	grey	-0.246924508	0.001444444		AT5G12830.1	
Sapur.006G019700.2	4.12068856	-0.466158392	0.146485417	-3.18228	0.00146185	0.002371764	grey	-0.111884074	0.163152966	GO:0005525	emb1688	Minichromosome maintenance (MCM2/3/5) family protein
Sapur.007G091600.2	6.513438359	-0.242078876	0.076097452	-3.18179	0.00146672	0.002375892	grey	-0.092697426	0.240823847	GO:0006950;GO:0006488;GO:0005524;GO:0004672	AT5G20940.1	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
Sapur.010G093600.1	0.638123585	-1.005270372	0.315080632	-3.18143	0.00146548	0.002378148	grey	0.24408673	0.002064138		AT5T1681.1	
Sapur.001G113100.1	0.373222177	1.321361796	0.416703875	3.180117	0.00147157	0.002388177	grey	0.305058888	0.00127			
Sapur.015G190400.1	161.8657887	-0.208654178	0.065435336	-3.17954	0.00147597	0.002392639	grey	-0.284325736	0.000307078		AT5G1745.1	Tudor/PWWP/MBT superfamily protein
Sapur.006G186900.1	644.6627251	-0.109776682	0.03455187	-3.17949	0.00147631	0.002392963	grey	-0.304534007	0.000185271		AT2G47470.1	phosphoglycerate/bisphosphoglycerate-related / PAF2-related
Sapur.003G063300.1	11.32615725	0.333403175	0.104908114	3.178307	0.00148139	0.002302186	grey	-0.247096571	0.010809312		AT4G12230.3	WWE protein-protein interaction domain protein family
Sapur.008G172300.1	0.8101201	0.855451513	0.269196179	-3.17766	0.00148665	0.002307185	grey	-0.21277729	0.007182219			
Sapur.005G051100.1	2.480188027	0.683181085	0.214733829	3.177369	0.00148677	0.002306426	grey	-0.210115179	0.002467511		AT3G13135.1	INH3
Sapur.017G012100.1	7.888859723	-0.893878794	0.281385328	-3.17671	0.00148958	0.002316611	grey	-0.287798672	0.002572523		AT5G04570.1	Plant protein of unknown function (DUF247)
Sapur.013G200600.1	207.7788744	-0.364841578	0.116323326	-3.17633	0.00149148	0.002317848	grey	-0.24924568	0.016444444		AT3G18461.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.003G167500.1	0.478273882	-1.167646209	0.367634182	-3.17611	0.00149252	0.002319051	grey	-0.294215947	0.000183885	GO:0006508;GO:0005622;GO:0004198	AT3G15350.3	ATDEK1;DEK1;EMB1275;EM
Sapur.009G248900.1	28.06672325	-0.470283	0.150281455	3.1480744*	0.17506	0.00151791	grey	-0.199275679	0.012301562	GO:0005515;GO:0016491;GO:0007017	AT1G07920.1	elongation factor-1-1
Sapur.010G093900.1	14.15420147	-0.290437875	0.091452137	-3.17574	0.00149547	0.002321809	grey	-0.220329398	0.005674945		AT5G3375.1	Metallo-hydrolase/oxidoreductase superfamily protein
Sapur.009G145100.1	21.54449164	-0.513172234	0.161780834	-3.17548	0.00149669	0.002322722	grey	-0.156274691	0.013237073	GO:0016042;GO:0006629	AT5G49650.1	alpha/beta-Hydrolases superfamily protein
Sapur.015G190400.1	108.0684265	0.176036072	0.055439748	3.175268	0.00149698	0.00232534	grey	0.272910338	0.000545972		AT5G29310.1	Pentatricopeptide repeat (PPR) superfamily protein
Sapur.005G046100.7	1.765727867	0.189187876	0.059577412	-3.18172	0.00148344	0.002375892	grey	-0.092697426	0.240823847	GO:0005515	AT2G4840.1	G2484-1-2;G2484-1
Sapur.008G151100.2	4.026593786	-0.631906425	0.199029347	-3.17494	0.00148665	0.002327737	grey	-0.159613184	0.046126577		AT1G10745.3	alpha/beta-Hydrolases superfamily protein
Sapur.016G159500.1	3.952529158	0.524337663	0.165149699	3.174923	0.00149876	0.002377776	grey	0.214834211	0.007109395	GO:0006499	AT4G42280.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.002G067500.1	3.055455009	-0.644632752	0.203264867	-3.16046351	-3.17383	0.00151816	grey	-0.364634007	0.000185271		AT5G47470.1	replication factor C subunit 5
Sapur.018G071200.1	11.33415485	0.349797467	0.110298833	3.171419	0.00151692	0.002355714	grey	0.267892605	0.006690088	GO:0007264;GO:0005525	AR4;AT4G27440.2;TA:AT	Ras-related small GTP-binding family protein
Sapur.009G051300.1	2.725079527	-0.273180095	0.19984837	-3.1714	0.00151752	0.002355741	grey	-0.238785926	0.002975677			
Sapur.016G239400.1	1.870142885	-0.870899693	0.27463709	-3.17109	0.00151866	0.002358139	grey	-0.185592721	0.019957687	GO:0005975;GO:0004650	AT5G14650.1	Pectin lyase-like superfamily protein
Sapur.005G261300.1	2.334120264	0.661867315	0.145026638	3.1704	0.00152249	0.002364152	grey	-0.214807613	0.006933964	GO:0008654;GO:0000015;GO:0004512	AT1P52;ATMIPS2;MIPS2	Myo-inositol 1-phosphate synthase 2
Sapur.T065000.1	7.477605529	-0.356499205	0.110610597	-3.16876	0.00153097	0.002376731	grey	-0.232664166	0.003232424		AT3G28370.1	
Sapur.003G068500.1	19.82926767	-0.403016647	0.127250128	-3.16851	0.00153249	0.002378603	grey	-0.254197365	0.001022322		AT3T7132.1	cobalt ion binding
Sapur.019G108100.1	218.7954889	0.296030964	0.093720711	3.168253	0.00153178	0.002380623	grey	0.214372325	0.007017087	GO:0043565;GO:0006355;GO:0003700	AT2G38470.1	WRKY DNA-binding protein 33
Sapur.015G275200.1	10.16050353	-0.352249859	0.110587382	3.168016	0.00153433	0.002383459	grey	0.253879424	0.003346607	GO:0044030;GO:0006400;GO:0008270	AT4G14980.1	Acyl-CoA N-acetyltransferase with RING/FYVE/PHD-type zinc finger protein
Sapur.002G046600.1	4.626716477	-0.348585368	0.110065511	-3.16707	0.00153816	0.002389967	grey	0.245057563	0.002406043	GO:0007165;GO:0005515;GO:0005515	AT5G36930.2	Disease resistance protein (TIR-NBS-LRR class) family
Sapur.001G154200.1	0.44425136	1.084392765	0.342468568	3.166401	0.00154338	0.002395164	grey	-0.302898796	0.001147762	GO:0016747;GO:0008610;GO:0016020;GO:0006633	AT5G26640.1	Hypoxia-responsive family protein
Sapur.019G066800.1	1.258179376	-0.707018842	0.223326014	-3.16629	0.00154508	0.002396129	grey	0.300046628	0.003134624	GO:0006355;GO:0003700	AT2G18160.1	Target of Myb protein 1
Sapur.010G241100.1	2.782624222	-0.604137772	0.191288353	-3.15806	0.00158826	0.002462912	grey	-0.247012566	0.010181588	GO:0016787;GO:0005634;GO:0004672	AT3G01120.2	dicer-like 2
Sapur.009G152300.1	73.69739873	-0.262618771	0.083061585	-3.15748	0.00159221	0.002467013	grey	-0.218235977	0.010460701		AT2G45675.1	
Sapur.018G093600.1	84.52443433	-0.245804049	0.07787926	-3.1567	0.00159574	0.002472988	grey	-0.24051392	0.002411611	GO:0006468;GO:0005634;GO:0004672	AT2G17560.1	Protein kinase family protein
Sapur.008G230300.1	6.492872646	-0.208198693	0.066000969	-3.15549	0.00160522	0.002486111	grey	0.140809621	0.151649	GO:0005515;GO:0016301	AT4G19210.1	mitogen-activated protein kinase 16
Sapur.019G090000.1	57.9306577	-0.124025165	0.039339681	-3.15367	0.00161827	0.002507923	grey	-0.302773595	0.000160065	GO:0045454;GO:0015035;GO:0006662	AT3MAA;ATM4;TRX-M4	MRX16
Sapur.006G227700.1	2.370789343	-0.623794584	0.208605022	-3.15367	0.00161864	0.002507923	grey	-0.243920063	0.002171123	GO:0005515;GO:0006508	THA1	thioredoxin M-type 4
Sapur.012G020300.2	11.13359864	0.309443604	0.09816751	3.1522	0.00163054	0.002511751	grey	-0.212997355	0.007299068	GO:0016491;GO:0003774		threonine aldolase 1
Sapur.005G131200.1	2.95015679	0.081653436	0.343207486	3.151602	0.00162274	0.002516739	grey	0.235249957	0.003019162	GO:0051015;GO:0007015		myosin heavy chain-related
Sapur.008G142200.1	123.9695412	0.201356161	0.064828971	3.15154	0.00162412	0.002517157	grey	0.227624437	0.004105728	GO:0005515		
Sapur.013G098200.1	297.3992847	0.149109537	0.047133704	-3.15151	0.00162426	0.00251731	grey	-0.247698843	0.001761526	GO:0019201;GO:0006139;GO:0005524	AM42	adenosine monophosphate kinase
Sapur.016G259300.1	0.486176234	-1.242804476	0.394435157	-3.15145	0.00162459	0.002517651	grey	0.210441029	0.008109488			
Sapur.007G039900.1	2.850630301	-0.548538137	0.174113686	-3.15046	0.00163038	0.002526129	grey	-0.207173232	0.009818178			Disease resistance protein (CC-NBS-LRR class) family
Sapur.001G080300.1	92.9617383	-0.313356846	0.099468528	-3.1525	0.00163124	0.002527731	grey	-0.2507821	0.015338877	GO:0009733	AT5G61600.1	SAUR-like auxin-responsive protein family
Sapur.019G013800.1	2.435401324	0.742595829	0.235640877	3.150115	0.00163263	0.002528664	grey	-0.233107305	0.003032604	GO:0003677	AT4G21730.1	BED zinc finger /hAT family dimerization domain
Sapur.004G142000.1	46.11881589	-0.232354125	0.105005502	-3.15011	0.00163328	0.002528664	grey	-0.27027365	0.000618459			
Sapur.013G190300.1	3.941033855	1.051261521	0.333725709	3.150077	0.00163227	0.002528852	grey	0.131739369	0.100363863	GO:0016788	AT5G03630.1	GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.012G081000.1	1.272019923	0.818323188	0.259801141	-3.14861	0.00163789	0.002531076	grey	-0.228101993	0.006054423	GO:0055085;GO:0016020;GO:0015297;GO:0015238;GO:0006855	AT5G33550.1	MATE efflux family protein
Sapur.003G063800.1	163.3491125	0.202378835	0.064188174	3.14878	0.00163937	0.002528664	grey	-0.205297483	0.008898684			
Sapur.017G021800.1	5.185665147	-0.558180429	0.177134564	-3.14934	0.00163296	0.002534878	grey	-0.263437272	0.008214154		AT4G42250.1	
Sapur.006G189000.1	536.429176	-0.099297541	0.031539448	-3.14806	0.00164093	0.002541554	grey	-0.252127994	0.004452275	GO:0005515	AT8P42;8PM2	BTB-POZ and MATH domain 2
Sapur.016G099900.1	36.46093792	-0.022530851	0.334815215	-3.14804	0.00164137	0.002545834	grey	-0.356328272	4.64E-06			
Sapur.006G184900.1	27.57629834	-0.402457142	0.127902984	-3.14658	0.00165192	0.002556418	grey	-0.273832157	0.005202183	GO:0006508;GO:0004185	AT4G15000.1	scp50
Sapur.002G191400.1	0.490067425	-0.079371181	0.343164629	-3.14524	0.00165913	0.002565155	grey	-0.238026923	0.002615767	GO:0006367;GO:0006810;GO:0005622	AT5G25150.2	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain
Sapur.019G088480.1	318.8724616	-0.149281884	0.047464614	-3.14524	0.00165924	0.002565991	grey	-0.255400237	0.001452367	GO:0008080;GO:0000159	AT3T2725.1	Protein phosphatase 2A regulatory subunit PR55
Sapur.014G134400.1	3.862632824	-0.429060303	0.136407112	3.145042	0.00166063	0.002571573	grey	-0.249303844	0.016682259	GO:0071165;GO:0000150;GO:0000160	AT4G35750.1	AHK2;HK2
Sapur.008G138300.1	73.70686249	-0.172485449	0.058395428	-3.14493	0.00166264	0.002572455	grey	-0.242884123	0.002232351	GO:0005515;GO:0004672	AT4G37580.1	Leucine-rich repeat protein kinase family protein
Sapur.003G083200.1	2.875378503	0.541295223	0.171152047	3.144319	0.00166747	0.002577588	grey	-0.242823612	0.010716394	GO:0003677	AT4G11400.1	ARID/BRIGHT DNA-binding domain;ELM2 domain protein
Sapur.008G196200.3	1.963075005	-0.989009256	0.31466774	-3.14303	0.00167103	0.002588956	grey	-0.113189866	0.181338681	GO:0055124;GO:0003676	AT5G59990.1	DEAD/H-box RNA helicase family protein
Sapur.017G037600.1	25.91555355	-0.060860868	0.019284754	-3.13987	0.00168246	0.002592607	grey	-0.227188255	0.007087227	GO:0016491;GO:0016646	AT2G46690.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.011G061700.1	819.4083711	0.153186827	0.048730117	3.139788	0.00169092	0.002617285	grey	-0.216869274	0.006411892	GO:0005515	T8L41	TRICHOME BIREFRINGENCE-LIKE 41
Sapur.013G088000.1	184.9487016	0.172368849	0.054959621	3.13849	0.00169216	0.002620794	grey	-0.262192674	0.000922916	GO:0006287;GO:0000535		RING-U box superfamily protein
Sapur.016G054700.1	13.12838835	-0.280614118	0.089431918	-3.1384	0.00169709	0.002629434	grey	-0.238178614	0.002665664		AT5G10140.1	REC42
Sapur.005G184800.2	4.054291931	-0.300987984	0.4173679	-3.13769	0.00170138	0.002633034	grey	-0.213610405	0.002725076		AT4G26280.1	KAS I;KAS1
Sapur.019G141300.5	0.397010886	-3.354971577	0.431696976	-3.13673	0.00170849	0.002646055	grey	-0.35256699	4.66E-06	GO:0005114;GO:0009088;GO:0008839	AT5G21100.1	crr1
Sapur.006G184200.1	1.023189065	-1.024664628	0.32671884	-3.1362	0.00171152	0.002648603	grey	-0.239164369	0.003026619	GO:0043565;GO:0006355;GO:0003700	AT4G37590.1	WRKY DNA-binding protein 63
Sapur.001G189100.1	37.80794557	-0.239839897	0.076478154	-3.13606	0.00172155	0.002669813	grey	-0.244112336	0.002062888	GO:0022900;GO:0005747;GO:0005739	AT5G14450.1	NADH dehydrogenase (ubiquinone) b
Sapur.018G035100.1	0.614318586	-1.4048763	0.448035657	-3.13581	0.00172838	0.002681863	grey	-0.277537235	0.000426544			
Sapur.010G007800.1	3.109954832	-0.484697483	0.154559191	-3.13471	0.00173207	0.002691686	grey	-0.329437068	2.52E-05			
Sapur.002G145500.1	231.4128608	-0.170953323	0.054539747	-3.13393	0.00173795	0.002698562	grey	-0.278353534	0.000415657		AT2G31360.1	PYL8;RCAR1
Sapur.012G049700.1	12.95049727	-0.353120364	0.113398085	3.133921	0.00173151	0.002678733	grey	0.166356658	0.037313639		AT4G27390.1	
Sapur.004G039900.3	0.923831305	-0.863407952	0.27565325	-3.1322	0.00173509	0.002683864	grey	-0.243947391	0.002077812		AT5G29240.1	Protein of unknown function (DUF688)
Sapur.016G138100.1	3.105882174	-0.329648429	0.10764522	3.131928	0.00173622	0.002686234	grey	0.237909697	0.010263389		AT2G42240.1	Protein of unknown function (DUF247)
Sapur.T045500.1	0.20663927	1.363783804	0.435478875	3.131688	0.00173847	0.002688227	grey	0.458385796	1.57E-09		AT1G70320.1	ATCIM1;ATXPO1;HET2;XPO
Sapur.016G302020.1	14.28065668	-0.352279202	0.112609403	-3.13168	0.00173874	0.002688277	grey	-0.22308205	0.006931795	GO:0043531	AT2T3190.1	NB-ARC domain-containing disease resistance protein
Sapur.010G203800.1	1.48559501	0.664957251	0.212308151	3.130711	0.00174836	0.02697014	grey	0.194746682	0.012411273			
Sapur.009G050500.1	226.5312018	-0.218188364	0.070011548	3.130657	0.00174918	0.002697386	grey	0.217814181	0.008136351		AT5G12190.1	DGS1
Sapur.010G052400.1	4.911794266	-0.497392181	0.158896126	-3.1303	0.00174292	0.00270052	grey	-0.218441863	0.002635862		AT3G01810.3	
Sapur.018G093300.1	17.26287504	0.463126682	0.145580975	3.130288	0.00174348	0.00270052	grey	0.212171184	0.007623891		AT5G10330.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.009G081400.4	2.835278503	0.541295223	0.171152047	3.164319	0.00166747	0.002577588	grey	-0.242823612	0.010716394	GO:0003677	AT4G11400.1	ARID/BRIGHT DNA-binding domain;ELM2 domain protein
Sapur.008G196200.3	1.963075005	-0.989009256	0.31466774	-3.14303	0.00167103	0.002588956	grey	-0.113189866	0.181338681	GO:0055124;GO:0003676	AT5G59990.1	DEAD/H-box RNA helicase family protein
Sapur.017G037600.1	25.91555355	-0.060860868	0.019284754	-3.13987	0.00168246	0.002592607	grey	-0.227188255	0.007087227	GO:0016491;GO:0016646	AT2G46690.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.011G061700.1	819.4083711	0.153186827	0.048730117	3.139788	0.00169092	0.02617285	grey	-0.216869274	0.006411892	GO:0005515	T8L41	TRICHOME BIREFRINGENCE-LIKE 41
Sapur.013G088000.1	184.9487016	0.172368849	0.054959621	3.13849	0.00169216	0.002620794	grey	-0.262192674	0.000922916	GO:0006287;GO:0000535		RING-U box superfamily protein
Sapur.016G054700.1	13.12838835	-0.280614118	0.089431918	-3.1384	0.00169709	0.002629434	grey	-0.238178614	0.002665664		AT5G10140.1	REC42
Sapur.005G184800.2	4.054291931	-0.300987984	0.4173679	-3.13769	0.00170138	0.002633034	grey	-0.213610405	0.002725076		AT4G26280.1	KAS I;KAS1
Sapur.019G141300.5	0.397010886	-3.354971577	0.431696976	-3.13673	0.00170849	0.002646055	grey	-0.35256699	4.66E-06	GO:0005114;GO:0009088;GO:0008839	AT5G21100.1	crr1
Sapur.006G184200.1	1.023189065	-1.024664628	0.32671884	-3.1362	0.00171152	0.002648603	grey	-0.239164369	0.003026619	GO:0043565;GO:0006355;GO:0003700	AT4G37590.1	WRKY DNA-binding protein 63
Sapur.001G189100.1	37.80794557	-0.239839897	0.076478154	-3.13606	0.00172155	0.002669813	grey	-0.244112336	0.002062888	GO:0022900;GO:0005747;GO:0005739	AT5G14450.1	NADH dehydrogenase (ubiquinone) b
Sapur.018G035100.1	0.614318586	-1.4048763	0.448035657	-3.13581	0.00172838	0.002681863	grey	-0.277537235	0.000426544			
Sapur.010G007800.1	3.109954832	-0.484697483	0.154559191	-3.13471	0.00173207	0.002691686	grey	-0.329437068	2.52E-05			
Sapur.002G145500.1	231.4128608	-0.170953323	0.054539747	-3.13393	0.00173795	0.002698562	grey	-0.278353534	0.000415657		AT2G31360.1	PYL8;RCAR1
Sapur.012G049700.1	12.95049727	-0.353120364	0.113398085	3.133921	0.00173151	0.002678733	grey	0.166356658	0.037313639		AT4G27390.1	
Sapur.004G039900.3	0.923831305	-0.863407952	0.27565325	-3.1322	0.00173509	0.002683864	grey	-0.243947391	0.002077812		AT5G29240.1	Protein of unknown function (DUF688)
Sapur.016G138100.1	3.105882174	-0.329648429	0.10764522	3.131928	0.00173622	0.002686234	grey	0.237909697	0.010263389		AT2G42240.1	Protein of unknown function (DUF247)
Sapur.T045500.1	0.20663927	1.363783804	0.435478875	3.131688	0.00173847	0.002688227	grey	0.458385796	1.57E-09		AT1G70320.1	ATCIM1;ATXPO1;HET2;XPO
Sapur.016G302020.1	14.28065668	-0.352279202	0.112609403	-3.13168	0.00173874	0.002688277	grey	-0.22308205	0.006931795	GO:0043531	AT2T3190.1	NB-ARC domain-containing disease resistance protein
Sapur.010G203800.1	1.48559501	0.664957251	0.212308151	3.130711	0.00174836	0.02697014	grey	0.194746682	0.012411273			
Sapur.009G050500.1	226.5312018	-0.218188364	0.070011548	3.130657	0.00174918	0.002697386	grey	0.217814181	0.008136351		AT5G12190.1	DGS1
Sapur.010G052400.1	4.911794266	-0.497392181	0.158896126	-3.1303	0.00174292	0.00270052	grey	-0.218441863	0.002635862		AT3G01810.3	
Sapur.018G093300.1	17.26287504	0.463126682	0.145580975	3.130288	0.00174348	0.00270052	grey	0.212171184	0.007623891		AT5G10330.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.009G081400.4	2.835278503	0.541295223	0.171152047	3.164319	0.00166747	0.002577588	grey	-0.242823612	0.010716394	GO:0003677	AT4G11400.1	ARID/BRIGHT DNA-binding domain;ELM2 domain protein
Sapur.008G196200.3	1.963075005	-0.989009256	0.31466774	-3.14303	0.00167103	0.002588956	grey	-0.113189866	0.181338681	GO:0055124;GO:0003676	AT5G59990.1	DEAD/H-box RNA helicase family protein
Sapur.017G037600.1	25.91555355	-0.060860868	0.019284754	-3.13987	0.00168246	0.002592607	grey	-0.227188255	0.007087227	GO:0016491;GO:0016646	AT2G46690.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.011G061700.1	819.4083711	0.153186827	0.048730117	3.139788	0.00169092	0.02617285	grey	-0.216869274	0.006411892	GO:0005515	T8L41	TRICHOME BIREFRINGENCE-LIKE 41
Sapur.013G088000.1	184.9487016	0.172368849	0.054959621	3.13849	0.00169216	0.002620794	grey	-0.262192674	0.000922916	GO:0006287;GO:0000535		RING-U box superfamily protein
Sapur.016G054700.1	13.12838835	-0.280614118	0.089431918	-3.1384	0.00169709	0.002629434	grey	-0.238178614	0.002665664		AT5G10140.1	REC42
Sapur.005G184800.2	4.054291931	-0.300987984	0.4173679	-3.13769	0.00170138	0.002633034	grey	-0.213610405	0.002725076		AT4G26280.1	KAS I;KAS1
Sapur.019G141300.5	0.397010886	-3.354971577	0.431696976	-3.13673	0.00170849	0.002646055	grey	-0.35256699	4.66E-06	GO:0005114;GO:0009088;GO:0008839	AT5G21100.1	crr1
Sapur.006G184200.1	1.023189065	-1.024664628	0.32671884	-3.1362	0.00171152	0.002648603	grey	-0.239164369	0.003026619	GO:0043565;GO:0006355;GO:0003700	AT4G37590.1	WRKY DNA-binding protein 63
Sapur.001G189100.1	37.80794557	-0.239839897	0.076478154	-3.13606	0.00172155	0.002669813	grey	-0.244112336	0.002062888	GO:0022900;GO:0005747;GO:0005739	AT5G14450.1	NADH dehydrogenase (ubiquinone) b
Sapur.018G035100.1	0.614318586	-1.4048763	0.448035657	-3.13581	0.00172838	0.002681863	grey	-0.277537235	0.000426544			
Sapur.010G007800.1	3.109954832	-0.484697483	0.154559191	-3.13471	0.00173207	0.002691686	grey	-0.329437068	2.52E-05			
Sapur.002G145500.1	231.4128608	-0.170953323	0.054539747	-3.13393	0.00173795	0.002698562	grey	-0.278353534	0.000415657		AT2G31360.1	PYL8;RCAR1
Sapur.012G049700.1	12.95049727	-0.353120364	0.113398085	3.133921	0.00173151	0.002678733	grey	0.166356658	0.037313639		AT4G27390.1	
Sapur.004G039900.3	0.923831305	-0.863407952	0.27565325	-3.1322	0.00173509	0.002683864	grey	-0.243947391	0.002077812		AT5G29240.1	Protein of unknown function (DUF688)
Sapur.016G138100.1	3.105882174	-0.329648429	0.10764522	3.131928	0.00173622	0.002686234	grey	0.237909697	0.010263389		AT2G42240.1	Protein of unknown function (DUF247)
Sapur.T045500.1	0.20663927	1.363783804	0.435478875	3.131688	0.00173847	0.002688227	grey	0.458385796	1.57E-09		AT1G70320.1	ATCIM1;ATXPO1;HET2;XPO
Sapur.016G302020.1	14.28065668	-0.352279202	0.112609403	-3.13168	0.00173874	0.002688277	grey	-0.22308205	0.006931795	GO:0043531	AT2T3190.1	NB-ARC domain-containing disease resistance protein
Sapur.010G203800.1	1.48559501	0.664957251	0.212308151	3.130711	0.00174836	0.02697014	grey	0.194746682	0.012411273			
Sapur.009G050500.1	226.5312018	-0.218188364	0.070011548	3.130657	0.00174918	0.002697386	grey	0.217814181	0.008136351		AT5G12190.1	DGS1
Sapur.010G052400.1	4.911794266	-0.497392181	0.158896126	-3.1303	0.00174292	0.00270052	grey	-0.218441863	0.002635862		AT3G01810.3	
Sapur.018G093300.1	17.26287504	0.463126682	0.145580975	3.130288	0.00174348	0.00270052	grey	0.212171184	0.007623891		AT5G10330.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.009G081400.4	2.835278503	0.541295223	0.171152047	3.164319	0.00166747	0.002577588	gr

Sapur.003G014900.2	10.0903362	2.07122896	0.088637671	3.059905	0.002214068	0.003399963	grey	0.239280588	0.002542423	GO:0005515		TOPLESS-related 1	topless-related protein
Sapur.014G032000.2	24.74150706	-0.22267623	0.072772382	-3.0599	0.002214077	0.003399963	grey	-0.250320558	0.001567221			PPP06 putative thiol peptidase family protein	PPP06 thiol peptidase family protein, putative
Sapur.016G014700.1	16.41803466	-0.45287007	0.148018915	-3.05656	0.002214611	0.003400695	grey	-0.24013915	0.002409014	GO:0042545;GO:0030598;GO:0005618		Pectin lyase-like superfamily protein	pectinesterase
Sapur.009G022100.4	0.356904152	-1.2105182	0.395672116	-3.0594	0.002217828	0.003405486	grey	-0.374651132	1.34E-06				transmembrane protein, putative
Sapur.016G230300.3	21.5883557	0.273589382	0.088994257	3.05868	0.002223121	0.003413375	grey	-0.250185537	0.001576731			ACT7 actin 7	actin
Sapur.15WG0013300.1	1.064828887	0.812574512	0.265734335	3.057845	0.002229346	0.003422773	grey	-0.210054307	0.008279197			mucin-related	mucin-like protein
Sapur.009G007000.1	7.577193904	0.314216331	0.102842234	-3.05532	0.002248176	0.003451524	grey	-0.228898286	0.003917482	GO:0003677;GO:0009725;GO:0006355;GO:0005634		ARF10 auxin response factor 10	auxin response factor
Sapur.15WG0041000.1	929.5230715	-0.16613794	0.054382355	-3.05499	0.002250647	0.003455156	grey	-0.24772064	0.0017584	GO:0016604;GO:0005634		EMB2733,ESP3 RNA helicase family protein	NA
Sapur.008G002000.1	0.334565519	-1.36603791	0.447155813	-3.05495	0.002250961	0.003455479	grey	-0.335612624	1.73E-05			ATKCC1,ATTPK1,KCC1,TTPK1 Outward rectifying potassium channel protein	outward rectifying potassium channel protein
Sapur.018G201700.1	13.02952038	-0.35281304	0.116796829	-3.05336	0.002258204	0.003468364	grey	-0.320519786	4.23E-05	GO:0005525		KAN GTPase 1	small GTPase family Ras-related nuclear family (Ran)/TC4 protein
Sapur.016G146600.1	765.1586574	0.102353171	0.033479706	3.054184	0.002259739	0.003470864	grey	0.201573654	0.011335345	GO:0045454;GO:0015035;GO:0009055		CAX interacting protein 1	monothiol glutaredoxin-S14 protein
Sapur.016G000300.1	44.46001037	-0.18582463	0.059329513	-3.06804	0.002274688	0.003496852	grey	-0.233437289	0.00225565			Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.006G146400.2	23.88958838	0.364685762	0.086656726	3.054049	0.002277755	0.003495105	grey	0.268421141	0.005676258				hypothetical protein
Sapur.016G113300.2	0.374623732	-0.24398167	0.080187692	-3.04267	0.002281023	0.003499461	grey	-0.305183231	0.003825943			HCF107 high chlorophyll fluorescent 107	high chlorophyll fluorescent 107 protein, putative
Sapur.002G001300.1	1765.911616	0.08809041	0.029281685	3.052776	0.002287255	0.003479514	grey	0.205499295	0.009834627	GO:0055114;GO:0020037;GO:0009769;GO:0004601		TAPX thylakoid ascorbate peroxidase	thylakoid-bound ascorbate peroxidase
Sapur.012G087700.1	3.365759052	-0.29291131	0.095941611	-3.05261	0.002287703	0.003481296	grey	-0.239387885	0.002545983			RDO2 bHLH-DNA-binding protein (RHD3)	ROOT HAIR defective-like protein
Sapur.006G002600.1	1575.132404	0.108298897	0.064996266	3.051231	0.002279206	0.003467214	grey	0.208315204	0.008841812			MEE9 maternal effect embryo arrest 9	maternal effect embryo arrest 9 protein, putative
Sapur.007G061100.1	255.3576533	0.250920509	0.082249434	3.050845	0.002281992	0.003501311	grey	-0.205708041	0.00978846	GO:0016757		PGM1,PGS1 plant glycogenin-like starch initiation protein 1	secondary cell wall-related glycosyltransferase family 8 protein
Sapur.005G136200.1	12.50965262	-0.45391362	0.127905054	-3.05041	0.002283210	0.003503969	grey	-0.263663661	0.001138361	GO:0005085;GO:0016021;GO:0016020;GO:0006810;GO:0005215		Major facilitator superfamily protein	peptide transporter PTR1
Sapur.T163100.1	1.280706127	-0.68623075	0.225203856	-3.04991	0.002289092	0.003511732	grey	-0.233410067	0.00326076				NA
Sapur.018G017600.1	10.53799232	-0.05188826	0.017796835	-3.04969	0.002291348	0.003513854	grey	-0.254889840	0.002767227			CHD3,CHR6,GYM,PKL,SSL2 chromatin remodeling factor CHD3 (PICKLE)	b-domodomain helicase DNA-binding protein, putative
Sapur.009G010900.1	735.2882518	-0.07846105	0.024102514	-3.04919	0.002299549	0.003519854	grey	-0.253853831	0.00134485			ATCPNIFS,ATNFS2,ATSUFS,CPNIFS chloroplastic NIFS-like cysteine desulfurase	Suf5 suffamily cysteine desulfurase
Sapur.017G046600.1	1.316645348	0.658786023	0.216101149	3.04851	0.002309881	0.003527684	grey	-0.258173884	0.005082211				NA
Sapur.005G177200.4	4.2853333	0.481288845	0.157881736	3.048412	0.002300054	0.003528639	grey	-0.254572172	0.012939272			APG6,ATAPG9 autophagy 9 (APG9)	autophagy protein Apg9 containing protein
Sapur.002G015500.1	0.52319311	-0.24398167	0.4080728	-3.04803	0.002301020	0.003529461	grey	-0.316747006	1.31E-05			AGL18,GEC16 lateral organ boundaries-domain 16	LOB domain protein, putative
Sapur.015G238900.2	5.822701629	0.77752964	0.255096164	3.047986	0.002303803	0.003533318	grey	-0.296206059	0.000145482	GO:0005524;GO:0003676;GO:0004386		DEAD/H-box RNA helicase family protein	NA
Sapur.001G051000.1	0.630645913	-0.19129478	0.390990353	-3.04694	0.002311858	0.003545586	grey	-0.254321445	0.001308126	GO:0046983		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.003G165500.1	13.15118864	0.704631832	0.241189545	3.04688	0.002312321	0.003546253	grey	-0.26093556	0.003692389			ATRAF1,RAF1,RAF2,RAF5,RAF6 rapid alkalinization factor	rapid alkalinization factor
Sapur.010G054000.4	19.03663634	0.325473292	0.108282424	3.046749	0.002313308	0.003547402	grey	-0.261240210	0.003297537	GO:0016787;GO:0008152		2o-dependent oxygenase superfamily protein	NOD 2o-dependent oxygenase family protein
Sapur.009G069700.1	314.8197924	0.108432211	0.04822783	3.0465	0.002315218	0.003550166	grey	-0.261232306	0.003197369	GO:0005634		DNA2 domain-containing protein / helicase domain-containing protein	chromatin remodeling complex subunit, putative
Sapur.15G205900.1	2.609189864	0.562696743	0.184802224	3.04645	0.002315561	0.003550693	grey	0.2296375	0.003816179				NA
Sapur.009G006100.1	232.6802796	0.272794555	0.089542129	-3.04569	0.002319145	0.003555872	grey	-0.246743461	0.003837668	GO:0004781		Pseudouridine synthase/archaeosine transglycosylase-like family protein	ATP sulfurylase
Sapur.017G082300.1	4.534546603	-0.49461271	0.162734822	-3.04509	0.002320075	0.003556157	grey	-0.263872721	0.00567686				NA
Sapur.009G022100.1	0.341862201	0.156494831	0.37984618	3.044223	0.002328602	0.003567164	grey	0.260815426	0.002109969				NA
Sapur.017G120400.1	105.1980944	-0.74152676	0.24485249	-3.0437	0.002336905	0.003582257	grey	-0.302971615	0.000114816	GO:0043531		LRR and NB-ARC domains-containing disease resistance protein	NBS-LRR type disease resistance protein
Sapur.014G026100.1	237.6134651	0.085209186	0.028142369	3.043119	0.002343652	0.003593731	grey	-0.283284603	0.000307306				signal peptidase I, putative
Sapur.002G006000.1	25.72748672	-0.53776724	0.176690935	-3.04134	0.002351298	0.003609784	grey	-0.229811136	0.003787118			CAM7 calmodulin 7	NA
Sapur.001G186400.1	729.1991244	0.255889858	0.08417298	3.041236	0.002353695	0.003610837	grey	-0.219850841	0.005661414			hetero(glycan) glucosidase 1	hypothetical protein
Sapur.010G075400.1	2.406761442	-0.72791368	0.237573725	-3.0409	0.002358743	0.003614729	grey	-0.227903484	0.00406959				NA
Sapur.001G143200.1	674.3085697	-0.20152799	0.066277595	-3.04066	0.002360156	0.003617937	grey	-0.277436013	0.000435142			Protein of unknown function (DUF2921)	transmembrane protein, putative
Sapur.004G022300.1	236.3705868	0.251898268	0.082880369	3.040288	0.002362142	0.003620849	grey	0.205291494	0.009908884				NA
Sapur.004G111900.1	3.983232733	0.560328026	0.184389756	3.039984	0.002365903	0.00362503	grey	-0.210325879	0.008223327	GO:0055114;GO:0020037;GO:0016705;GO:0005506		allene oxide synthase	fatty acid hydroperoxide lyase
Sapur.005G188000.1	37.38078604	-0.20479741	0.074265518	-3.03961	0.002368874	0.003629413	grey	-0.218547963	0.002632992			Pentatricopeptide repeat (PPR) superfamily protein	NA
Sapur.009G017900.1	4.930883591	-0.847734714	0.278818558	-3.03865	0.002373272	0.003640722	grey	-0.315697603	5.64E-05			Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/LTP family protein
Sapur.006G002200.1	0.639963248	0.191951651	0.33367742	3.038612	0.002376708	0.003646179	grey	-0.229317996	0.003766712			alpha/beta-Hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.005G164600.1	19.75016279	-0.27402998	0.090485358	-3.03833	0.002378966	0.003646389	grey	-0.223872025	0.004806612				hypothetical protein
Sapur.T182300.1	0.373681741	0.985496401	0.324358611	3.038274	0.002379377	0.003646883	grey	0.284269803	0.000388741			Exostosin family protein	NA
Sapur.006G110000.1	76.3696274	-0.318949186	0.104879127	-3.03773	0.002383666	0.003655123	grey	-0.279312665	0.001398407			Thioesterase superfamily protein	MeaC-like dehydratase
Sapur.010G171700.1	4.070205712	0.527667861	0.17370802	3.037667	0.002384175	0.003655983	grey	0.225062314	0.006597809				hypothetical protein
Sapur.005G187500.1	2.290838468	0.722761368	0.238177458	3.037592	0.002386244	0.003658253	grey	-0.218482634	0.006378879				NA
Sapur.016G145100.1	0.418135844	1.171742409	0.385811468	3.037038	0.002389151	0.003659124	grey	0.23343008	0.032358192	GO:0006355;GO:0003677		NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC domain protein
Sapur.005G071100.1	1.861180604	0.302215242	0.099583369	3.036208	0.002392143	0.003666873	grey	-0.252624121	0.004494365	GO:0005515		26S proteasome non-regulatory subunit, putative (RPN5)	26S proteasome non-ATPase regulatory subunit
Sapur.010G097700.2	14.16691616	-0.39985422	0.131770394	-3.03447	0.002409042	0.003690132	grey	-0.249163325	0.001652137	GO:0004680;GO:0004672;GO:0048544		ARK2,BRK1 receptor kinase 3	Serine/Threonine-kinase
Sapur.009G028100.1	19.36619968	-0.30247874	0.114288444	-3.03368	0.002412143	0.003694238	grey	-0.252234526	0.003199176				Oxidoreductase,2ffoxo/Sem-2p family protein
Sapur.010G033800.1	3.053046632	-0.511342841	0.168523973	-3.03408	0.002412689	0.003694353	grey	-0.265946603	0.000759525			RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.016G023800.1	0.858631008	-0.357404509	0.121812473	-3.03407	0.002413711	0.003694553	grey	-0.238777212	0.003088889	GO:0005515		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.T168200.1	5.167503114	-0.732617253	0.241558726	-3.03287	0.002422265	0.003708962	grey	-0.272039678	0.000567594				NA
Sapur.012G106400.1	3.132661773	0.496078636	0.163798652	3.032788	0.002423058	0.003709851	grey	0.231828064	0.002969349	GO:0043661;GO:0009966;GO:0004864		phosphoprotein phosphatase inhibitors	protein phosphatase inhibitor 2 containing protein
Sapur.016G000400.1	0.669449424	0.975627621	0.321501784	-3.03227	0.002426155	0.003710411	grey	-0.260838377	0.005968619	GO:0005515		SH3 domain-containing protein	Rho guanine nucleotide exchange factor
Sapur.016G180600.1	0.667514783	-1.030226819	0.339795832	-3.0319	0.002430201	0.003720649	grey	-0.19019848	0.017034695			DEGP protease 2	DEGP protease 2a
Sapur.018G261300.1	6.690723224	-0.48211488	0.159021103	-3.03179	0.002431103	0.003721652	grey	-0.253383488	0.002462154	GO:0043531		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.012G018800.3	0.621503629	-1.036278497	0.341863383	3.031522	0.002432241	0.003724753	grey	0.07854831	0.32814697			transducin family protein / WD-40 repeat family protein	transducin/WD40 domain protein
Sapur.009G028100.1	33.21668024	0.334519905	0.108117888	-3.03143	0.002433962	0.003725884	grey	-0.33479461	1.81E-05				NA
Sapur.010G054400.1	0.474026166	-1.132009882	0.373764227	-3.03111	0.002436554	0.00372921	grey	-0.295223868	0.00017413			DNA repair metallo-beta-lactamase family protein	NA
Sapur.006G181700.1	5.867029377	-0.503192117	0.18861267	-3.03111	0.002436556	0.00372921	grey	-0.229318663	0.005288172	GO:0009733		SAUR-like auxin-responsive family protein	NA
Sapur.005G164000.2	18.62237328	-0.259065513	0.085780198	-3.02991	0.002446244	0.003743791	grey	0.082054917	0.3068451	GO:0005975;GO:0004553		Glycosyl hydrolase family 17 protein	glycoside hydrolase family 17 protein
Sapur.015G203300.1	8.414453268	-0.182581164	0.061251176	-3.02926	0.002450703	0.003749823	grey	-0.230419397	0.003043032	GO:0004683;GO:0005524;GO:0004672	SNC4	suppressor of npr1-1 constitutive 4	NA
Sapur.016G165400.1	1098.039805	0.156740892	0.051738708	3.029471	0.002449828	0.00374893	grey	-0.208947076	0.008634937			Thioredoxin superfamily protein	gamma-interferon-inducible lysosomal thiol reductase
Sapur.010G094000.1	121.2529905	-0.167860700	0.056438147	-3.02789	0.002462662	0.003768316	grey	-0.253595628	0.001644486	GO:0003676		AT4H6,AT4H5 homeobox protein 54	NA
Sapur.009G034600.1	2.126257909	0.587184124	0.202190858	2.027885	0.002462721	0.003768184	grey	-0.251606208	0.001675542	GO:0016831;GO:0008299		GMP synthase family protein	mevalonate diphosphate decarboxylase
Sapur.002G182000.1	628.4314773	-0.362085024	0.109502886	-3.02765	0.002466659	0.003770928	grey	-0.312963877	6.58E-05			PHD finger protein	Phd finger protein, putative
Sapur.004G067700.1	28.31446872	-0.314288444	0.103868207	-3.02748	0.002467142	0.003769248	grey	-0.227609373	0.003796484	GO:0005515		Oxidoreductase/2ffoxo/Sem-2p family protein	P61 domain protein
Sapur.009G091600.1	665.4257267	-0.167162819	0.055218045	-3.02732	0.002467307	0.00377463	grey	-0.251863012	0.001219213	GO:0005524;GO:0006020;GO:0000103		AKN1,APK,APK1,ATAKIN1 APS kinase	adenylylsulfate kinase
Sapur.015G026200.1	9.513161674	0.474968668	0.156539738	3.026829	0.002473137	0.003780652	grey	-0.227531731	0.004218504				NA
Sapur.013G120000.1	2.253060875	-0.593776379	0.196179913	-3.02669	0.002474449	0.003782146	grey	-0.205632394	0.009775807				monothiol glutaredoxin-S11 protein, putative
Sapur.016G009400.2	71.13625075	-0.14808028	0.049095142	3.026424	0.002478546	0.003785346	grey	0.197336507	0.013243092	GO:0008886		ENT6/HNT6/GAT	NA
Sapur.006G087300.1	372.4482015	-0.287911757	0.095145546	-3.02614	0.002476966	0.003788705	grey	-0.240990055	0.002362559				NA
Sapur.007G085500.1	1.108732001	0.872150844	0.288220179	3.025988	0.002479322	0.003790488	grey	0.207305596	0.009187371	GO:0005085;GO:0016020;GO:0008810;GO:0015171;GO:0003333		BAT1 bidirectional amino acid transporter 1	bidirectional amino acid transporter 1
Sapur.T024500.1	1.661202704	0.852760664	0.281824566	3.025963	0.002479427	0.003790589	grey	0.217567553	0.006196525			RNA-binding (RRM/RBD/RNP motifs) family protein	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.017G047200.1	5.388556117	-0.600286135	0.198408532	-3.02563	0.002481188	0.003794628	grey	-0.242970303	0.001833273	GO:0003824;GO:0006470;GO:0004722		Protein phosphatase 2C family protein	NA
Sapur.015G085800.1	0.983553882	0.802329402	0.265188181	3.025567	0.002482167	0.003795292	grey	-0.268686423	0.00208827	GO:0005975;GO:0006532		Glycosyl hydrolase family protein with chitinase insertion domain	Glycosyl hydrolase family protein
Sapur.016G147000.1	315.5142332	-0.082939599	0.027413181	-3.02552	0.002482211	0.003795681	grey	-0.230795526	0.002488895			RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein, putative
Sapur.005G189000.1	1.694841117	0.650281457	0.215764488	3.02484	0.002487455	0.003804031	grey	-0.208073024	0.009317785			Regulator of chromosome condensation (RCC1) repeat protein	chromosome condensation regulator RCC1 repeat protein
Sapur.002G105200.1	104.5552075	-0.258723723	0.085537235	-3.02469	0.002488871	0.003805683	grey	-0.251226683	0.001504749			Protein of unknown function, DUF617	plant-specific domain TIGR01570 family protein
Sapur.002G170700.1	17.47495464	0.365618302	0.088031308	2.023608	0.002490126	0.003811577	grey	-0.223238842	0.004902386				transmembrane protein, putative
Sapur.013G025500.3	0.460456299	-1.136043617	0.375799896	-3.02332	0.002500151	0.003822223	grey	-0.283873138	0.000314682	GO:0003824;GO:0006470;GO:0004722			protein phosphatase 2C
Sapur.009G000300.1	2.318687749	-0.52461469	0.173126878	-3.02299	0.002502673	0.003826077	grey	-0.219346605	0.007545682				NA
Sapur.004G231100.1	133.6565772	-0.111743869	0.036971386	-3.02244	0.002507441	0.003832838	grey	-0.30671216	0.356 35				PPR containing plant protein
Sapur.009G132900.2	137.0742207	0.323191622	0.106945512	3.022144	0.002509999	0.003836557	grey	0.248639994	0.005689383	GO:0005515;GO:0005086		SEC7-like guanine nucleotide exchange family protein	brefeldin A-inhibited guanine nucleotide-exchange protein
Sapur.002G170300.2	2.701337908	-0.505932386	0.168410364	-3.02196	0.002510456	0.003838362	grey	-0.194329195	0.014737113	GO:0005515		AT1USE,ATSK31,COP11,CSN1 26S proteasome subunit RPN12	COP9 signalosome complex subunit 6 protein
Sapur.010G164000.1	1.760284681	0.657828353	0.217650203	3.021283	0.002510763	0.003847012	grey	0.231780804	0.004951188				NA
Sapur.009G049000.1	2.334419915	-1.362638734	0.45086455	3.02101	0.002513311	0.003850271	grey	-0.362932251	2.88E-06	GO:0055114;GO:0020037;GO:0016705;GO:0005506		CB8,CYP90,CYP90A,CYP90A1 Cytochrome P450 superfamily protein	cytochrome P450 family 90 monooxygenase, putative
Sapur.008G167000.1	10.63532232	0.328069814	0.108604598	3.019775	0.002519629	0.003865861	grey	0.235868463	0.002925935				NA
Sapur.009G044200.1	7.105015114	-0.307488844	0.224432201	-3.0189	0.002519723	0.003874829	grey	-0.219397272	0.007168868	GO:0006629		alpha/beta-Hydrolases superfamily protein	triacylglycerol lipase
Sapur.009G005900.3	4.588671761	-0.277332016	0.12408551	-3.01808	0.002543855	0.003887242	grey	-0.274908864	0.010734946	GO:0005885;GO:0008642		Zinc finger (C3HC4-type RING finger) family protein	Zinc finger (C3HC4-type RING finger) family protein
Sapur.T005400.1	0.705242211	-0.8542662	0.283137589	-3.01714	0.002551706	0.003888878	grey	-0.178074629	0.016826415	GO:0008270;GO:0008022;GO:0006625;GO:0005779		APM4,ATPX12,PEX12 peroxin 12	peroxin 12
Sapur.T041800.1	0.236953924	1.181620604	0.391275512	3.016089	0.002560586	0.003912283	grey	0.27656512	9.45E-07			ATCIRM1,ATKPO1,HET2,XPO1 exportin 1A	NA
Sapur.017G048500.1	14.01862998	-0.295272836	0.098059789	-3.01574	0.002563529	0.003916283	grey	-0.238812293	0.003939446	GO:0029900;GO:0005747;GO:0005739		NADH dehydrogenase (ubiquinone)	NA
Sapur.007G067000.2	2.785828941	0.743951738	0.246730433	3.015217	0.002567951	0.003922976	grey	-0.221788385	0.005244358			BSD domain-containing protein	BSD domain protein
Sapur.003G099700.5	0.770002725	-0.836062349	0.277607814	-3.01499	0.002569907	0.003925782	grey	-0.259207211	0.010394855	GO:0005515;GO:0006468;GO:0005524;GO:0004672		Leucine-rich repeat protein kinase family protein	receptor-like kinase, putative
Sapur.015G111100.1	36.90247735	-0.561838204	0.186197344	-3.01486	0.002570905	0.003927217	grey	-0.214113102	0.005937926	GO:0055114;GO:0016491		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase, putative
Sapur.008G058100.3	4.471691823	-0.774547513	0.125199692	-3.01482	0.002571336	0.003927556	grey	0.068861229	0.39078259				autophagy-related protein
Sapur.015G009400.1	147.9029277	0.151939401	0.050261645	3.010988	0.002573579	0.003931178	grey	-0.228624724	0.004934775			emb2735 embryo defective 2735	embryo defective 2735 protein, putative
Sapur.012G111200.2	2.133129521	-0.506072162	0.16794251	-3.01337	0.002583476	0.003946086	grey	-0.238720324	0.002406666	GO:0006412;GO:0005840;GO:0003735		Ribosomal protein S5 domain 2-like superfamily protein	30S ribosomal protein S9
Sapur.014G081800.1	4.903810109	-0.703846188	0.233584951	-3.01126	0.002587719	0.003949025	grey	-0.332604291	-2.04E-05	GO:0048364;GO:0016762;GO:0005507;GO:0005618;GO:0005975;GO:0004553		xyloglucan endotransglycosylase/hydrolase	xyloglucan endotransglycosylase hydrolase
Sapur.013G155400.2	1.468072446	0.680751583	0.226102631	3.010644	0.002600946	0.003981257	grey	-0.183624683	0.028362229			FRIGIDA like 1	frigida-like protein, putative
Sapur.009G166600.1	39.23230097	-0.254329124	0.08451027	3.009446	0.002607245	0.003990683	grey	-0.255868429	0.001227122	GO:0006355;GO:0003677		BLH1,EDA29 BELL1-like homeotic protein	BELL1-related homeotic protein, putative
Sapur.009G112900.1	751.2914934	-0.124657328	0.041423083	-3.00936	0.002617958	0.003997707	grey	-0.253212254	0.001350435			ATIP1/FL7,ATIP3FL1,FIP1/FL1 homolog of yeast FIP1 [V]	Fip1 motif protein, putative
Sapur.005G002300.3	1.238344857	0.793422446	0.263730615	-3.00889	0.002623801	0.004004495	grey	0.191457165	0.016303586				plant IF-like protein
Sapur.018G261200.1	0.47443511	1.147744338	0.381522307	3.00853	0.002626876	0.004009515	grey	-0.218450096	0.003229088				hypothetical protein
Sapur.017G301300.5	0.870567759	-0.880688823	0.292795899	-3.00786	0.002630956	0.004017	grey	-0.26072278	0.003698888				Mpl/SANT-like DNA-binding domain protein
Sapur.005G120800.13	9.788157632	-0.704084264	0.239758185	-3.00657	0.002640214	0.004030624	grey	-0.242874016	0.007172088	GO:0005515		Protein of unknown function (DUF3245)	RN-binding protein, putative
Sapur.006G029900.1	4.2762232	-0.752033489	0.249607099	-3.00582	0.002646831	0.004043239	grey	-0.231671644	0.002545813	GO:0016020;GO:0008810;GO:0005215		Major facilitator superfamily protein	NA
Sapur.016G144200.4	2.328618008	-0.587929758	0.195571333	-3.00491	0.002655174	0.004051177	grey	-0.223238374	0.004926425	GO:0005524;GO:0016021;GO:0006810;GO:0005524	ATHAP6,NAP8	non-intrinsic ABC protein 8	NA
Sapur.016G208800.1	19.71902825	-0.306235482	0.101925027	-3.00465	0.002658906	0.004058595	grey	-0.248515862	0.001696023	GO:0005524	AATP1	AAA-ATPase 1	AAA-family ATPase
Sapur.009G000300.1	1.357394015	-0.248882363	0.11610763	-3.00404	0.002660609	0.004061462	grey	-0.261373834	0.004966182				hypothetical protein
Sapur.012G083900.1	0.500927358	0.513182908	0.34339239	3.003934	0.002663112	0.004067489	grey	-0.261373834	0.004966476	GO:0005515		F-box/RNI-like/FBD-like domains-containing protein	F-box/RNI-like/FBD-like domains protein
Sapur.006G080000.1	47.03561219	-0.412287861	0.137127463	-3.00383	0.002664	0.004068689	grey	-0.273564898	0.003538814	GO:0003333		Transmembrane amino acid transporter family protein	sodium-coupled neutral amino acid transporter
Sapur.002G008000.1	5.418284944	-0.376515373	0.126021167	-3.00372	0.002667002	0.004069968	grey	-0.198317618	0.012780175				hypothetical protein
Sapur.016G123000.2	0.438668801	-0.457578336	0.484028811	-3.00349	0.002668341	0.004071335	grey	-0.285365342	0.002915579	GO:0005975;GO:0004553		beta glucosidase 17	glycoside hydrolase family 1 protein
Sapur.015G091300.1	94.28515107	-0.110591546	0.03673482	-3.0079	0.002674374	0.004087324	grey	-0.205604905	0.010670999	GO:0005515;GO:0005798;GO:0003690		Mitochondrial transcription termination factor family protein	mTERF family protein
Sapur.001G106500.1	303.3182845	-0.140082685	0.046727316	-2.99788	0.002718685	0.0041475	grey	-0.258166786	0.001086513			D111/G-patch domain-containing protein	DEAH box splicing factor-binding site protein
Sapur.016G039200.1	2.393828241	-0.514604154	0.171828669	-2.99736	0.002723123	0.004158381	grey	-0.308098384	1.81E-05			NADPH-binding Rossmann-like superfamily protein	short-chain dehydrogenase reductase
Sapur.002G204900.1	41.12001783	-0.225858029	0.075308824	-2.99702	0.002726313	0.004158752	grey	-0.256582231	0.001027081	GO:0016773;GO:0016020;GO:0006520	ATMPK1,MPK1	mitogen-activated protein kinase 1	MAP kinase
Sapur.016G017900.1	586.4607799	-0.248182079	0.082786418	-2.99678	0.002728	0.004161802	grey	-0.243875275	0.003844505				hypothetical protein
Sapur.004G091200.4	2.123234646	-0.564249492	0.188306274	-2.99645	0.002731147	0.004166235	grey	-0.257328668	0.001119308			RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.006G057900.1	1.342882645	-0.649932437	0.216774499	2.995947	0.002735	0.004170945	grey	-0.196238936	0.032281836	GO:0043565;GO:0006355;GO:0003700;GO:0003677	HAT14	homeobox-leucine zipper protein hat14	NA
Sapur.012G068800.2	0.91276704	-0.809428137	0.270273322	-2.994861	0.002745696	0.004187161	grey	-0.051124722	0.124849468	GO:0006355;GO:0003677	CDF3	cycling DOF factor 3	Dof zinc finger protein, putative
Sapur.016G120200.1	170.0640948	0.520852388	0.173939226	2.994525	0.002748729	0.004191593	grey	-0.219828265	0.006419753			N-ASPP/-linked oxidoreductase superfamily protein	carbohydrate-binding protein
Sapur.014G056100.2	1.306091797	-0.700329361	0.233969179	2.993926	0.002754128	0.004200592	grey	-0.242224446	0.003883363	GO:0016746;GO:0008152		calcineurin-B subunit-related	1-acylglycerophosphocholine O-acyltransferase
Sapur.002G144600.1	1.123401758	-0.754958472	0.252226071	-2.99318	0.002760854	0.004206695	grey	-0.295171781	0.00174766				NA
Sapur.016G113100.1	17.08951617	-0.689293707	0.230363862	-2.99271	0.002765119	0.004210024	grey	-0.221838171	0.005973346				hypothetical protein
Sapur.010G084000.5	1.090685541	0.772631155	0.258254538	2.991751	0.002773828	0.004228892	grey	-0.261643837	0.000931204			Heat shock protein DnaJ, N-terminal with domain of unknown function (DUF3977)	chaperone protein DnaJ
Sapur.015G167200.1	5.892449869	-0.275000993	0.092000551	-2.99165	0.002775695	0.004191542	grey	-0.229820739	0.004466868			Protein of unknown function (DUF247)	DUF274 family protein
Sapur.009G159300.1	31.71625663	-0.631660431	0.211105567	-2.99152	0.002775954	0.004201744	grey	-0.247091644	0.001809563			C2H2 and C3HC zinc fingers superfamily protein	nucleic acid-binding protein, putative
Sapur.008G208400.1	322.6841059	-0.250587931	0.083937846

Sapur.016G231900.1	2.65087325	-5.52342845	0.17867882	-2.94279	0.00325262	0.04930257	grey	-0.24979483	0.00160471	ENSG00000171240.10	AT3G11140.1	hydroxyproline-rich glycoprotein family protein
Sapur.002G097700.1	152.7117085	0.41253854	0.14021168	2.941262	0.00328242	0.04938504	grey	0.24558875	0.01932719		AT1G27685.1	glycine-rich protein
Sapur.016G181800.1	20.02726787	0.21887572	0.07884376	2.941312	0.00328249	0.04963444	grey	0.21537793	0.00832654	GD0005515	AT5G41610.1	receptor like protein 6
Sapur.016G259800.1	0.28872106	1.40482135	0.47741093	2.941248	0.00328936	0.04954243	grey	0.33193052	2.01E-05		AT4G29281.1	LCR21
Sapur.007G201700.1	340.8545165	0.22568256	0.076736	2.940853	0.00327517	0.04960074	grey	0.18282626	0.02184633		AT4G25480.1	NRR.L1
Sapur.009G125700.1	21.62131101	-0.41404121	0.14096926	-2.94004	0.00328167	0.04973098	grey	-0.24838911	0.01709882		AT2G27310.1	F-box family protein
Sapur.019G286900.1	104.4871772	-0.19401039	0.06610125	-2.93958	0.00328627	0.04980158	grey	-0.22929734	0.03988567		AT5G58100.1	PDC85
Sapur.T100300.1	0.39556153	0.61377959	0.21043888	2.939405	0.00328934	0.04982627	grey	0.24269404	0.02419366		AT4G26860.1	SEC7-like guanine nucleotide exchange family protein
Sapur.005G290600.1	2466.202669	0.07777569	0.03677409	2.938739	0.00329507	0.04990156	grey	0.19093102	0.01606663	GD0010021;GD0006486;GD0057883;GD0004579	AT5G76400.1	Ribophorin I
Sapur.005G241700.1	80.68854619	0.34988826	0.08477587	2.938623	0.00329551	0.04991351	grey	-0.21750028	0.01609251	GD0001047	AT5G15570.1	ATSG13,SG13
Sapur.010G043400.1	0.27392514	1.5628371	0.53208706	2.937139	0.00331251	0.0501852	grey	0.38832501	5.02E-07			
Sapur.004G208000.1	93.68443944	0.29960148	0.10202789	2.936011	0.00332819	0.05018093	grey	-0.23283968	0.03341103	GD0005885;GD0016297;GD0015297;GD0015138;GD0006855	AT3G21680.1	MATE efflux family protein
Sapur.010G154100.1	0.35016289	1.89063873	0.64382953	2.93655	0.00331885	0.05027372	grey	0.34681914	8.67E-06		AT3G21133.1	Disease resistance-responsive (dirigent-like protein) family protein
Sapur.004G173700.1	1.96532374	0.49007629	0.16682404	2.936238	0.00332467	0.05040438	grey	0.21537793	0.00832654	GD0006483;GD0005534;GD0004672	AT4G30840.1	receptor like protein 6 family protein
Sapur.002G169900.1	20.95601817	-0.27204588	0.09250517	-2.93403	0.00334568	0.05067815	grey	-0.26382478	0.00841869			hypothetical protein
Sapur.T116200.1	0.61767886	0.86663281	0.29513968	2.933966	0.00336291	0.05088243	grey	-0.32754367	0.00615249	GD0007165;GD0005515	AT4G16950.1	RPP5
Sapur.008G245400.1	811.8193407	0.11167649	0.03792582	2.931826	0.00338118	0.05070778	grey	0.20015764	0.01952559	GD0006457	AT4G55520.1	
Sapur.019G263400.1	0.32845251	-0.29355477	0.4077232	-2.93361	0.0033506	0.05074002	grey	-0.35978497	3.69E-06		AT5G18320.2	Kinase interacting (KIP1-like) family protein
Sapur.010G141600.1	177.7379179	-0.07465422	0.05132469	-2.931369	0.00337829	0.05076289	grey	-0.2427384	0.01087184	GD0006355;GD0003700	AT2G40340.1	ATERF4,DREB2C
Sapur.010G209100.1	50.2924809	-0.35890004	0.12240761	-2.93274	0.00339863	0.05087867	grey	-0.23615623	0.02905699		AT5G07010.1	ATST2A,ST2A
Sapur.007G201500.2	2.48501899	0.24176467	0.08246837	2.931468	0.00340697	0.05096868	grey	0.07127806	0.37056168		AT4G03690.2	
Sapur.003G051800.3	1.80479003	0.55937245	0.19077185	-2.93216	0.00341058	0.05096949	grey	0.10876276	0.17504814	CLPR4	AT1G70480.1	CLPR4
Sapur.004G212200.1	14.15870362	0.49387202	0.16819305	2.931066	0.00341873	0.05100074	grey	0.24479411	0.02005517		AT4G16820.1	vacuolar ATP synthase catalytic subunit-related / V-ATPase-related / vacuolar proton pump-related
Sapur.017G085600.1	3.10857605	-0.5832453	0.19893579	-2.93183	0.00339745	0.05101888	grey	-0.23459846	0.03102581	GD0071651;GD0005515;GD0043531	AT5G17680.1	disease resistance protein (TIR-NBS-LRR class), putative
Sapur.T100500.1	254.7977444	0.49007629	0.16723546	2.931123	0.00337735	0.05101346	grey	-0.22807323	0.03920984			
Sapur.002G304800.4	2.62906633	-0.47261705	0.16123472	-2.9309	0.00337869	0.05116757	grey	0.00193122	0.98096515	GD0008080	AT5G56630.1	BGT.GCN5.HAC1.HAG2.HL
Sapur.006G245700.2	28.3952213	-0.23947013	0.08178842	-2.93042	0.00338507	0.05124315	grey	-0.2199966	0.05572391		AT5G12150.1	
Sapur.009G158200.1	28.86869602	0.31331888	0.10694364	2.929913	0.00339565	0.05132241	grey	0.24519032	0.01947722		AT5G08550.1	
Sapur.019G247500.1	3.42362705	0.50363324	0.17189107	2.929797	0.00339184	0.05133931	grey	0.23137859	0.00882416	GD0006355;GD0005634;GD0070D;GD0046983;GD0033077	AGL12,XAL1	AGAMOUS-like 12
Sapur.006G009200.1	128.0453877	0.14988334	0.05110142	2.92926	0.00339701	0.05142574	grey	0.22440344	0.00973889	GD0005515	AT4G15281.1	CPR30
Sapur.T181000.1	0.35682874	-1.02430749	0.34970682	-2.92905	0.00340042	0.05145884	grey	-0.36029502	3.57E-06			
Sapur.005G127400.5	0.75071616	0.49017467	0.16736221	2.929327	0.00340159	0.05148387	grey	0.07127806	0.37056168		AT5G58020.1	
Sapur.017G003700.1	3.38994351	-0.81847849	0.27880222	-2.92718	0.00340529	0.05157416	grey	-0.22969112	0.00584402	GD0007735;GD0005622	AT4G44065.2	
Sapur.004G224100.1	2.75363834	0.47186632	0.16128383	2.926385	0.00343211	0.05192344	grey	0.25187851	0.00446120	GD0010021;GD0004679;GD0006486;GD0004668;GD0006672	AT4G18130.1	WAK2
Sapur.008G121100.1	504.1139414	-0.13664979	0.04773424	-2.92614	0.00343971	0.05193257	grey	-0.23197852	0.03461792	GD0016787;GD0005234;GD0036727;GD0042393	AT2G06030.1	ATCHR12
Sapur.006G045800.1	97.51113179	0.36455483	0.12463258	2.925267	0.00345157	0.05198994	grey	-0.22604512	0.03682445	GD0005515	AT5G66860.1	ATPGIP1,PGIP1
Sapur.010G099100.3	4.41767027	-0.46700489	0.15961861	-2.92576	0.00343671	0.05199137	grey	-0.09348833	0.21574089		AT5G13310.1	
Sapur.T150200.1	11.19955477	-0.41837925	0.14290391	-2.92568	0.00347033	0.05200203	grey	-0.23894068	0.03195516			
Sapur.005G112500.1	0.90864867	0.76692323	0.26215121	2.92561	0.00347914	0.05201146	grey	-0.25183074	0.01479654	GD0005114;GD0020037;GD0008679;GD0004601	AT5G30870.1	
Sapur.008G025600.1	5.54205675	0.40957984	0.14000878	2.925293	0.00348132	0.05206212	grey	0.18514621	0.03262858			
Sapur.016G075400.1	1.71644999	0.52319194	0.2105114	2.925268	0.00349198	0.05206391	grey	0.22944288	0.01841717			
Sapur.008G091600.1	2.42764596	-0.46719193	0.15968528	-2.92525	0.00344173	0.05206422	grey	-0.2723123	0.00565066			
Sapur.009G125300.1	1.78007844	0.61092147	0.21000471	2.924661	0.00349752	0.05209182	grey	0.24518032	0.01972192	GD0068872	AT1G29880.1	RING/FYVE/PHD-type zinc finger family protein
Sapur.010G084600.1	43.77714833	0.32304158	0.11010726	2.924719	0.00347676	0.05216871	grey	0.23144124	0.00324984	GD0007735;GD0005511;GD0004175	AT4G16470.2	PAB4
Sapur.008G021500.1	9.33916869	0.42408536	0.15468782	2.924675	0.00348347	0.05215362	grey	0.23246265	0.02274316	GD0005514;GD0046334	AT1G07240.1	ARA4,ARAF1,ARG1,ATAGD1
Sapur.010G170700.6	7.40440275	0.31651547	0.10927443	2.923073	0.00345594	0.05229001	grey	0.23268193	0.00331922		AT2G39290.1	PGPS,PGPS1,PGS1
Sapur.009G058300.1	21.75562791	0.38125307	0.13051273	2.921458	0.00351423	0.05230368	grey	-0.2073723	0.03923684			
Sapur.009G080000.1	210.9451093	-0.18794803	0.06404093	-2.92305	0.00346247	0.05242006	grey	-0.23757629	0.00423244		AT5G20230.1	CYO1,SCO2
Sapur.005G146400.4	1.48824168	0.70025637	0.24168385	2.922777	0.00349253	0.05246311	grey	0.08705849	0.28925543		AT5G21450.1	SCL1
Sapur.005G138300.1	7.65383775	-0.54586139	0.18911336	-2.92151	0.00347224	0.05250564	grey	0.19052388	0.01838479	GD0045454;GD0015035;GD0006662	AT5G35010.2	ATOL,TOL1
Sapur.019G069300.1	7.20793199	0.60631511	0.20758143	-2.922	0.00347994	0.05258899	grey	-0.27063311	0.00506872			
Sapur.010G264900.1	156.8424849	0.15496165	0.05847151	2.92103	0.00349746	0.05259961	grey	-0.3193918	3.75E-06			
Sapur.008G088000.5	3.33063714	-0.66179818	0.22809447	-2.92121	0.00346772	0.05271184	grey	-0.19446321	0.01467935		AT5G16180.1	
Sapur.015G007605.1	13.83557922	0.51005605	0.19472839	2.920686	0.00350419	0.05280047	grey	0.24816665	0.0151256		AT5G05185.3	NFD6
Sapur.001G145500.1	0.26242503	1.32121042	0.45617055	2.920517	0.00349506	0.05282567	grey	0.33125769	2.00E-05		AT5G16695.1	
Sapur.013G092500.1	44.85955244	0.21103192	0.07196827	2.919865	0.00350171	0.05293827	grey	0.25278164	0.01402504			
Sapur.009G041000.1	218.6772229	0.10819543	0.03705724	-2.91966	0.00350682	0.05296318	grey	-0.23947014	0.00252115	GD0005515	AT5G32030.2	
Sapur.008G237900.3	30.83575657	0.21608954	0.07231271	2.917682	0.00352635	0.05329616	grey	-0.06803053	0.39747771		AT1G26520.1	Cobalamin biosynthesis CobW-like protein
Sapur.009G080500.1	40.17838154	-0.44208556	0.15228315	-2.91766	0.00353742	0.05329856	grey	-0.20850292	0.08881577		AT5G05180.1	HSP20-like chaperones superfamily protein
Sapur.I59G214300.1	0.53268773	-2.42431247	0.83835764	-2.91653	0.00353946	0.05348546	grey	-0.38842458	4.85E-07		AT4G21440.1	B7D
Sapur.005G120100.1	14.70764982	0.35211247	0.12127441	2.916463	0.00354167	0.05350374	grey	0.24237084	0.02225326		AT2G39290.1	PGP1,PGP1,PGS1
Sapur.I59G050000.3	1.0127696	-0.75685362	-0.25952904	-2.91628	0.00354455	0.05352604	grey	0.25776128	0.01117031		AT5G48550.1	
Sapur.009G125900.1	57.53582287	-0.22021986	0.07552159	-2.91599	0.00356152	0.05357142	grey	-0.23850561	0.02675511	GD0005885;GD0016021	AT3G51290.1	ATPIN1,PIN1
Sapur.005G175500.1	4.85479887	-0.37500304	0.1288395	-2.91556	0.00355056	0.05364355	grey	-0.29509414	0.00175525			
Sapur.010G182700.1	1.62847338	0.66450739	0.22829164	2.911479	0.00359021	0.05364641	grey	-0.28916849	0.00239665		AT5G32040.2	
Sapur.010G072200.2	1.51603527	-0.66370739	0.22717414	-2.91524	0.00355473	0.05369328	grey	-0.24338692	0.01288187	GD0016020;GD0015031;GD0007030	AT4G26840.1	
Sapur.005G191000.3	2.76210605	-0.52376834	0.18117634	-2.91507	0.00355635	0.05372373	grey	-0.27303085	0.00554186	GD0015031	AT4G34160.1	CPT5A
Sapur.T075200.1	10.97123222	0.29312568	0.10054788	2.914713	0.00358152	0.05373871	grey	-0.18629513	0.03948573	GD0003676	AT5G07810.1	
Sapur.018G241800.1	8.85881506	-0.39061677	0.13405887	-2.91402	0.00358122	0.05389663	grey	-0.23672718	0.00599946	GD0046295	AT2G21660.1	ATGRP7,CCR2,GR-RBP7,GRP
Sapur.I16G184600.2	2.29905771	-0.46015441	0.15757122	-2.91352	0.00357833	0.05398004	grey	0.04968191	0.53674872	GD0003676	AT2G20030.3	
Sapur.010G080600.1	2.57143726	0.83435113	0.28645052	2.912722	0.00358296	0.05411298	grey	0.26305107	0.00873108		AT5G47540.1	
Sapur.007G090400.1	158.1093393	0.10286687	0.07043871	2.91268	0.00358412	0.05411777	grey	0.19885926	0.01532766		AT3G24320.1	ATPAD4,PAD4
Sapur.009G120900.1	2705.43629	-0.15910769	0.05462694	-2.91203	0.00359863	0.05422528	grey	-0.27864223	0.00142486	GD0005975;GD0004553	AT5G20910.2	
Sapur.T087500.1	2.61664884	0.47457563	0.16457976	2.910892	0.00360398	0.05440296	grey	0.22615425	0.03227732		AT3G61510.1	NUMA1-related protein 5
Sapur.014G061200.1	1.03270157	0.83219326	0.28597124	2.910501	0.00360895	0.05448656	grey	0.28300405	0.00364005		AT2G27330.2	ATMYB13R-1,ATMYB13R1,MY
Sapur.005G075400.1	5.58928757	0.31995249	0.10992318	2.910342	0.00361049	0.05449462	grey	0.24148128	0.0308776	GD0006464;GD0004077	AT5G25230.1	HCS1
Sapur.I02G099800.3	0.81041932	0.90737492	0.31190397	2.910312	0.00363076	0.05451203	grey	0.14332481	0.07332533	GD0006468;GD0006672	AT3G09030.1	
Sapur.007G071500.1	653.0078819	0.09700501	0.03357189	2.909816	0.00363647	0.05459623	grey	0.17504208	0.02832258	GD0045454	AT4G04330.1	PLP3b
Sapur.009G083300.4	2.41724577	-0.54216026	0.18640934	-2.90936	0.00363598	0.05470214	grey	-0.01918207	0.88287204	GD0005515;GD0016787	AT4G26220.1	BSL2
Sapur.010G047000.3	17.92113391	0.36670955	0.12609569	2.903969	0.00368429	0.05558281	grey	-0.05499744	0.49391956	GD0063051;GD0056349;GD0070D;GD0046983;GD0033077	AT4G24260.1	AGL15,SEP3
Sapur.008G026600.1	585.0149661	0.07964197	0.03357685	2.903902	0.00368508	0.05581224	grey	-0.22929097	0.00609214	GD0006284;GD0006508	AT5G07730.1	Cysteine proteinase superfamily protein
Sapur.009G030200.1	496.5691567	-0.13100628	0.04515328	-2.90352	0.00370761	0.05584129	grey	-0.22769234	0.00413178	GD0005234;GD0006476	AT5G46960.1	RNA helicase, ATP-dependent, SK12/DDX21 protein
Sapur.I06G138000.1	152.7363825	-0.54491376	0.18779757	-2.90174	0.00371627	0.05597325	grey	-0.24898209	0.01658913		AT4G27690.2	Duplicated homologous-like superfamily protein
Sapur.I02G038800.1	22.58175568	-0.37278281	0.12847585	-2.90127	0.00371676	0.05605966	grey	-0.23916597	0.00441763		AT5G76180.1	ALPHA DOX2
Sapur.I02G025400.1	1.53243727	0.64487447	0.22230441	2.900904	0.00372878	0.05616122	grey	-0.24973078	0.01608247	GD0006351;GD0008899	AT4G14660.1	NRP.T
Sapur.005G164000.2	1.80213322	-0.63776261	0.21988539	-2.90066	0.00373829	0.05616394	grey	-0.25763139	0.00112749	GD0006396	AT3G07580.2	
Sapur.006G088700.3	1.02678684	-0.70375887	0.24150875	-2.90057	0.00373460	0.05617753	grey	0.01534642	0.84836569		AT2G35530.1	
Sapur.012G108200.1	4.51464769	0.59013876	0.20347957	2.90023	0.00372888	0.05623511	grey	0.19456221	0.01461388		AT5G21250.1	AtMYB17,MYB17
Sapur.005G102600.1	0.34739882	1.63828073	0.56508537	2.899173	0.00374485	0.05642252	grey	0.32734156	2.86E-05			
Sapur.010G081500.1	16.74119172	0.27127452	0.09358599	2.898604	0.00374579	0.05661334	grey	0.06479492	0.55263816		AT4G14746.1	
Sapur.018G053000.1	2.17997059	0.51246636	0.17668749	2.898607	0.00374842	0.05661926	grey	0.24864393	0.02377740	GD0003676	AT5G19960.1	CAT7
Sapur.008G207000.1	14.44243	0.29665148	0.10228859	2.898651	0.00374899	0.05663362	grey	0.19912467	0.01341862	GD0016020;GD0015171;GD0003033	AT3G16620.1	CATC
Sapur.004G123300.1	477.8715112	0.14995823	0.05176288	2.898508	0.00374932	0.05663206	grey	0.17890723	0.02416749	GD0015985;GD0015078;GD0002076	AT5G13230.1	
Sapur.010G285800.2	6.93964009	0.35602167	0.12274118	2.897816	0.00377464	0.05664482	grey	0.20010456	0.00843572	GD0006486	AT4G04320.1	GAMMA-SNAP,GSNAP
Sapur.I59G086300.1	80.37041245	0.18863347	0.0684626	2.897456	0.00378029	0.05671423	grey	0.20216785	0.01111099	GD0005524	AAT91	AAA-ATPase 1
Sapur.003G086000.2	21.59880203	0.45663353	0.16288875	2.896662	0.00377245	0.05687059	grey	-0.07536633	0.17332825		AT4G28720.1	x-ray induced transcript 1
Sapur.005G160700.1	0.29686519	1.23795273	0.42747337	2.896029	0.00379172	0.05696488	grey	0.30982449	8.05E-05	GD0016021	AT2G30890.1	Cytochrome b561/ferric reductase transmembrane protein family
Sapur.010G170300.2	3.80261267	-0.68003229	0.23709639	-2.89587	0.00378071	0.05699909	grey	-0.15277179	0.05169293		AT5G55060.1	
Sapur.T100100.1	7.71928114	-0.35404863	0.12160188	-2.8957	0.00378128	0.05700191	grey	-0.21534608	0.00675724		AT5G46150.1	
Sapur.004G135800.1	178.8225	0.20622802	0.07127619	2.895265	0.00378391	0.05706603	grey	-0.18122078	0.02312418	GD0046482;GD0005524;GD0046672	AT4G34500.1	Protein kinase superfamily protein
Sapur.013G117700.1	148.6244231	0.07503626	0.03881929	2.895027	0.00378610	0.05707673	grey	-0.26274618	0.00073883		AT2G36010.1	
Sapur.016G246700.1	54.24859383	0.29548456	0.10215427	-2.89339	0.00381055	0.05742976	grey	-0.21105657	0.00795674	GD0005885;GD0016020	AT5G76610.1	MSL6
Sapur.I02G038200.1	2.75330202	0.47053811	0.16257978	2.893505	0.00381166	0.05748809	grey	-0.22451174	0.00470211		AT5G61160.1	SDE5
Sapur.019G097600.2	3.93457533	0.47732879	0.16508105	2.890917	0.00384196	0.05787868	grey	-0.22562156	0.00449617		AT2G07240.1	
Sapur.007G088100.1	2.22862714	0.60883836	0.21064267	2.890429	0.00384287	0.05801885	grey	-0.42730725	2.37E-08	GD0046983;GD0006477;GD0006255;GD0005634;GD0033700	AT5G42620.2	AGL6,AGL32,TT16
Sapur.018G189400.1	25.75392183	0.21245705	0.07431341	2.889751	0.00385547	0.05808847	grey	-0.19843681	0.01272629		AT3G19180.1	
Sapur.I59G211500.4	0.73913688	0.96756885	0.33812235	2.889675	0.00386175	0.05821995	grey	0.06679804	0.45852393		AT5G03670.1	Histone superfamily protein
Sapur.003G132200.1	0.30542887	-1.24957163	0.43255587	-2.88881	0.00386706	0.05825743	grey	-0.3397169	4.46E-05		AT3G24060.1	Plant self-incompatibility protein S1 family
Sapur.I59G204000.1	48.7505223	0.38456868	0.06888570	2.88864	0.00388914	0.05828646	grey	-0.23772801	0.00717394		AT5G53345.1	
Sapur.005G186400.1	198.2145251	-0.16195886	0.05595883	-2.88802	0.00387674	0.05829969	grey	-0.22994568	0.00376847		AT5G66840.1	SAP domain-containing protein
Sapur.016G176700.1	57.24744865	0.12182455	0.04218349	-2.88801	0.00387824	0.05830669	grey	-0.26394535	0.00591929	GD070461	AT4G33890.2	
Sapur.008G202400.1	3.00747568	0.48183624	0.16697029	2.887935	0.00388377	0.05836737	grey	0.23288855	0.00493171		AT2G18960.1	Pectin lyase-like superfamily protein
Sapur.007G113300.1	487.7659498	0.08948579	0.03100325	2.88356	0.00389731	0.05866972	grey	0.19109263	0.01651242	GD0043085;GD0046385	AT2G31440.1	
Sapur.I02G038400.1	428.0979687	0.07610221	0.0263629	2.886318	0.00389735	0.05866972	grey	0.19225195	0.01579853		AT5G61600.1	ERF104
Sapur.013G084000.6	36.5313062	0.36863583	0.09131314	-2.88437	0.00392391	0.05906028	grey	-0.12466784	0.12038786	GD0085836;GD0006886	AT5G17030.1	ATCRM1,ATXPO1,HET2,XPO1
Sapur.I16G081700.1	2.18174038	0.48944681	0.16952164	2.884287	0.00392409	0.05906257	grey	0.26747047	0.00707757		AT1G14140.1	
Sapur.002G047400.1	2.06337033	0.49661837	0.17231584	2.882028	0.00395125	0.05949962	grey	0.20879608	0.00682784		AT4G22940.1	
Sapur.017G021200.1	20.47552886	0.98358333	0.34126801	2.881151	0.00396243	0.05966214	grey	0.27917812	0.00198932	GD0082304;GD0006508	AT5G08690.1	ULP1B
Sapur.I59G014700.1	0.31918807	-0.66425228	0.23066203	-2.88124	0.00396365	0.05968052	grey	-0.4097906	9.86E-08		AT3G05190.1	Plant protease inhibitor family protein (DUF247)
Sapur.004G071500.1	427.9099113	0.17340715	0.06018861	2.880956	0.00396674	0.05969361	grey	0.19627782	0.01735511		AT5G15530.1	BCCP2,CAC1-B
Sapur.010G281600.1	4.76802873	0.36401784	0.12616622	2.88049	0.00395539	0.05977587	grey	-0.25455571	0.01288714	GD0008270	AT5G65615.1	zinc ion binding
Sapur.012G089900.1	353.7923342	-0.42687428	0.14820557	-2.88032	0.00397665	0.05980515	grey	-0.2634989	0.00858712	GD0043531	AT5G14470.1	NB-ARC domain-containing disease resistance protein
Sapur.005G040600.1	1.32088944	0.52889142	0.18367524	2.879866	0.00398354	0.05991156	grey	-0.18939515	0.01751592	GD0045454;GD0006468;GD0005524;GD0046672	AT5G60600.1	RLK1
Sapur.007G126700.1	392.287664	-0.37796295	0.13119105	-2.88025	0.00397651	0.05981455	grey	-0.26060187	0.00988624	GD0016758;GD0081152	AT4G38820.1	AT5G47160.1
Sapur.I59G087900.1	3.42080167	-0.27398795	0.42349344	-0.64827	0.00398631	0.05988679	grey	-0.22439185	0.00308366		AT4G26170.2	CLF2,CLFR2,NCLFR2
Sapur.014G070900.1	65.15439853	0.2011904	0.06986558	2.879679	0.00398799	0.05991669	grey	0.22614329	0.00443647		AT3G46170.2	
Sapur.005G237100.1	3.3797577	-0.65406895	0.23108369	-2.87969	0.00398	0.05992306	grey	0.23372102	0.00348818		AT5G55530.1	
Sapur.010G094900.1	1123.311366	-0.09319154	0.03237812	-2.87922	0.00399294	0.06001959	grey	-0.27591006	0.00466334		AT5G14210.1	CLF2,CLFR2,NCLFR2
Sapur.007G117500.2	11.60705335	-0.42437474	0.14738242	-2.87809	0.00400921	0.06021134	grey	-0.23056572	0.00370167		AT2G03320.1	RNA-binding ASCH domain protein
Sapur.010G029300.1	210.3116204	-0.60833703	0.23216092	-2.87798	0.00402301	0.06023027	grey	-0.22061265	0.00518855	GD0082304;GD0006508	AT5G02230.1	ULP1 protease family protein
Sapur.017G162600.1	52.10075339	-0.96279592	0.33453664	-2.87786	0.00400383	0.06024963	grey	-0.30726468	2.58E-07		AT5G62590.1	HERK1
Sapur.003G204300.2	2.77648924	0.49487697	0.16958185	2.877604	0.00400979	0.06029569	grey	0.25740617	0.01513563	GD0005634;GD0006255	AT4G00502,MFD2	MATH/CONDAM, MATH DOMAIN 2
Sapur.007G120900.1	2.89832676	0.86639352	0.29629132	2.876868	0.00401637	0.0604311	grey	0.21902748	0.05348076		AT5G14520.1	GAL6,GAL2
Sapur.014G007300.1	3.66381874	-0.66491197	0.17557645	-2.87674	0.00403473	0.06041134	grey	0.14772922	0.07604134	GD0005515	AT5G27461.1	ATCSA-1
Sapur.010G094600.1	441.2328827	0.37607797	0.13079157	2.876232	0.00403537	0.06045746	grey	0.18356114	0.02138589	GD0005514;GD0010277	AT5G26530.2	ACD1-like,PTC52,TIC55-IV
Sapur.I59G124700.1	847.5124759	-0.1383562	0.04814578	-2.87422	0.00406675	0.06068602	grey	0.20280609	0.01835409		AT2G37820.1	
Sapur.I02G089200.4	1.49205241	-0.70581007	0.24561947	-2.8708	0.00405569	0.06100658	grey	-0.16385805	0.16491553	GD0005515;GD0006468;GD0046672	AT4G03190.1	SRF3
Sapur.I59G145700.1	0.43561821	-0.96158224	0.33478898	-2.86947	0.00407573	0.06102178	grey	-0.29273648	0.00108467		AT5G57220.1	Arabidopsis protein of unknown function (DUF241)
Sapur.I02G097800.1	18.38913313	0.41558144	0.14463975	2.873133	0.00416241	0.06211518	grey	0.15154092	0.05813636	GD0015514;GD0016491;GD0018081	AT1G76690.1	ATPRD2,DPR2
Sapur.I02G062700.3	0.47751276	-0.99200502	0.34558723	-2.87308	0.00408884	0.06112222	grey	-0.03587824	0.65437564	GD0015515;GD0006468;GD0015134;GD0046672	AT5G58300.2	Leucine-rich repeat protein kinase family protein
Sapur.I02G038500.1	0.95304032	-0.81840344	0.28224149	-2.87132	0.00409507	0.06118459	grey	-0.22743456	0.02775522	GD0006457;GD0005770;GD0043	AT5G65570.1	rootamer-containing protein
Sapur.008G014000.1	1.22207848	-0.66051996	0.2302755	-2.87112	0.00409174	0.06150697	grey	-0.2310235	0.00590174		AT3G02040.1	Mitochondrial substrate carrier family protein
Sapur.I59G204900.1	24.50226495	0.15188871	0.0887849	2.870447	0.00410337	0.06155338	grey	0.19341578	0.01522407	GD0005524	AT4G13120.1	arabinose kinase
Sapur.005G178500.1	77.8518604	0.26606526	0.09260075	2.87029	0.0041095	0.06165779	grey	0.1981089	0.01287508		AT3G11180.1	ATMYB14,MYB14,MYB14A7
Sapur.I16G298300.1	2.91844850	-0.50137528	0.1829697	-2.87001	0.00411071	0.06181152	grey	-0.19891489	0.02158607		AT4G18810.2	
Sapur.I06G178300.1	132.2741145	-0.18712769	0.06526726	-2.8671	0.00414546	0.06227467	grey	-0.26814512	0.00072692		AT5G60360.1	
Sapur.I02G062700.2	9.69561272	0.27427666	0.09568061	2.866252	0.00416179	0.06238964	grey	-0.25739724	0.00118909	GD0082270;GD0005515	AT5G58190.1	RING-U box protein
Sapur.I01G001200.3	10.39507276	-0.32432837	0.11315564	-2.86623	0.00415393	0.06246015	grey	-0.13225126	0.09870117	GD0005885;GD0016020;GD0015297;GD0015138;GD0006855	AT3G21690.1	MATE efflux family protein
Sapur.I01G181100.3	19.60485868	0.80507203	0.14134089	2.86592	0.00417598	0.06268966	grey	0.21425847	0.00748205		AT5G19320.1	lactoylglutathione lyase-like family protein
Sapur.I02G062800.1	2.21321892	0.75180847	0.26225679	2.865021	0.00418069	0.06280875	grey	0.18283102	0.02245727	GD0016491;GD0016491	AT

Sapur.01G0231400.1	1.42085483	0.725804676	0.256790583	2.825609	0.004739089	0.007363684	grey	0.120872399	0.13156514	GO:0006508,GO:0004195	AT1G11080.2	scp31	serine carboxypeptidase-like 8	NA	
Sapur.008G118800.1	53.06698614	-0.15462758	0.054517699	-2.82528	0.004723981	0.007070686	grey	-0.223203796	0.004955293		AT1G24095.1		Putative thiol-disulphide oxidoreductase DCC	thiol-disulfide oxidoreductase DCC, putative	
Sapur.008G288300.1	0.935627331	0.85964731	0.306215444	2.825123	0.004726246	0.007037755	grey	-0.198728836	0.012532087					NA	
Sapur.007G019600.1	3.416096258	-0.63355577	0.224259347	-2.82421	0.004739726	0.007093611	grey	-0.205997193	0.009664174		AT4G36500.1			hypothetical protein	
Sapur.005G050300.1	2.322237843	0.514894622	0.182342225	2.821763	0.004794325	0.007103203	grey	-0.205294883	0.008896641		AT1G71730.1			late embryogenesis abundant protein, putative	
Sapur.01G238700.1	8.687744626	-0.60520602	0.214364085	-2.82273	0.004761657	0.007125468	grey	-0.213889399	0.007149239					transmembrane protein, putative	
Sapur.002G077200.1	298.5747148	0.224764613	0.079648354	2.82162	0.004778214	0.007149918	grey	-0.206229721	0.000993588		AT1G78170.1			WW domain protein, putative	
Sapur.005G050600.1	3.168076311	0.752378751	0.266653384	2.821561	0.004779059	0.00715086	grey	-0.203189856	0.010702727		AT1G16030.1		Leucine-rich repeat (LRR) family protein	LRR amino-terminal domain protein	
Sapur.002G011100.1	4.1594551	0.370731544	0.131196337	2.821475	0.004780329	0.00752436	grey	0.13852155	1.45E-05	GO:0055085,GO:0016021	AT1G16980.2		Major facilitator superfamily protein	hippocampus abundant transcript 1 protein	
Sapur.003G062800.1	775.6682284	0.224984759	0.079647904	2.821436	0.004781294	0.007163234	grey	0.203970512	0.011391786		AT5G45490.1		Plastid-lipid associated protein PAP / fibrillin family protein	plastid-lipid associated protein, putative	
Sapur.002G050400.1	10.59052512	-0.25402507	0.090194264	-2.82086	0.004789557	0.007165585	grey	-0.190958651	0.015189879		AT1G71730.1		DNAse I-like superfamily protein	type I inositol-1\3\4-trisphosphate 5-phosphatase	
Sapur.004G208300.1	1.364129662	0.488851052	0.173701869	2.815021	0.004818951	0.00717885	grey	-0.222682669	0.005058243	GO:0006355,GO:0003677	AT2G28320.2		Dof type zinc finger DNA-binding family protein	Dof zinc finger protein	
Sapur.009G031900.1	1010.279461	0.136316464	0.048418409	-2.81993	0.004804931	0.007185376	grey	-0.226219536	0.004387078	GO:0005524,GO:0009506,GO:0004222	AT4G07060.1	ftsh7	FTSH protease 7	ATP-dependent zinc metalloprotease FtsH	
Sapur.004G317000.2	2.178076865	0.487220192	0.173097466	2.813721	0.004908428	0.007359187	grey	-0.227778408	0.005184964	GO:0008270,GO:0006355	AT4G38370.1	FR18	FAR1-related sequence 9	FAR1-related sequence protein	
Sapur.008G135900.3	8.552298896	-0.292665891	0.103891021	-2.81924	0.004817152	0.007200164	grey	-0.225748289	0.004473273		AT3G23280.1	XBAT35	RING-H2 zinc finger protein	E3 ubiquitin-protein ligase XBAT34, putative	
Sapur.008G288300.1	0.935627331	0.85891169	0.318313630	2.810604	0.005165754	0.007633589	grey	-0.198762111	0.033641289		AT5G26110.1		Metal-dependent phosphohydrolase	metal-dependent phosphohydrolase HD domain protein	
Sapur.01G076200.1	344.8157732	-0.594347393	0.210850118	-2.81881	0.004830135	0.007200659	grey	-0.229173671	0.003887888					hypothetical protein	
Sapur.008G060000.1	413.2185351	0.217192754	0.077065498	2.818288	0.004828051	0.007205573	grey	0.196253529	0.01376248					NA	
Sapur.01G413900.1	8.623662275	-0.754637723	0.115233391	-2.81809	0.004835277	0.007224763	grey	-0.208459377	0.008032602	GO:0006468,GO:0005524,GO:0004672	AT5G55540.1		Protein kinase superfamily protein	MAP Kinase like protein	
Sapur.008G050900.1	216.9370911	0.095044309	0.033729501	2.817839	0.004834801	0.007200014	grey	0.178833357	0.024203976	GO:0043565,GO:0006355,GO:0003700	AT5G58550.1	ARGEO,DPBF3	ABA-responsive element binding protein 3	BZIP transcription factor	
Sapur.01G177200.1	74.60450644	-0.345631757	0.478318108	-2.81331	0.004903443	0.007328381	grey	-0.228613784	0.004825948	GO:0045454,GO:0015035,GO:0009055	AT5G42930.1		Thioredoxin family protein	monothiol glutaredoxin-S2 protein	
Sapur.008G068400.1	732.7741467	-0.317232216	0.112631529	-2.81735	0.004842219	0.007240289	grey	-0.235661108	0.002946459	GO:0033897,GO:0003723	AT3G02980.1	ATRNL1,RNS1	ribonuclease T	ribonuclease T2	
Sapur.005G032100.1	1.016650917	0.776570971	0.274929925	-2.81724	0.004843229	0.007240289	grey	-0.251514048	0.004854417	GO:0043565,GO:0006355,GO:0003700	AT5G47390.1	AWRKY47,WRKY47	WRKY family transcription factor	WRKY transcription factor	
Sapur.003G076100.1	55.57426886	0.144538303	0.051306883	2.817133	0.004854491	0.007304227	grey	-0.20605885	0.009622026		AT4G17250.1			plant/MNU7-17 protein	
Sapur.004G061100.1	1.368713303	0.682024855	0.242188556	2.812609	0.004908828	0.007324865	grey	-0.190769828	0.017262667		AT1G77460.1			hypothetical protein	
Sapur.01G119900.1	25.50973607	-0.629469479	0.223435271	-2.81676	0.004851051	0.007252947	grey	-0.227629989	0.006142654	GO:0005975,GO:0004553	AT4G44680.1	BGLU17	beta glucosidase 17	beta-glucosidase	
Sapur.01G412300.1	26.94358815	0.469292427	0.159518758	2.810591	0.004853632	0.007255877	grey	0.219828559	0.005711474					pollen protein Ole E 1-like protein	
Sapur.009G194600.1	3.906869009	-0.47268275	0.172727792	-2.81569	0.004888035	0.007307076	grey	-0.197027653	0.013383762	GO:0016788	AT5G22810.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase	
Sapur.002G030800.1	86.93545356	-0.342416049	0.092583174	-2.81548	0.004870402	0.007280289	grey	-0.220742358	0.005466882	GO:0008270	AT5G27280.1		Zim17-type zinc finger protein	DNL zinc finger protein	
Sapur.005G139800.1	1.182044284	0.819000117	0.297154142	2.808588189	0.005188257	0.007813589	grey	-0.181882423	0.022618404	GO:0102246,GO:0016020,GO:0008378,GO:0006486	AT3G58010.1	GALT1	galactosyltransferase 1	beta-1\2\3-galactosyltransferase	
Sapur.009G038100.4	23.5218055	-0.34875563	0.125508785	-2.81497	0.004878249	0.00729136	grey	0.07848531	0.32814487					NADP(H)-quinone oxidoreductase chain, putative	
Sapur.01G177200.1	74.60450644	-0.345631757	0.478318108	-2.81331	0.004903443	0.007328381	grey	-0.184167526	0.020931724		AT5G19580.1		Tryptophan/tyrosine permease family protein	tryptophan/tyrosine permease family protein	
Sapur.01G097300.1	61.10702566	-0.444185021	0.157809892	-2.81308	0.004906945	0.007332216	grey	-0.236177707	0.002846311		AT5G03670.1		ankyrin repeat family protein	NA	
Sapur.01G000100.1	45.68466829	0.716600	0.254978864	2.808452283	0.005067	0.007332216	grey	0.36492101	2.61E-06					NA	
Sapur.006G085500.1	14.42854704	0.358105051	0.127313348	2.811785	0.004914551	0.007339327	grey	0.193210709	0.01533085		AT2G38310.1	PYL4,RCAR10	PYR1-like 4	abscisic acid receptor PYL4	
Sapur.006G208400.1	2.180469676	0.525621504	0.187034284	2.810594842	0.005024	0.007345264	grey	-0.181819558	0.023931724	GO:0006468,GO:0005524,GO:0004672	AT5G38280.1	PRSK	PRS-like receptor kinase	NA	
Sapur.01G561100.2	1.496388956	0.717699864	0.255282013	2.812013	0.004918376	0.007354242	grey	-0.203115501	0.010575363					NA	
Sapur.005G097900.1	25.43535626	0.232212623	0.082554578	-2.81174	0.004927503	0.007362316	grey	-0.234337728	0.003137439		AT3G18350.1	AHB24,HB24	homeobox protein 24	2\-HD homeobox protein cyc/tcp-rich dimerization domain protein	
Sapur.7G008B0.1	0.243496668	0.787867298	0.458056749	2.811613	0.004929828	0.007364788	grey	0.362918723	2.99E-06		AT2G38180.1		Melibiase family protein	NA	
Sapur.1SZG037300.1	42.00655485	0.267807568	0.095282010	2.811273	0.004934586	0.007372233	grey	0.213267181	0.007321694	GO:0082720,GO:0003676				NA	
Sapur.005G140600.1	295.1840437	0.164964254	0.058685189	2.810687	0.004943439	0.007385124	grey	0.176043439	0.034792526		AT3G04330.1		NHL domain-containing protein	NHL domain protein	
Sapur.002G157300.1	2.178038833	0.625888807	0.222785547	2.809375	0.004963783	0.007414889	grey	0.222593927	0.005077912	GO:0045454,GO:0015035,GO:0009055	AT3G03020.1		Thioredoxin superfamily protein	monothiol glutaredoxin-S6 protein	
Sapur.7G0430.2	0.46370004	0.875122205	0.311423973	2.809287	0.004965	0.007416	grey	-0.181618156	7.03E-05	GO:0005975,GO:0004553	AT1G05200.1		O-Glycosyl hydrolases family 17 protein	glucan endo-1\3\2-beta-glucanase	
Sapur.002G076600.2	10.3028162	-0.246288282	0.087707591	-2.80806	0.004984076	0.007444489	grey	-0.208175171	0.009331144	GO:0008168,GO:0008152	AT5G39140.1		5-adenosylmethionine-dependent methyltransferase, putative	5-adenosylmethionine-dependent methyltransferase, putative	
Sapur.003G090600.1	57.36208854	0.554661365	0.197548736	2.807719	0.005009	0.007452064	grey	-0.178169225	0.025181407	GO:0009055	ABPN		plastocyanin	basic blue protein	
Sapur.01G092100.1	6.460696128	-0.874027583	0.311325728	-2.80744	0.004993734	0.007458241	grey	-0.243093531	0.002100791				Disease resistance protein (TIR-NBS-LRR class) family	NA	
Sapur.01G027300.1	71.71196006	-0.58975895	0.208320412	-2.80701	0.005000413	0.007467979	grey	-0.235228354	0.000293664	GO:0004674,GO:0048544,GO:0006468,GO:0004672	AT5G27290.1		S-locus lectin protein kinase family protein	protein kinase family protein	
Sapur.7D97200.1	372.3024761	0.160438825	0.154380572	2.806959	0.005050115	0.007486663	grey	0.263869222	0.000940089		AT2G17630.1		Phosphatidylinositol 3- and 4-kinase family protein with FAT domain	NA	
Sapur.7D7400.1	8.750745105	-0.796378403	0.28388305	-2.80664	0.005060095	0.00747569	grey	-0.264894906	0.01184919					NA	
Sapur.01G022000.1	106.8288027	-0.555000413	0.198154371	-2.80633	0.005066125	0.007481393	grey	-0.219292592	0.006855651		AT1G70150.1		zinc ion binding	WD40 finger protein	
Sapur.01G178600.1	0.324904656	1.171880602	0.417582916	2.806342	0.005092743	0.007481956	grey	0.203819786	0.000115772	GO:0003677,GO:0005515	AT3G19510.1	HAT3.1	Homeodomain-like protein with RING/FYVE/PHD-type zinc finger domain	PHD-Finger protein	
Sapur.01G025400.1	304.1885167	0.158075566	0.055186182	2.806202	0.005092924	0.007484671	grey	0.205549765	0.009896611	GO:0016021,GO:0004190	AT5G07010.1	PS1	Presenilin-1	presenilin-like protein	
Sapur.01G261800.1	18.68159904	0.297961779	0.106176946	2.806087	0.005064171	0.007487203	grey	0.248118252	0.001729037		AT5G22730.1		SNARE-like superfamily protein	transmembrane protein, putative	
Sapur.01G082200.1	10.87635631	0.527384491	0.187905267	2.805681	0.005101681	0.00749	grey	-0.222703984	0.005005589					NA	
Sapur.01G089600.1	2.46097411	0.601894327	0.214528303	2.805661	0.005021144	0.007496092	grey	0.223531603	0.00338262					hypothetical protein	
Sapur.7D66D0.1	17.53716234	0.388956564	0.138528133	2.805162	0.005023888	0.007498054	grey	-0.171335898	0.032416474					NA	
Sapur.008G154900.1	1.121834552	-0.712476014	0.253999114	-2.80503	0.005023136	0.007510032	grey	-0.23315579	0.003709016		AT1G58840.2	CCI4	cofactor assembly of complex C	DUF2930 family protein	
Sapur.7D91100.1	1.21991318	0.859156075	0.299239709	2.804294	0.005242692	0.007529643	grey	0.231827794	0.003919387					NA	
Sapur.01G022800.2	-0.561172866	0.851880904	0.303608804	2.803688	0.005061144	0.007554466	grey	0.251982613	0.001459636		AT1G71140.3	SWEETIE	HEAT repeat-containing protein	NA	
Sapur.01G623B700.1	83.51489739	-0.219854069	0.078446527	-2.80262	0.005088883	0.007565023	grey	-0.199491829	0.012263674		AT5G48020.1			heat- and acid-stable phosphoprotein	
Sapur.01G604540.1	4.931728747	-0.460826354	0.167123285	-2.80249	0.005070937	0.007567786	grey	-0.400842654	1.97E-07		AT3G27610.3		Cysteine proteinases superfamily protein	OTU-like cysteine protease	
Sapur.7D3500.1	7.030577784	0.358871947	0.128412818	2.802461	0.005071431	0.007568132	grey	0.215795978	0.006154845					NA	
Sapur.7D7600.1	0.268952683	1.164604448	0.56302479	2.802187	0.005078891	0.007578361	grey	0.372050651	1.82E-06					NA	
Sapur.009G015500.1	2.516237677	-0.572565864	0.204362402	-2.80172	0.005083129	0.007584562	grey	-0.20404646	0.01184919					NA	
Sapur.01G018200.2	14.92105061	-0.551854291	0.197124398	-2.80146	0.005088712	0.007589224	grey	0.020211104	0.835622644	GO:0006468,GO:0004672	AT4G15490.2	CRLK1	Protein kinase superfamily protein	serine/Threonine kinase domain protein	
Sapur.01G083400.1	10.42885669	-0.553814541	0.197688974	-2.80145	0.005087428	0.007589955	grey	-0.224894684	0.006429076		AT5G62360.1		Carbohydrate-binding-like fold	Carbohydrate-binding-like protein	
Sapur.009G013300.1	1336.787241	0.136705838	0.048796562	2.801393	0.005083535	0.007596803	grey	0.196026346	0.015368215	GO:0005515,GO:0003723	AT5G7870.2	eIFiso4G1	MIF4G domain-containing protein / MA3 domain-containing protein	eukaryotic translation initiation factor iso4G	
Sapur.01G058500.1	6.057417019	-0.439452451	0.156908908	-2.80069	0.005089424	0.007607161	grey	-0.213676929	0.007208554					NA	
Sapur.01TG139000.1	38.00745279	-0.362447395	0.129453343	-2.79983	0.005123972	0.007670206	grey	-0.180491535	0.023691756	GO:0016788	AT4G09960.1	GLIP1	GDSL lipase 1	GDSL esterase/lipase	
Sapur.01G113300.1	16.50822284	-0.570051136	0.181838988	-2.79965	0.005115875	0.007678367	grey	-0.152276297	0.050924804	GO:0005515,GO:0003723	AT3G27830.1		Gro/Sin1 interacting protein	Gro/Sin1 interacting protein	
Sapur.003G079000.2	8.322626867	0.310505786	0.110974706	2.799294	0.005121454	0.007686646	grey	0.231609661	0.005196341	GO:0006468,GO:0005524,GO:0004672	AT4G28540.1	CKL6,FAP61	casein kinase I-like 6	casein kinase-like protein	
Sapur.006G198600.2	2.163663334	0.527141758	0.191935088	2.798657	0.005132946	0.007695096	grey	0.191692742	0.016160818		AT3G60500.1			hypothetical protein	
Sapur.7T48600.1	139.7631201	0.362806623	0.129479243	-2.79881	0.005140232	0.007705616	grey	-0.19118819	0.016451821		AT5G11510.2	AtMYB38A,MYB38-4	myb domain protein 3r-4	NA	
Sapur.01G620000.1	2.175379481	0.509214506	0.182073	2.797777	0.005165679	0.007732047	grey	-0.210246156	0.008206688		AT2G40420.1		Uncharacterized P-loop containing NTP hydrolase family protein UCP029193	NA	
Sapur.01G042700.1	119.2891512	0.153083586	0.054706557	2.797445	0.005150853	0.007806417	grey	0.173530077	0.029746388	GO:0009439	AT2G34860.1	CYN	cyanase	cyanate hydratase	
Sapur.01G187800.2	14.73662609	0.362806168	0.129654991	-2.79708	0.005155668	0.007808704	grey	0.218133666	0.006055795	GO:0009231,GO:0003935,GO:0008686	AT4G04500.1	ATGCH_ATRIBA3,GCH_RFD1	GTP cyclohydrolase II	3\,5,2\-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	
Sapur.01G002300.1	5.719625049	0.425010175	0.152034326	2.797012	0.005157727	0.007809017	grey	0.223508291	0.003737573					NA	
Sapur.006G217000.1	12.63177155	-0.349882968	0.089346228	-2.79678	0.005161448	0.007805173	grey	-0.248802706	0.001677187					hypothetical protein	
Sapur.007G034800.1	0.835506786	-0.784661668	0.280531983	-2.79669	0.005163237	0.007807464	grey	0.167284934	0.032515325	GO:0008168	AT1G11480.1	ATBSMT1,BSMT1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NA	
Sapur.006G048100.2	2.873449814	-0.451712458	0.161543195	-2.79624	0.005189858	0.007870317	grey	0.082314548	0.355411904		AT1G80530.1		Major facilitator superfamily protein	nodulin-like protein	
Sapur.01G218300.1	7.628836797	-0.685226569	0.245135125	-2.79535	0.005183049	0.007706947	grey	0.193979758	0.015020914		AT2G37230.1		Protein of unknown function (DUF1635)	DUF1635 family protein	
Sapur.01G261200.3	5.410369371	-0.391830059	0.140176305	-2.79527	0.005185517	0.007729395	grey	-0.214873651	0.006989702		AT5G42370.2	ATSOS3,CBL4,SOS3	Calcium-binding EF-hand family protein	calcineurin B-like protein 4-1	
Sapur.008G058200.1	6.967551698	0.402832231	0.143849772	2.794808	0.005193503	0.007760214	grey	0.197319855	0.013123307	GO:0006355,GO:0003700,GO:0007275	AT5G42520.1	ASAL1,ATWIL1,WIL,WRI1	Integrase-type DNA-binding superfamily protein	AP2 domain transcription factor	
Sapur.01G134800.1	667.0601993	-0.122039422	0.043988557	-2.79455	0.005197269	0.007766134	grey	-0.223031377	0.009773146	GO:0046488,GO:0016307	AT5G19180.1	ATPIP5K1,ATPIPK1,PIP5K1	phosphatidylinositol-4-phosphate 5-kinase 1	phosphatidylinositol-4-phosphate 5-kinase	
Sapur.008G082200.1	2.653170016	0.497187827	0.184121659	-2.79324	0.005210704	0.007774737	grey	-0.182313609	0.022604595					NA	
Sapur.01G247900.8	8.250175872	0.289720641	0.103718928	2.793325	0.005219393	0.007774737	grey	0.210432328	0.008160907		AT1G76700.1	BEH4	BES1/BZR1 homolog 4	brassinosteroid signaling positive regulator-like protein	
Sapur.008G000900.1	13.32786215	-0.468802194	0.167661253	-2.79307	0.005219455	0.007783194	grey	-0.175071817	0.038303193	GO:0008261,GO:0008803,GO:0005576	AT5G49780.1	ATPK2-PORMER SYNBDK1	phosphoribulokinase precursor protein	phosphoribulose precursor protein	
Sapur.009G011700.1	4.008765227	-0.457650451	0.163848593	-2.79313	0.005230071	0.007778718	grey	0.188712927	0.017931959	GO:0007165	AT2G36980.4	CIPK3,SnRK3.17	CBL-interacting protein kinase 3	CBL-interacting Serine/Threonine-kinase	
Sapur.008G142700.1	0.570599666	1.085618465	0.388680705	2.790686	0.005202788	0.007794635	grey	-0.242866616	0.003431325		AT4G42230.1			hypothetical protein	
Sapur.007G117200.1	148.6841058	-0.226282269	0.08457985	-2.793	0.005222194	0.007798118	grey	-0.224120296	0.003955356		AT5G07680.1		Plant protein of unknown function (DUF936)	NA	
Sapur.009G196600.3	10.41608077	0.30884885	0.110591299	2.792705	0.005236937	0.007787896	grey	0.173506167	0.029788021		AT5G16330.1			NA	
Sapur.01G618300.1	20.07503939	0.364522765	0.130217671	2.791931	0.005239451	0.007806019	grey	0.214526275	0.006975365	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G37570.1		Leucine-rich repeat protein kinase family protein	Leucine-rich repeat protein kinase family protein	
Sapur.006G188800.1	104.1232602	0.215161495	0.077070115	2.791789	0.005241753	0.007809268	grey	0.190831125	0.016663788		AT3G26110.1		Protein of unknown function (DUF761)	transmembrane protein, putative	
Sapur.008G205300.1	1.872664972	0.509016833	0.182340684	2.791571	0.005245293	0.007814189	grey	0.195237102	0.014242607		AT2G27520.1			NA	
Sapur.003G085300.1	3.174002254	-0.485439931	0.174104072	-2.79111	0.005252838	0.007824725	grey	-0.219264444	0.005832072	GO:0006468,GO:0005524,GO:0004672	AT5G18100.1	PEPKR1	phosphoenolpyruvate carboxylase-related kinase 1	calcium-dependent kinase	
Sapur.7D21100.1	-0.294780281	0.922884294	0.338628777	2.790601	0.005255242	0.007828584	grey	-0.237261529	0.005283691		AT1G08140.1	ATCOMT1,ATXROI1,HET2,XPO	exportin 1A	NA	
Sapur.005G177400.1	0.21910267	1.540820047	0.55216785	2.790492	0.005262798	0.007838855	grey	0.41341255	7.36E-08	GO:0005515,GO:0016491	AT4G10500.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA	
Sapur.006G085100.1	2.538607748	0.498802197	0.178698553	2.79066	0.005263803	0.007849594	grey	-0.219630576	0.008093722		AT5G46680.1		Pentatricopeptide repeat (PPR-like) superfamily protein	PPR containing plant protein, putative	
Sapur.01TG125800.1	1115.7943	0.108632231	0.038943642	2.789493	0.005279393	0.007862864	grey	0.200260018	0.011909863		AT4G02720.1		Class I glutamine amidotransferase-like superfamily protein	intracellular protease	
Sapur.7T23100.1	3.805074651	-0.459134576	0.164602392	-2.78929	0.005280754	0.007864538	grey	-0.221297988	0.006242404		AT5G28455.1	CLE25	CLAVATA/ESR-RELATED 25	NA	
Sapur.01G029300.9	24.81308214	0.290696941	0.10434528	2.788501	0.005295255	0.007885778	grey	0.22880607	0.004272622	GO:0016787	AT4G38960.1	amuB,NUDT4	nudix hydrolase homolog 4	nudix hydrolase	
Sapur.006G155600.1	0.365955154	1.311786369	0.471234803	2.787965	0.005300459	0.00789821	grey	0.243092296	0.003215181	GO:0007165	AT4G15731.3	SCR,111	SCR-like 11	NA	
Sapur.008G268800.1	2.844418374	0.641760066	0.230239335	-2.78761	0.005318809	0.007906385	grey	-0.221837374	0.005239546					NA	
Sapur.01G025300.1	49.33775915	-0.28665805	0.10283825	-2.78747	0.005312215	0.007906611	grey	-0.219712771	0.005698806		AT1G01300.2			transmembrane protein, putative	
Sapur.01G052900.1	0.658817464	-0.931745296	0.33175168	-2.787	0.005319443	0.007920012	grey	-0.210744013	0.010192091	GO:0055114,GO:0046872,GO:0006801	AT1G18100.1	CSD3	copper/zinc superoxide dismutase 3	NA	
Sapur.01G024100.1	44.57323798	0.201000489	0.072118199	2.786712	0.005324584	0.007927315	grey	0.223827822	0.005303569		AT5G15980.1		Pentatricopeptide repeat (PPR) superfamily protein	NA	
Sapur.006G344300.1	106.0145326	0.205027358	0.074341661	2.78668	0.005325102	0.007937739	grey	-0.175527017	0.036104218	GO:0005085,GO:0016020,GO:0008810,GO:0015171,GO:0003333	AT5G40420.1		Amino acid permease family protein	amino acid transporter, putative	
Sapur.01G027700.1	1.12237004	0.68279334	0.245054584	2.786241	0.005323237	0.007938128	grey	-0.214203138	0.007061171	GO:0016787	AT3G26040.1		H|XOD-type acyl-transferase family protein	NA	
Sapur.01G138700.1	259.4499669	0.145984416	0.052418357	-2.78528	0.005348093	0.007956219	grey	-0.228379798	0.004616753	GO:0006468,GO:0005524,GO:0004672	AT5G08670.1		Protein kinase superfamily protein	receptor-like kinase	
Sapur.01G502100.1	256.8577884	0.118319291	0.046675346	2.784767	0.005369604	0.007971696	grey	0.185188884	0.037776572		AT4G08830.1		Uncharacterized conserved protein UCP029193	hypothetical protein	
Sapur.007G002100.3	5.269660696	0.346782484	0.124538468	2.784541	0.005363052	0.007976612	grey	0.204949427	0.010198112	GO:0006468,GO:0005524,GO:0004672	AT5G17220.1		Protein kinase superfamily protein	Serine/Threonine-kinase Cx32, putative	
Sapur.01G062600.1	232.3313	0.108632231	0.038943642	2.784197	0.005374893	0.007991185	grey	0.224793806	0.004664857		AT5G05610.1	AtmuB,NUDT14	nudix hydrolase homolog 6	DUF1421 family protein	
Sapur.009G217000.5	0.80541127	-0.813201963	0.292106138	-2.78395	0.005370208	0.007992362	grey	-0.225029629	0.004598308	GO:0006468,GO:0005524,GO:0004672	AT3G44200.1	ATNEK6,IBO1,NEK6	NIMA (never in mitosis, gene A)-related 6	protein kinase family protein	
Sapur.01G207700.1	5.46357774	-0.343681328	0.123168411	-2.78389	0.005374893	0.007997696	grey	0.215885804	0.007384736		AT5G67060.1			transmembrane protein	
Sapur.1SWG271300.2	1.660689952	-0.67156709	0.241261257	-2.78357	0.005376461	0.008000948	grey	-0.258790567	0.001606408	GO:0008440	GO:0017601	ATIPK2BETA,IPK2B,IPK2BET	inositol polyphosphate kinase 2 beta	inositol polyphosphate multikinase	
Sapur.01G029000.9	0.632862606	1.260686461	0.452857211	2.784251	0.005388112	0.008060021	grey	0.22880607	0.004272622	GO:0016787	AT4G38960.1	amuB,NUDT4	nudix hydrolase homolog 6	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region	
Sapur.01G103600.1	231.9777562	0.129489316	0.051200353	2.783105	0.005380138	0.008011653	grey	0.197302923	0.012251115	GO:0006468,GO:0005524,GO:0004672	AT3G09830.1		Protein kinase superfamily protein	kinase APK1A, putative	
Sapur.01G062900.1	102.5680368	0.147760066	0.058396	2.783025	0.005390641	0.008036285	grey	0.202408663	0.010960605	GO:0055114,GO:0016021,GO:0005375	AT5G44420.1	COPT1	copper transporter 1	copper transporter	
Sapur.01G189900.1	24.21152022	-0.284289848	0.102161749	-2.78274	0.005390188	0.008019922	grey	-0.216375251	0.006546156	GO:0005515,GO:0043531	AT5G63020.1		Disease resistance protein (CC-NBS-LRR class) family	NBS-LRR type disease resistance protein	
Sapur.01G089800.1	185.8760845	0.145321665	0.052868182	-2.7804	0.005415202	0.008052409	grey	-0.190759896	0.015341721	GO:0005524,GO:0003676,GO:0004386	AT4G39380.1	DEAH9,HCA1	DEAD/H-box helicase family protein	ATP-dependent RNA helicase, putative	
Sapur.01G052400.1	6.026745622	0.318882976	0.116635479	2.781061	0.005419429	0.008061	grey	-0.112467847	0.187926706		AT1G69510.1		DOT domain-containing protein	aminoacyl-tRNA synthetase	
Sapur.01G069600.1	31.17083487	0.334760343	0.12039557	2.780338	0.005430239	0.00807807	grey	0.212306432	0.007588393	GO:0006355,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AT5G16692.1	AGL12,XAL1	AGAMOUS-like 12	AGAMOUS-like 12	
Sapur.01G139300.1	9.521484	0.513000321	0.189417939	-2.78043	0.005437	0.008082832	grey	-0.208479229	0.009332116	GO:0016491	AT5G14170.2	GLR3.6	aldehyde dehydrogenase 6B2	NA	
Sapur.004G139800.1	10.60776436	0.523256427	0.188215366	-2.7801	0.005439429	0.008083369	grey	-0.178023134	0.024872092		AT2G34630.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative	
Sapur.01TG108600.1	0.347205532	0.93681113	0.337763869	2.778873	0.005458019	0.008085454	grey	0.275268651	0.000475532	GO:0032012,GO:0005886	AT5G58010.1		SEC7-like guanine-nucleotide exchange family protein	NA	
Sapur.01G041200.2	0.578722888	-0.905132405	0.326163203	-2.77975	0.005440051	0.008091231	grey	-0.248581695	0.001828486	GO:0016787	GO:0081030.1		N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	licesparyl/peptidase/L-asparaginase	
Sapur.006G205300.1	96.23733908	0.182011207	0.066000187	-2.78

Sapur.012G068000.1	215.0680165	0.553327211	0.202515669	2.752269	0.006289983	0.00929846	grey	0.194920748	0.014431283		CBG03180.1	Pectin lyase-like superfamily protein
Sapur.008G168300.1	1591.835598	0.137009726	0.050160237	2.731461	0.006205804	0.009214162	grey	0.192461897	0.015750963	GO:0046872;GO:0030001	CBG06130.1	Heavy metal transport/detoxification superfamily protein
Sapur.012G018200.2	70.83699795	0.894369976	0.327641316	2.731282	0.006208852	0.009225541	grey	0.323400047	1.61E-05		CBG05145.1	RING/U-box superfamily protein
Sapur.016G188900.1	0.493401581	-1.10603117	0.404964881	-2.73118	0.006303838	0.009328059	grey	-0.272642352	0.005511144	GO:0016758;GO:0008108	CBG22360.1	UDP-glucosyltransferase 85A2
Sapur.006G113000.1	0.52319868	0.925051158	0.338826439	2.73053	0.006322921	0.009358664	grey	-0.23934096	0.02253356		CBG03180.1	Pectin lyase-like superfamily protein
Sapur.008G145400.4	0.975023224	-0.661989434	0.242509214	-2.72975	0.006338245	0.009367313	grey	-0.235668807	0.002965745	GO:0006351;GO:0005634;GO:0003700	CBG13450.2	Homeodomain-like superfamily protein
Sapur.005G114100.1	84.96282131	0.368807513	0.135041667	2.729584	0.006344148	0.009371195	grey	0.226889804	0.006394455	GO:0016021;GO:0005215	CBF28220.1	purine permease 3
Sapur.7G004000.1	152.8654072	-0.186355679	0.068319693	-2.7277	0.006377743	0.009424625	grey	-0.209519053	0.009385363	GO:0016811	CBF27585.1	Acetamidase/Formamidase family protein
Sapur.012G025300.3	12.26079681	0.290614281	0.106647697	2.724994	0.006430275	0.00949693	grey	0.027153404	0.735683777	GO:0055085;GO:0016020;GO:0008811;GO:0005216	CBG17700.1	ATCNGC20;CNBT;CNGC20 cyclic nucleotide-binding transporter 1
Sapur.009G127200.1	261.5961132	0.163308833	0.060091146	2.724949	0.006431177	0.009500794	grey	0.202516823	0.029395974		CBG22190.1	Cytochrome P450, family 87, subfamily A, polypeptide 2
Sapur.016G010600.1	44.0448943	0.278242314	0.138812295	2.724887	0.006433122	0.009503287	grey	0.241600665	0.022101041		CBG17020.1	ATCRMLA;ATKPCI;HET2;KPCI exportin 1a
Sapur.012G018900.1	15.00183845	-0.305230305	0.1451788315	-2.72442	0.006441375	0.009510523	grey	-0.156894955	0.049508058		CBG21440.1	MYB-like 102
Sapur.016G088700.1	325.2957566	0.117714857	0.043210043	2.724248	0.006444816	0.009519712	grey	0.169660746	0.033646691	GO:0048871;GO:0000160	CBG03430.1	AHPS
Sapur.7G004000.1	109.7692017	0.411284412	0.151000117	2.724037	0.006453728	0.009530202	grey	0.322400047	1.61E-05		CBG05145.1	RING/U-box superfamily protein
Sapur.003G004800.1	41.25681154	0.306651641	0.112594964	2.723507	0.006459529	0.009539812	grey	-0.17323309	0.030303308		CBG08730.1	hypothetical protein
Sapur.016G020100.1	0.479537818	-0.668583816	0.245385267	-2.7228	0.006473048	0.009559149	grey	-0.345376606	0.005916187	GO:0055114;GO:0020037;GO:0016705;GO:0005506	BAS1;CYP72B1;CYP73A4	Cytochrome P450 superfamily protein
Sapur.018G112600.1	0.49851763	1.056303449	0.388102497	2.721713	0.006494461	0.009590042	grey	0.175563014	0.02785442	GO:0005515	RPP27	RNI-like superfamily protein
Sapur.006G042800.1	0.552558718	1.228354087	0.451469432	2.720912	0.006533223	0.009642446	grey	0.204223848	0.010300731	GO:0043531	CBG14470.1	NB-ARC domain-containing disease resistance protein
Sapur.005G058500.1	72.34417662	-0.462183329	0.170000585	-2.72027	0.006547754	0.009664574	grey	-0.183749591	0.012435514	GO:0016887;GO:0005524;GO:0016020	ABCG11;ATWBC11;COF1;D5	white-brown complex homolog protein 11
Sapur.008G134600.1	0.6806199	1.088269335	0.399245584	2.720755	0.006551336	0.009661513	grey	0.15805305	0.048038785	GO:0043531;GO:0003700	CBG23230.1	Integrase-type DNA-binding superfamily protein
Sapur.003G088300.1	0.290227608	0.7208024	0.265000264	2.720522	0.006560992	0.009702202	grey	0.32350249	1.92E-05	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP87A2	cytochrome P450, family 87, subfamily A, polypeptide 2
Sapur.006G007000.1	3.507028256	-0.53025207	0.191292029	-2.71848	0.006583268	0.009861672	grey	-0.190849997	0.012430364	GO:0046983	BEE1	bHLH protein 92
Sapur.016G088200.1	159.4705661	-0.138370171	0.051027918	-2.7186	0.006584638	0.009860209	grey	-0.249924749	0.001818657			acylphosphatase
Sapur.010G043400.1	21.90441056	0.267610776	0.098454511	2.718116	0.006595483	0.009891024	grey	0.221947398	0.05231082		CBG07600.1	Heavy metal transport/detoxification superfamily protein
Sapur.004G021100.1	3.3237365	0.511389127	0.188126547	2.718069	0.006597372	0.009894381	grey	0.252194934	0.004573207		CBG45470.1	Protein of unknown function (DUF594)
Sapur.002G190200.1	344.8813883	0.108434941	0.039893982	2.718003	0.006599642	0.00896128	grey	-0.251920129	0.01458844		CBG20570.1	RPM1 interacting protein 4
Sapur.016G245600.1	0.56849899	-0.870315671	0.320264139	-2.71693	0.006618928	0.009724076	grey	-0.18813381	0.038058023	GO:0030170;GO:0009058	CBG22532.3	AAT;ATAAT;WIE17 aspartate aminotransferase
Sapur.003G118800.1	38.76637313	0.472824461	0.174061988	-2.71692	0.006618947	0.009724512	grey	-0.248208325	0.001727231	GO:0006488;GO:0005234;GO:0004672;GO:0030246	CBG27720.1	RLK	receptor kinase
Sapur.016G202500.1	36.45888956	0.318462661	0.117226569	-2.71665	0.006594552	0.00973176	grey	-0.212742984	0.007471715		CBG19450.1	
Sapur.016G207000.1	388.7393449	0.202681589	0.0746267	2.715876	0.006660603	0.009753344	grey	0.183438687	0.015188025	GO:0008270	CBG18290.1	zinc finger protein-related
Sapur.013G097000.1	288.458764	-0.400458382	0.147468289	-2.71556	0.00661646	0.009762349	grey	-0.251427607	0.001491221	GO:0055114;GO:0016491;GO:0010181	BTS;EMB2454	zinc finger protein, putative
Sapur.014G201000.1	594.2581684	0.227680674	0.083873201	2.71448	0.006629392	0.009793681	grey	0.176398146	0.029292268	GO:0016620;GO:0050662	CYP78A7;CYP78A7	12-oxophytodienoate reductase 2
Sapur.009G030600.1	623.6934611	0.112327137	0.041607555	2.71434	0.006640756	0.009797322	grey	-0.29135399	0.000488404	GO:0045454;GO:0015035;GO:0009055	AWG1;VEP1	cytochrome P450 family 87, subfamily A, polypeptide 2
Sapur.006G296000.1	27.27964614	0.562502548	0.208086276	2.71429	0.006642197	0.009798459	grey	-0.23705312	0.022965655		ATBPC4;BBR;BPC4	Glutaredoxin family protein
Sapur.016G256900.1	1.360832213	0.676713847	0.249335175	2.714073	0.006646154	0.00980461	grey	0.248123019	0.001728748	GO:0080017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	CBG06370.1	GATA6-like transcription factor
Sapur.006G000300.1	0.305058644	0.778739177	0.288126547	2.713969	0.006653788	0.009821631	grey	0.217618278	0.006376586		CBG22360.1	basic helix-loop-helix (bHLH) family protein
Sapur.006G081600.3	26.71641311	-0.19925	0.073534899	-2.71334	0.006660922	0.009825321	grey	0.195374327	0.014099844		CBG01460.1	Amidase family protein
Sapur.001G188000.2	3.028810875	0.48856133	0.180008948	2.713311	0.006661458	0.009825673	grey	0.202133342	0.011125048		CBG18645.1	LMBR1-like membrane protein
Sapur.005G081100.1	0.037666873	0.963856259	0.111349445	-2.71277	0.006673272	0.009854811	grey	-0.214757128	0.030484851	GO:0055556;GO:0016020	CBG04570.1	Cornichon family protein
Sapur.012G076900.1	7.328244616	0.285987605	0.105464615	2.712161	0.006686621	0.009885959	grey	0.236205579	0.002896344			
Sapur.005G088600.1	0.607970584	0.966956835	0.3687523	2.711734	0.006693227	0.009897771	grey	0.222606266	0.005316021		CBG16830.1	vacuolar ATP synthase catalytic subunit-related / V-ATPase-related / vacuolar proton pump-related
Sapur.001G187000.1	241.7279911	0.190371169	0.070211164	2.711409	0.006699796	0.00987071	grey	0.175230313	0.028154174	GO:0016020;GO:0008810;GO:0005215	CBG19740.1	Major facilitator superfamily protein
Sapur.003G183800.1	272.7188322	0.097587389	0.036434104	2.711404	0.006699898	0.009870971	grey	0.18180888	0.021871337			hypothetical protein
Sapur.009G176100.1	1308.155322	0.11873215	0.051170286	2.71119	0.006704227	0.009885671	grey	0.178663643	0.025188803	GO:0019236;GO:0007186;GO:0016021	CBS18520.1	Lung seven transmembrane receptor family protein
Sapur.001G188900.1	28.93774269	-0.562389646	0.206098682	-2.7094	0.006735765	0.009938319	grey	-0.272015155	0.005431323		CBG37530.1	hypothetical protein
Sapur.006G017500.6	4.115356462	0.273568917	0.13792658	-2.70804	0.006762014	0.009969548	grey	0.352882377	5.78E-06		CBG22160.3	Cysteine proteinases superfamily protein
Sapur.010G064800.1	6.653283611	0.407980555	0.150682129	2.708355	0.006765052	0.009988853	grey	-0.149873662	0.046001276		CBG45420.1	ovate family protein 12
Sapur.017G127200.1	0.632819954	-0.857084117	0.316620311	-2.70698	0.006788882	0.010009742	grey	-0.246248087	0.007059643		CBG22160.1	Protein of unknown function (DUF789)
Sapur.003G033300.1	0.491485934	-0.971336762	0.358862278	-2.70641	0.006800491	0.010026352	grey	-0.316582021	7.62E-05	GO:0048500;GO:0045900;GO:0008310;GO:0006614	CBG49100.1	Signal recognition particle, SRP9/SRP14 subunit
Sapur.008G097000.1	187.6103154	0.300102038	0.111037922	2.706388	0.006805750	0.010026352	grey	0.223113127	0.009470613			hypothetical protein
Sapur.007G035400.1	681.8974259	0.179054708	0.219652532	2.706337	0.006808998	0.010037786	grey	0.224249671	0.004752073		ATMES1;MES1	methyl esterase 1
Sapur.004G098100.1	0.328693024	-0.452517784	0.167338483	-2.70466	0.006828174	0.010077654	grey	-0.215374256	0.036689225			Plant protein of unknown function (DUF868)
Sapur.013G053500.1	34.60222801	0.212474865	0.078576574	2.704048	0.006850503	0.010095283	grey	0.208736904	0.008702369			
Sapur.003G183800.1	4.197720000	0.651611853	0.241134384	-2.70349	0.006861559	0.010110054	grey	-0.198052658	0.031720915	GO:0005815;GO:0009022;GO:0000226	CBG28245.2	Spc97 / Spc98 family of spindle pole body (SBP) component
Sapur.008G064500.1	3.060764744	0.404181937	0.149554506	2.702387	0.006884636	0.010164953	grey	0.198341199	0.012768397	GO:0006508;GO:0004197	AMCA;ATMCS;ATMCP28;M	metacaspase 5
Sapur.008G207300.1	0.668253232	-0.52591154	0.195369188	-2.70273	0.006886943	0.010165359	grey	-0.254404304	0.010309064		CBG40380.1	DNA/RNA-like superfamily protein
Sapur.006G060600.1	0.382094384	-1.111668287	0.411389969	-2.70231	0.006895998	0.010164642	grey	-0.38137051	6.23E-07		CBG47670.1	L1L_NF-Y8G	nuclear factor Y, subunit B6
Sapur.016G197300.1	3734.518844	0.300159669	0.037006547	-2.70217	0.006898933	0.010150334	grey	-0.25420332	0.001311177		CBG14040.1	PHT2;1	phosphate transporter 2;1
Sapur.010G057500.1	24.14073355	0.100351588	0.074157442	2.70188	0.006904727	0.010158624	grey	-0.214759906	0.006912669			
Sapur.006G045300.1	0.934960201	1.056348853	0.391049512	2.700837	0.006935518	0.010200072	grey	0.173869966	0.02942163	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP71Z4;CYP71Z4	cytochrome P450, family 71Z, subfamily A, polypeptide 1
Sapur.005G080600.1	8.149496043	0.312127882	0.121119366	-2.70075	0.006938308	0.010192367	grey	0.197735648	0.033050809		CBG44050.1	hypothetical protein
Sapur.004G092000.1	0.37613849	0.907629212	0.336089279	2.700559	0.006982205	0.010097689	grey	0.214240807	0.007059643			
Sapur.008G134100.1	1.6323763	0.767842019	0.27601509	-2.70046	0.006984324	0.010200021	grey	-0.218842237	0.008822367	GO:0055114;GO:0047134	CBG46800.1	Cysteine/Histidine-rich C1 domain family protein
Sapur.005G132600.6	0.15288661	0.948804072	0.351490336	-2.69876	0.006959797	0.010255151	grey	-0.11567799	0.14911805		CBG22060.1	
Sapur.013G136600.1	111.8075269	0.100302968	0.037169891	2.698597	0.006964998	0.010309091	grey	-0.207277478	0.008302216		CBG22160.1	ATP binding;nucleic acid binding;helicases
Sapur.006G043900.2	0.755832321	0.820337256	0.304261307	2.69616	0.007004139	0.010331045	grey	0.168380032	0.035303023	GO:0008270;GO:0003677	CBG51200.1	A20/AN1-like zinc finger family protein
Sapur.005G052000.1	2.423709869	0.455354549	0.168787327	2.69568	0.007009156	0.010345488	grey	-0.305431336	0.008486181	GO:0003700;GO:0006355	CBG21440.1	Dof type zinc finger DNA-binding family protein
Sapur.010G034100.1	0.287528312	-1.522021114	0.564718975	-2.69518	0.007034993	0.010360487	grey	-0.182318566	7.76E-07	GO:0008725;GO:0006284	CBG29705.2	DNA glycosylase superfamily protein
Sapur.012G091500.1	91.6618863	0.147172764	0.054629221	2.694031	0.007059348	0.010395901	grey	0.168438996	0.039692295		CBG24165.1	hypothetical protein
Sapur.016G289900.1	4.352616199	0.648821404	0.191406013	2.693695	0.007066487	0.010405786	grey	0.197983847	0.012934681		CBG29770.1	AvrRPT2-9 rapidly elicited protein, putative
Sapur.018G002200.1	84.49676262	-0.279905327	0.10391171	-2.69368	0.007066709	0.010405786	grey	-0.224376415	0.004726956		CBG10330.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.006G201100.2	0.587754844	0.865634552	0.31175027	-2.69353	0.007069489	0.010410151	grey	-0.168025268	0.041283611	GO:0016831;GO:0009058	AGA2;ATHANSYNA8	anthranilate synthase 2
Sapur.009G287900.1	105.0897207	-0.52302711	0.193229857	-2.69279	0.007085723	0.010432189	grey	-0.174423278	0.028302218			anthranilate synthase alpha 1
Sapur.7G005000.1	20.53641884	-0.512591154	0.191369188	-2.69273	0.007086021	0.010431687	grey	-0.219389022	0.015768728			transmembrane protein, putative
Sapur.005G010100.1	1.039693204	0.676467814	0.251242467	2.69249	0.007092068	0.010440337	grey	0.23017235	0.005602009		CBG18630.1	NA
Sapur.016G077800.1	1.273863809	0.682681835	0.253562118	2.69225	0.007097137	0.010447104	grey	-0.37004667	1.82E-06	GO:0006355	PTAC13	Galactose oxidase/kelch repeat superfamily protein
Sapur.005G047700.1	147.1323851	0.116604873	0.04257351	2.691929	0.007104004	0.010456977	grey	0.182886613	0.021871246			plastid transcriptionally active 13
Sapur.002G135900.1	73.08613389	0.293802699	0.096363132	-2.69154	0.007121237	0.010488807	grey	-0.203813633	0.030439546	GO:0055114;GO:0016491;GO:0016616;GO:0016615;GO:0006108	CBG44910.1	Lactate/malate dehydrogenase family protein
Sapur.007G067000.1	2.070601427	-0.464379124	0.16132772	-2.69129	0.007127703	0.010475641	grey	-0.181383527	0.022968858		CBG16860.1	ubiquitin-protein ligase 1
Sapur.017G047300.1	0.598669987	-0.856287232	0.318169914	-2.69127	0.007127785	0.010475641	grey	-0.233027754	0.002334822			
Sapur.017G047300.1	0.598669987	-0.856287232	0.318169914	-2.69127	0.007127785	0.010475641	grey	-0.233027754	0.002334822			
Sapur.010G055600.1	290.1491646	0.395492337	0.146973486	2.690909	0.007152754	0.010486664	grey	0.238898981	0.002806063	GO:0018342;GO:0008318	ATRGTA1;RGTA1	RAB geranylgeranyl transferase alpha subunit 1
Sapur.005G199500.1	2.216987014	0.595385479	0.221276754	-2.69068	0.007155258	0.010491391	grey	-0.262835775	0.009501763			
Sapur.007G069900.1	0.592438847	0.957417133	0.3558283	2.690664	0.007130995	0.010490439	grey	0.19577658	0.031999624		CBG05530.1	
Sapur.008G000300.1	366.1887573	0.102604318	0.060056457	2.690428	0.007158324	0.010500078	grey	0.160737911	0.048852122	GO:0005515;GO:0051087	CBG22560.1	ATBAG1;BAG1 BAG1-associated athanogene 1
Sapur.010G146300.1	1.997833331	0.778101299	0.28925316	-2.69004	0.007164444	0.010512387	grey	-0.219996615	0.00768766			
Sapur.008G061600.1	0.506838446	0.952601101	0.354128148	2.690005	0.007165099	0.010513379	grey	0.223670003	0.010047503			
Sapur.015G051600.1	0.877010213	0.848091938	0.315299076	2.689769	0.007174959	0.010518851	grey	0.209212236	0.008547527	GO:0006468;GO:0004672		
Sapur.010G136100.1	1087.178816	0.147087993	0.054697977	2.689586	0.007154081	0.010525889	grey	0.214198853	0.007064886	GO:0008725;GO:0006284	CBG29720.1	Leucine-rich repeat transmembrane protein kinase
Sapur.016G274000.1	3.864916284	0.515418837	0.205830973	-2.68964	0.007164646	0.010541316	grey	0.142284466	0.052237557	GO:0006508;GO:0008233	CBG22560.1	DNA glycosylase superfamily protein
Sapur.012G016900.2	0.208834446	-0.433942951	0.16146151	-2.68759	0.007196889	0.010586625	grey	0.128656691	0.107252507	GO:0055085;GO:0016020;GO:0008811;GO:0005216	CBS13130.1	serine/threonine-protein kinase 1
Sapur.016G160700.1	3.816413707	0.905065407	0.33767887	-2.68748	0.007199296	0.010589705	grey	-0.221283611	0.015035592		CBG21520.1	ATCNGC;CNGC1 cyclic nucleotide gated channel 1
Sapur.006G141600.1	75.7554222	0.205147821	0.076337237	2.687389	0.007202312	0.010592189	grey	0.208876014	0.008656768	GO:0005515	Protein of unknown function (DUF674)	
Sapur.005G087400.1	5558.713227	0.113884664	0.04268893	-2.6869	0.007217377	0.010607327	grey	-0.220002674	0.005630241	GO:0003677;GO:0000786	ATNPR1;NIM1;NPR1;SAI1	regulatory protein (NPR1)
Sapur.017G097300.1	0.881602913	0.774058227	0.288108724	2.686688	0.007164634	0.010614988	grey	0.173450543	0.029692626	GO:0003047;GO:0006468;GO:0055114;GO:0004672	CBS12560.1	Histone superfamily protein
Sapur.008G000600.1	2.033578619	0.529210841	0.197008872	2.686252	0.007234938	0.010624894	grey	0.210268161	0.007273891	GO:0004197;GO:0006508	CBG47000.1	Protein kinase superfamily protein
Sapur.015G262800.3	0.4839319	0.964878431	0.359247455	-2.68583	0.007234938	0.010639763	grey	-0.245125268	0.001624716	GO:0008168;GO:0008152	CBG11330.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.006G098600.1	3.457525251	0.428051956	0.159362216	-2.68576	0.007236422	0.010645475	grey	-0.186721265	0.033028659	GO:0008324;GO:0004176;GO:0004722	CBG54430.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.003G036600.1	85.23680892	0.137362266	0.051147791	-2.6856	0.007240073	0.010646371	grey	-0.213757516	0.007188655		CBG48430.2	Protein phosphatase 2C family protein
Sapur.006G107700.1	10699.91469	0.096085474	0.036119235	-2.68515	0.007243978	0.010660171	grey	-0.238804693	0.002617601	GO:0005525	CBG02340.1	GTP binding Elongation factor Tu family protein
Sapur.005G128500.1	18.03958884	0.223626727	0.083128291	2.685197	0.007251449	0.010682211	grey	-0.253484654	0.001938845		CBG20750.1	F-box family protein
Sapur.016G059500.1	0.330546555	-1.689967893	0.629387376	-2.6836	0.007283135	0.010708581	grey	0.005592742	0.945421975	GO:0008168	CBS18470.1	nucleic acid binding;methyltransferases
Sapur.003G105900.1	686.8173472	0.103657889	0.039261236	2.683116	0.007293127	0.010720367	grey	0.208369097	0.008886668		CBG10840.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.017G084600.1	6.730316853	0.536099921	0.199845122	2.682577	0.007305734	0.010740536	grey	0.191326633	0.016378305			TIR-NBS-LRR TIR type disease resistance protein, putative
Sapur.7G023000.1	1.389609223	0.551357429	0.205611208	2.682349	0.007317139	0.010757127	grey	-0.259161139	0.003207803			NA
Sapur.015G037000.1	530.6477609	-0.451209097	0.168234325	-2.68203	0.007317743	0.010757127	grey	-0.254145564	0.011318878		CBG11840.5	GTGX1;GLX1 glyoxalase I homolog
Sapur.016G030000.2	7.223147416	0.313325809	0.12056483	2.681934	0.007319765	0.010757127	grey	0.203087827	0.010349668		ATCBL2;CBL3	calcineurin B-like protein
Sapur.15WG027400.1	426.5663221	0.219957272	0.079797966	2.681714	0.007323605	0.010763685	grey	0.216792878	0.006393086	GO:0030170;GO:0009058	AtCLB;CLB5;ZTP;FdRR11;LC	long-chain base1
Sapur.010G217400.7	4.708049409	-0.449874485	0.165935318	-2.68169	0.007325069	0.010766589	grey	-0.208336687	0.009315722	GO:0140140;GO:0140141;GO:0016787;GO:0005524;GO:0003677;GO:0016818;GO:0006323	CHR11	chromatin remodeling protein 11
Sapur.7G003000.1	6.366823242	0.301644176	0.110756047	-2.67994	0.007364488	0.010802076	grey	-0.185235391	0.020351586	GO:0071949	AT4G04640.1;SQE1;KF1	FAD/NAD(P)-binding oxidoreductase family protein
Sapur.014G134100.5	0.49124986	-0.940077452	0.351122565	-2.67961	0.007364159	0.010825582	grey	-0.27310723	0.00047862		CBF18150.1	PAT1	GRAS family transcription factor
Sapur.005G088000.1	10.42883449	0.515418837	0.205830973	-2.67866	0.007364640	0.010841316	grey	-0.215361661	0.009753282	GO:0016021;GO:0006952	CBG22560.1	Seven transmembrane MLO family protein
Sapur.15WG104000.2	1.569452608	-0.687705591	0.256579135	-2.6702	0.007396962	0.010864113	grey	-0.196327327	0.012184821	GO:0005515	CBG45160.1	ATNPR3;NPR3 NPR1-like protein 3
Sapur.016G138700.1	74.07057528	0.473618870	0.175873285	2.670607	0.007399	0.010869453	grey	0.247436318	0.001756275	GO:0005515;GO:0005634	ARF1-BP;ARF2;HS;SHI;CE	auxin response factor 2
Sapur.008G147500.1	0.81002766	-0.751054587	0.280360579	-2.67889	0.007387671	0.010853784	grey	-0.254606096	0.001323413	GO:0003676	CBG11930.1	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.006G283000.1	76.5267	0.248343671	0.092195251	2.678	0.007514	0.010882261	grey	-0.231004646	0.015738845	GO:0006486;GO:0005783;GO:0005579	CBG22620.1	Ribophorin I
Sapur.008G145200.1	0.814882662	0.674920018	0.252178255	2.678468	0.007514615	0.010905453	grey	0.136569118	0.088100383	GO:0016887;GO:0005524;GO:0050185;GO:0042626;GO:0016021;GO:0006810	CBS13080.1	ATMRP3;MRP3 multidrug resistance-associated protein 3
Sapur.006G094600.1	3.751013637	0.400511851	0.149709279	2.674193	0.007609934	0.010998861	grey	0.263682604	0.000829441		CBG08670.1	
Sapur.01G030000.1	32.51324795	0.336003164	0.125671744	2.673657	0.007702291	0.011022086	grey	0.187445242	0.018733559			hypothetical protein
Sapur.001G051300.1	26.20753499	-0.490079218	0.183354895	-2.6785	0.007522182	0.010648229	grey	-0.225487977	0.004519362		CBG19180.1	
Sapur.009G209700.1	417.6609955	0.307350568	0.114982579	-2.67227	0.007733888	0.010506612	grey	0.249860307	0.001950638	GO:0050662;GO:0003824	CBG48490.1	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.013G091000.2	2.887672054	0.416672072	0.230798149	2.671951	0.007542060	0.011077644	grey	-0.018985997	0.813421712	GO:0006887;GO:0000145	CBG71820.1	SEC6 SEC6
Sapur.014G020200.1	23.11308094	0.112327137	0.042041555	2.671	0.007579558	0.011102862	grey	-0.199947134	0.013130862	GO:0004857;GO:0016021	CBG06170.1	Galactosyl transferase GMA12/MNN10 family protein
Sapur.003G081200.1	0.410607237	0.775829984	0.402895582	2.670243	0.007579648	0.011103862	grey	0.236290603	0.002831693			hypothetical protein
Sapur.016G000300.1	3.79584666	0.455118204	0.170469931	-2.67022	0.007580161	0.011103862	grey	-0.130028488	0.089232164	GO:0006355;GO:0003677	CBG35180.3	NTL9 NAC transcription-like 9
Sapur.010G069300.1	10.04623167	0.341770328	0.090573264	2.669331	0.007600149	0.011160125	grey	0.22274802	0.0050466			NA
Sapur.006G242000.1	138.3853041	0.102803592	0.039267009	2.669	0.007611	0.011178784	grey	-0.240018537	0.004156186	GO:0016747	CBG26040.1	HXXXD-type acyl-transferase family protein
Sapur.014G058800.2	7.113414341	0.3796651	0.142257874	2.668854	0.007610152	0.011174023	grey	0.203779979	0.010471108	GO:0016559;GO:0005779	CBG45740.1	PEX11D peroxisomal biogenesis factor 11
Sapur.002G161800.1	45.47513883	0.144788566	0.05427926	-2.66763	0.007638782	0.011231719	grey	-0.226828095	0.005501023		CBG22370.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.012G042200.1	0.625888328	1.000434296	0.374951619	2.667514	0.007654154	0.011237231	grey	0.187507643	0.018951592			PPR containing plant protein
Sapur.003G063300.6	12.30996022	0.318762336	0.082014826	2.667351	0.007645176	0.011222188	grey	0.06459526	0.42153825	GO:0016020	ATPB;CEO;CICO;RCD1	WWE protein-protein interaction domain protein family
Sapur.005G167500.1	0.42497466	0.720554426	0.270554426	2.667068	0.007652626	0.011231047	grey	0.231273565	0.005547764	GO:0016597;GO:0008152	ACS3	ACT domain repeat 3
Sapur.013G023300.1	235.7391939	0.124921574	0.046838845	2.667051	0.007652012	0.011231047	grey	0.24287775	0.001276054	GO:0004648;GO:0005524;GO:0004672	CBG09600.1	ANP3;MAPKKK11;NPK1 NPK1-related protein kinase 1
Sapur.005G167500.1	9.602189153	0.720554426	0.270554426	2.667068	0.007652626	0.011231047	grey	-0.231004646	0.015738845		CBG18420.1	Glutamyl-tRNA reductase family protein
Sapur.002G043300.1	1189.794223	0.104148414	0.039051373	2.666689	0.007660323	0.011242346	grey	-0.207468831	0.009127318	GO:0006355;GO:0005634;GO:0003677;GO:0009725	CBG19220.1	ARF11;ARF19;IAA22 auxin response factor 19
Sapur.002G071400.1	633.2316887	0.118098857	0.044079429	2.66625	0.007670319	0.011260564	grey	-0.231824303	0.006633025		CBG36960.1	
Sapur.012G086700.1	26.19505379	0.257199588	0.096465049	2.66625	0.007670345	0.011260564	grey	-0.212468862	0.00755129	GO:0043531	CBG14470.1	NB-ARC domain-containing disease resistance protein
Sapur.006G266000.1	136.4349038	0.102803592	0.039267009	2.66605	0.007679	0.012083	grey	-0.243173804	0.010346803	GO:0046983	CBG41130.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.001G191800.1	2.02627074	0.567904973	0.210047758	2.66562	0.007686585	0.011275952	grey	-0.197686872	0.012941793			
Sapur.006G203500.1	56.53364164	0.399767724	0.149690382	2.66526	0.007692868	0.011287288	grey	-0.205167765	0.009792544	GO:0055114;GO:0020037;GO:0016705;GO:0005506

Sapur.002G005300.2	-2.63027839	-0.55382825	0.210895187	-2.62544	0.008653784	0.012635877	grey	-0.006849662	0.935756782	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G08850.1	Leucine-rich repeat receptor-like protein kinase family protein	receptor kinase-like protein
Sapur.018G097000.1	241.8142186	-0.235544133	0.089720144	-2.62522	0.008656744	0.012639643	grey	-0.215511223	0.006714171		AT3G56850.1	AT3P42B,PAP26	purple acid phosphatase 26	NA
Sapur.003G027000.1	2.245658849	0.505829163	0.192681169	-2.62509	0.008659174	0.012643231	grey	0.187313118	0.018818718		AT2G40840.1		Protein of unknown function (DUF1677)	DUF1677 family protein
Sapur.006G046700.1	8.565916579	0.39497634	0.150648178	-2.625165	0.008660696	0.012644295	grey	0.168854694	0.036740251					hypothetical protein
Sapur.019G089800.1	74.48178629	0.363454338	0.1625543	-2.624584	0.008675124	0.012658077	grey	-0.185513998	0.0320113	GO:0006355,GO:0005739,GO:0003690	AT4G44030.1	Mitochondrial transcription termination factor family protein	transcription termination factor family protein, putative
Sapur.016G270400.11	9.160262191	-0.346790017	0.132136497	-2.62468	0.008678057	0.012680524	grey	-0.178891768	0.032365924	GO:0055114,GO:0016491,GO:0008152	AT4G34240.1	ALDH3,ALDH3I1	aldehyde dehydrogenase 3I1	NA
Sapur.008G291200.2	0.824804126	-0.863224615	0.329073719	-2.62321	0.008730615	0.012715482	grey	0.024480116	0.768376922	GO:0003926	AT5G25310.1	At-AlN-like,UNV-E	alkaline/neutral invertase	alkaline/neutral invertase
Sapur.004G164600.1	7.980375281	-0.36291565	0.138378385	-2.62303	0.008735333	0.012735852	grey	0.189506052	0.017488848		AT2G27950.1		Ring/U-box superfamily protein	RING/U-box protein, putative
Sapur.014G092000.1	99.19788836	-0.188487221	0.071887412	-2.62188	0.008742106	0.012795036	grey	-0.104335186	0.014733987		AT4G47115.1			transmembrane protein, putative
Sapur.016G277400.1	0.288875231	-0.362855691	0.138278164	-2.62115	0.008786864	0.012796851	grey	-0.406113717	0.1					transmembrane protein, putative
Sapur.019G031900.1	1.590876647	-0.519345537	0.198121046	-2.62015	0.008789288	0.012826256	grey	-0.201806048	0.119239226	GO:0008270,GO:0005515	AT3G56340.1	ATCRT1	RING/U-box superfamily protein	zinc finger protein
Sapur.002G037500.1	1794.102824	-0.145458994	0.05489745	-2.62001	0.008789779	0.012830524	grey	-0.212293605	0.007926264	GO:0008270,GO:0005622,GO:0005515	AT2G37620.1	CONSTANS-like 4	CONSTANS-like 4	NA
Sapur.001G107900.1	36.1150075	0.230558472	0.088000384	-2.619822	0.008797566	0.01283732	grey	0.221528782	0.052985597	GO:0008168	AT5G19120.2	ERD3	S-adenosyl-L-methionine-dependent methyltransferases superfluoro family protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.016G242400.1	706.5981671	-0.82353781	0.312479491	-2.619645	0.008800353	0.012845511	grey	-0.173171181	0.03145269		AT3G17130.1	UBP15	ubiquitin-specific protease 15	ubiquitin carboxyl terminal hydrolase
Sapur.018G042500.1	0.524105323	-0.853561543	0.325019326	-2.61891	0.008821014	0.012869832	grey	-0.127635656	0.006141018					NA
Sapur.006G183000.1	465.4552038	-0.218098231	0.083279211	-2.617154	0.008858507	0.012894882	grey	-0.263418807	0.004370987	GO:0016887,GO:0005524,GO:0016020	AT5G06530.2		ABC-2 type transporter family protein	ABC transporter G family protein
Sapur.T039300.1	12.19371823	0.594830362	0.227188784	-2.618221	0.008883963	0.012894882	grey	-0.284930531	0.00298601					NA
Sapur.006G048900.1	137.4178698	-0.148852562	0.056355442	-2.617877	0.008886786	0.012907392	grey	-0.215102704	0.006836152	GO:0008270	AT2G32592.1	TIP1	Ankyrin repeat family protein with DHHC zinc finger domain	S-acylstearoyltransferase TIP1
Sapur.005G139200.1	529.5215495	-0.305119206	0.116422429	-2.617517	0.008875089	0.012920054	grey	-0.220570624	0.028420725		AT5G37330.1		Protein of unknown function (DUF231)	polyacetoxide biosynthesis protein
Sapur.002G080900.1	87.12824606	-0.183777753	0.07021091	-2.61751	0.008857391	0.012000056	grey	0.19404748	0.014884735		AT5G15230.1			FAMILIA1 protein
Sapur.004G284400.1	139.4918326	-0.198771303	0.075941113	-2.617404	0.008859127	0.012921136	grey	-0.192275291	0.017164	GO:0005524,GO:0051082,GO:0006457	AT2G35120.1		TCP-1/cpn60 chaperonin family protein	NA
Sapur.007G029900.1	689.6568849	-0.24673246	0.094267584	-2.61736	0.008861122	0.012924501	grey	-0.17842296	0.02602277					NA
Sapur.002G092000.2	0.51957884	0.817861277	0.340703282	-2.6197	0.008867198	0.012931525	grey	-0.242483498	0.00221187		AT5G15980.1	NDH1_NDH48	NDH-dependent cyclic electron flow 1	plastid T24018.8 protein
Sapur.010G149600.1	1.394176467	-0.816189355	0.311909745	-2.61675	0.008877172	0.012966627	grey	-0.025624154	0.749893195	GO:0005826	AT5G15960.1	ESK1,TBL29	Plant protein of unknown function (DUF828)	Pm5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.002G018200.2	0.642989775	-0.82353781	0.314024888	-2.61628	0.008885162	0.012995664	grey	-0.195834938	0.017293984	GO:0005515,GO:0003723	AT3G08610.1		binding RNA binding	NA
Sapur.003G070100.1	85.05033181	0.189331121	0.072416011	-2.61493	0.008936002	0.013031275	grey	-0.207658855	0.00960234					transmembrane protein, putative
Sapur.007G029900.1	2767.924787	-0.117352023	0.044888074	-2.61403	0.008940389	0.013070989	grey	-0.214346239	0.007024221	GO:0005618,GO:0030156,GO:0005524,GO:0004812,GO:0004838,GO:0004832	AT4G14510.1	TWN2,VAL#5	valyl-tRNA synthetase / valine -tRNA ligase (VAL#5)	valyl-tRNA synthetase
Sapur.010G181800.5	0.453937505	-0.815635497	0.332116014	-2.613621	0.008958679	0.013083354	grey	-0.140426683	0.07938607	GO:0008270,GO:0003676	AT5G26280.1		RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain	RNA binding protein 42 (RBM42)-like RNA recognition motif protein
Sapur.002G084600.1	126.9362414	-0.364457869	0.131182258	-2.61357	0.008960043	0.013084606	grey	-0.23788167	0.02699647					NA
Sapur.003G139300.1	77.34730327	-0.224883183	0.08208931	-2.61224	0.008995703	0.013118864	grey	-0.210807653	0.008045418					NA
Sapur.015G104700.1	571.7521385	0.118118427	0.045220089	-2.612308	0.008999357	0.013120773	grey	-0.215130349	0.00681417	GO:0005524	AT3G15130.1		F-box containing nucleoside triphosphate hydrolases superfamily protein	AAA family ATPase
Sapur.T145900.1	41.63623277	0.348802991	0.140216184	-2.61118	0.009060497	0.013150867	grey	-0.237318836	0.0	GO:0015270,GO:0009058	AT2G22502.2	AAT,ATAAT,MEE17	aspartate aminotransferase	NA
Sapur.001G029400.1	1993.15005	0.146466191	0.056081702	-2.611657	0.009060045	0.013157788	grey	0.1823732	0.022469832	GO:0008152,GO:0003824	AT4G21240.1	AC1,ATAC1,2	4-coumarate:CoA ligase 8	4-coumarate:CoA ligase
Sapur.003G208300.1	27.65627534	0.511949161	0.19606452	-2.61113	0.009062468	0.013165645	grey	-0.185839362	0.03978852		AT5G46160.1		Disease resistance protein (βgrgrf-like protein) family protein	NA
Sapur.018G079300.1	0.65702588	0.904253359	0.34632129	-2.61103	0.009066991	0.013187473	grey	0.204854607	0.01002282		AT5G18430.2		Calcium-binding EF-hand family protein	calcineurin subunit B
Sapur.003G208800.3	34.46101101	0.192785173	0.073826411	-2.61024	0.009069848	0.013188388	grey	-0.219898918	0.017329841		AT3G07480.1	CIP1	COPS-interactive protein 1	constitutive photomorphogenic 9, putative
Sapur.017G087100.1	0.60950876	-0.877904429	0.344003832	-2.6097	0.009082194	0.013208531	grey	-0.186126	0.019598426		AT5G38790.1			hypothetical protein
Sapur.017G074000.1	371.8902588	-0.281585344	0.107919059	-2.60923	0.009076697	0.013224787	grey	-0.188329069	0.019244912		AT5G01060.1			DUF4336 domain protein
Sapur.019G077100.1	1.006489372	-0.763721882	0.293017468	-2.60883	0.009085162	0.013246564	grey	-0.256045621	0.013200055					NA
Sapur.016G007000.1	2.058865867	0.619951355	0.237685256	2.608539	0.009092975	0.013250256	grey	0.212608388	0.007485116					transmembrane protein, putative
Sapur.005G075200.1	1.615476667	0.602452127	0.231288155	2.608423	0.009097176	0.013261022	grey	-0.206831932	0.030347423	GO:0007017,GO:0005875	AT2G32320.1		Dynein light chain type 1 family protein	dynein light chain
Sapur.007G077000.1	115.2227984	-0.206918746	0.079319364	-2.60736	0.009124232	0.013296622	grey	-0.218609965	0.007157076	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT5T18330.1	AT5SRK1,SSRK1	somatic embryogenesis receptor-like kinase 1	somatic embryogenesis receptor-like kinase
Sapur.001G010500.1	1.960623132	-0.750750224	0.288102849	-2.60264	0.009150752	0.013357992	grey	0.165756571	0.018034868	GO:0016758,GO:0008152	AT5G19900.1		UDP-Glycosyltransferase superfamily protein	NA
Sapur.001G182100.1	85.15101045	-0.672087304	0.257808085	-2.60694	0.009135541	0.013309916	grey	-0.249620904	0.005617066		AT5G25532.1	CPCdRF14	conserved peptide upstream open reading frame 14	NA
Sapur.003G131400.1	46.16917237	-0.364297743	0.141410475	-2.60686	0.009160203	0.013346407	grey	0.167426477	0.038386575	GO:0007264,GO:0005525	AT4G20520.3	ARAC4,ATROP6,RAC3,RHO5	RAC like 3	Ras small GTPase family Rac protein
Sapur.004G033700.1	26.1827822	0.3145567	0.120708182	2.605693	0.009168869	0.013357317	grey	0.201919163	0.011514306	GO:0016021,GO:0006952	AT3G20320.1	ATMLO12,MLO12	Seven transmembrane MLO family protein	MLO-like protein
Sapur.006G133200.1	0.270882203	-0.947097965	0.360490867	-2.60567	0.009180664	0.013400383	grey	-0.184173658	0.796-07		AT5G45481.1		Protein of unknown function (DUF231)	NA
Sapur.014G129900.1	162.1567566	-0.243622442	0.093563335	2.604226	0.009208206	0.013413442	grey	-0.134733428	0.092394324	GO:0046872	AT5G66590.1		Zinc finger C-x8-C-x5-C-x3-H type family protein	NA
Sapur.001G148800.1	1040.739935	0.086300053	0.033148562	2.603433	0.009229535	0.01343392	grey	0.200269417	0.011908392	GO:0004387,GO:0006229	AT3G18640.1	ATPDAT,PDAT,PDAT1	phospholipid:diacylglycerol acyltransferase	phospholipid:diacylglycerol acyltransferase
Sapur.006G277500.1	0.820661553	-0.740334452	0.28452637	-2.60307	0.009233111	0.013465623	grey	-0.229101007	0.02557065		AT4G27080.1	CAD8	cinnamoyl-coA reductase-like protein	calcium-binding protein CML7
Sapur.011G033500.1	1.734297146	0.640465693	0.246057141	2.602915	0.009243475	0.013463039	grey	0.18024758	0.023878708	GO:0008146	AT5T07J7,AT5T5E_3DT17		sulfotransferase family protein	flavonol 3-sulfotransferase, putative
Sapur.008G152200.1	5.362627984	0.368246512	0.125006152	2.602727	0.009247127	0.013467765	grey	-0.079898873	0.930888661	GO:0005515	AT5G57820.1	AT5ATRNR2,RPN8A	RP non-ATPase like 2	26S proteasome regulatory subunit RPN8 non-ATPase subunit
Sapur.004G051000.1	87.68570226	0.256460144	0.088547947	2.60239	0.009257664	0.013482518	grey	0.185363232	0.020111914	GO:0046872,GO:0030001	AT5G01490.1		Heavy metal transport/detoxification superfamily protein	NA
Sapur.008G171200.1	318.5187511	-0.275308224	0.097431691	-2.60176	0.009276248	0.013500275	grey	0.187749459	0.018185604	GO:0016787,GO:0005634	AT4G35220.1	AGB1,TRP4,WD7	anthranilate synthase beta subunit 1	anthranilate synthase component II
Sapur.001G124600.2	16.47177647	-0.220347371	0.084719465	-2.6009	0.009297854	0.013539857	grey	-0.215783603	0.00644719		AT5G17620.1		glycine-rich protein	DcnD-like protein
Sapur.006G034500.1	2.303886609	-0.41503871	0.159536364	-2.60073	0.009299683	0.013541923	grey	-0.204621216	0.010139		AT3G37113.1			NA
Sapur.013G111200.1	85.86641935	0.789669749	0.306336853	2.593102	0.009539153	0.013871391	grey	0.201258754	0.010726709		AT3G05950.1	RmlC-like cupins superfamily protein	RmlC-like cupins superfamily protein	germin family protein
Sapur.001G139300.1	6.429468236	-0.366170728	0.140878288	-2.592	0.009544154	0.013905483	grey	-0.185362876	0.019707654		AT4G01080.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.018G088200.1	23.68067511	-0.313822273	0.091586986	-2.59873	0.009558965	0.013921863	grey	-0.240517558	0.018494622		AT4G11120.2			transmembrane protein, putative
Sapur.006G069200.2	30.86949476	0.229371164	0.088276429	2.598381	0.009566444	0.013936738	grey	0.212354436	0.007583905	GO:0016787	AT5G08410.3		Pectinacetylesterase family protein	pectinacetylesterase
Sapur.003G055001.1	18.02245029	0.257395765	0.100290263	2.595	0.009578879	0.013983076	grey	0.179020057	0.028476617		AT5G47260.1		Protein of unknown function (DUF231)	transmembrane protein, putative
Sapur.015G226300.1	56.41378594	-0.251308021	0.086759793	-2.59718	0.009309321	0.0156814	grey	-0.193361609	0.014204705		AT5G46530.1		AWPM19-like family protein	AWPM19-like protein
Sapur.002G129500.1	62.13958889	0.294786799	0.113528215	2.59703	0.009439138	0.013888704	grey	0.155647218	0.051888816		AT4G21960.1		Plant protein of unknown function (DUF868)	Plant protein of unknown function (DUF868)
Sapur.005G027300.1	24.6840053	-0.18586129	0.071576738	-2.59667	0.009441184	0.013702375	grey	-0.240841668	0.002367583	GO:0005515	AT5G07630.1		F-box family protein	F-box protein interaction domain protein
Sapur.014G136600.1	8.975968601	-0.347237432	0.134000729	-2.58275138	0.009583	0.014136127	grey	0.085749372	0.381204056		AT2G27120.3		GPT2 chromosome	NA
Sapur.006G097000.1	43.05767692	-0.755142287	0.28261304	-2.59528	0.009654149	0.013758682	grey	-0.246423208	0.001863008		AT5G45480.1		Protein of unknown function (DUF594)	transmembrane protein, putative
Sapur.005G097100.1	1614.794628	-0.313888331	0.120631362	-2.595198	0.009663649	0.013759646	grey	0.203838312	0.010745229	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G21230.1	CYP706A6	cytochrome P450, family 706, subfamily A, polypeptide 6	NA
Sapur.T192800.1	0.794085623	-0.73353354	0.282656622	-2.59514	0.009645136	0.013761165	grey	-0.254362614	0.001325815					NA
Sapur.006G230800.1	2120.931569	0.070816901	0.027206441	2.594934	0.009692001	0.013768864	grey	0.179802213	0.02410052		AT2G26570.1			hypothetical protein
Sapur.019G080500.2	0.920393162	-0.441887879	0.257799079	-2.59456	0.009697027	0.013783	grey	0.244151513	0.005055375	GO:0008374,GO:0004792,GO:0016787	AT4G27600.1	PFH1,TAP38	thylakoid-associated phosphatase 38	protein phosphatase 2C
Sapur.005G095400.3	1.087949077	-0.663355829	0.255730732	-2.59416	0.009842097	0.013796427	grey	-0.172351585	0.030888468	GO:0005524,GO:0003676,GO:0004386	AT4G20160.1		helicase domain-containing protein / ISR domain-containing protein / zinc finger protein-related	ATP-dependent RNA helicase, putative
Sapur.010G098800.2	29.2120303	-0.171838444	0.066160984	-2.5933	0.009859017	0.013806067	grey	-0.223380602	0.07938604		AT5G55730.1		Glucose-binding protein with Leucine-rich repeats	D-glucose-binding protein with LRR domain
Sapur.017G075600.1	0.767904931	0.780869402	0.301139031	2.593123	0.009861089	0.013872391	grey	0.205760875	0.009731217	GO:0055114,GO:0051287,GO:0016616	AT5G26160.2		UDP-glucose 6-dehydrogenase family protein	UDP-glucose 6-dehydrogenase
Sapur.004G054300.1	64.10804965	-0.153880494	0.207833366	2.59273	0.009863683	0.013914933	grey	-0.236182756	0.000818863		AT1G68010.2		F-box/cyclophilin/tetratricopeptide hydrolases superfluoro family protein	NA
Sapur.013G111200.1	0.858641935	0.789669749	0.306336853	2.592102	0.009639153	0.013871391	grey	0.199729547	0.012144144	GO:0006351	AT5G59600.1	NRPB8B,NRPD8B,NRPE8B	RNA polymerase RpB8	DNA-directed RNA polymerase I, II, III
Sapur.016G025700.1	1671.626116	-0.059769164	0.023052283	2.591895	0.009649691	0.013884029	grey	0.144769083	0.036410994	GO:0016887,GO:0005524	AT5G28260.1	RFB1	regulatory particle triple-A ATPase 2	26S proteasome regulatory subunit 6B
Sapur.011G174400.4	3.446509469	0.378583371	0.146075328	2.5917	0.009655311	0.013892322	grey	0.204813693	0.952290017		AT2G46680.3	MEE13	myosin heavy chain-like protein	myosin heavy chain-like protein, putative
Sapur.010G089800.1	4.539199907	-0.481959793	0.185988251	-2.59149	0.009682163	0.013905923	grey	-0.202827174	0.010671503		AT4G18670.1		Ankyrin repeat family protein	ankyrin repeat protein
Sapur.003G186600.1	20.91005568	-0.363468564	0.11842964	-2.59127	0.009562107	0.013904634	grey	-0.187969653	0.018702527		AT5G48830.1			DUF3685 family protein
Sapur.011G111700.1	41.90882299	-0.284412163	0.109780547	-2.59072	0.009577419	0.013929786	grey	-0.194574265	0.014609733	GO:0055114,GO:0016491	AT4G10500.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	aminocyclopropanecarboxylate oxidase, putative
Sapur.018G088300.1	0.446613328	-0.953328822	0.368945652	2.589349	0.009615766	0.013965554	grey	0.209262631	0.008456861		AT1G48130.1			hypothetical protein
Sapur.010G155500.1	0.963768191	-0.767728675	0.296557205	-2.5888	0.009630971	0.014004652	grey	-0.193409691	0.015228661					NA
Sapur.005G142400.2	0.574411517	-0.776537861	0.300011294	-2.58856	0.009643155	0.014007964	grey	-0.187093516	0.017331181	GO:0005524	AT2G16180.1	EMB3968,RFC4	ATPase family associated with various cellular activities (AAA)	replication factor C subunit 2/4
Sapur.017G113500.1	5.574034798	0.64859881	0.250608368	2.588097	0.009650775	0.014034019	grey	0.262502278	0.008895987	GO:0005852,GO:0005737,GO:0003743	AT4G26070.1		Translation initiation factor eIF3 subunit	translation initiation factor eIF3 subunit
Sapur.006G175400.1	5.968675348	-0.332466166	0.127608751	-2.58802	0.009661293	0.014036329	grey	-0.19810241	0.023763595	GO:0005275,GO:0008237,GO:0006508	AT3G15120.1		peptidase M17 family protein	leucine aminopeptidase 4
Sapur.009G117100.1	391.0748886	0.271661327	0.104968283	2.587842	0.009679328	0.014043186	grey	0.196004778	0.013852208		AT3G44716.1			NA
Sapur.003G049400.1	0.429004631	-0.66624922	0.257800262	-2.58787	0.009684153	0.014049207	grey	-0.258266056	0.008988688	GO:0009733	AT2G43430.1		SAUR-like auxin-responsive protein family	auxin/indole-3-acetic acid-induced protein
Sapur.003G151000.1	0.302877864	1.178715252	0.455642784	2.586972	0.009682338	0.014077442	grey	2.282329254	0.000739243	GO:0016787	AT5G26020.1	atnuh16,NUDT16	nudix hydrolase homolog 16	nudix hydrolase
Sapur.007G092400.1	0.381552006	1.183389517	0.457452591	2.586298	0.009700129	0.014104376	grey	0.208740246	0.008701271	GO:0008168,GO:0008152	AT5G08330.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosylmethionine-dependent methyltransferase, putative
Sapur.015G256600.1	5.510752807	-0.265042838	0.101838941	-2.585857	0.009749554	0.014122314	grey	-0.210047554	0.03168273		AT5G06100.1	MEDB	mediator subunit 8	mediator of RNA polymerase II transcription subunit 8, putative
Sapur.T047700.2	13.6408872	0.199951615	0.077121109	-2.58547	0.009749158	0.014163641	grey	-0.185068527	0.019973344	GO:0009165,GO:0004749,GO:0000287	AT3G46530.1		Phosphoribosyltransferase family protein	ribose-phosphate pyrophosphokinase
Sapur.003G511000.3	4.41528848	0.553328822	0.213704641	-2.58349	0.009801766	0.014188954	grey	0.348819739	0.066493331	GO:0016192	AT3G08570.1		Golgi/SPK2-like vesicle trafficking protein family	vesicle transport protein GOT1B, putative
Sapur.L052G51100.5	0.321086608	1.257316993	0.486437082	2.584895	0.009740871	0.01415881	grey	0.138880613	0.082797527		AT3G03810.3		18S pre-ribosomal assembly protein gar2-related	hypothetical protein
Sapur.003G084900.1	0.363614634	-0.138245557	0.049608218	-2.5842	0.009774154	0.014177754	grey	-0.272245631	1.48E-06		AT3G14510.1		Protein of unknown function (DUF3527)	DUF3527 domain protein
Sapur.015G181900.3	2.935085792	-0.461159403	0.178480611	-2.58381	0.009776154	0.014202306	grey	-0.203019196	0.010768912		AT3G54880.1			transmembrane protein, putative
Sapur.008G117200.1	0.394100192	1.004681163	0.423796063	2.582382	0.009812102	0.014204648	grey	0.212183663	0.005425211		AT3G19260.1	APG6,ATAPG6	autophagy 6 (APG6)	autophagy protein Apg6 containing protein
Sapur.015G170000.1	23.76222939	0.311611399	0.120675522	2.581932	0.009815101	0.014261874	grey	0.199873558	0.010080859					hypothetical protein
Sapur.015G183800.3	3.807817177	-0.264851903	0.102562575	2.581668	0.009833663	0.014275048	grey	-0.45733716	1.75E-09	GO:0055114,GO:0016491,GO:0008270	AT5G55580.1		Zinc-binding dehydrogenase family protein	alcohol dehydrogenase
Sapur.013G138800.1	3.359442023	-0.609134147	0.235839196	-2.58186	0.009836875	0.0142788	grey	-0.221296556	0.005347834	GO:0005885,GO:0016021	AT4G26980.3	PHTA;3	phosphate transporter 4;3	anion transporter, putative
Sapur.016G239400.1	126.6238832	-0.430670731	0.166820525	2.581641	0.009863168	0.014287317	grey	0.207620271	0.009057569	GO:0016020	AT5G03660.1	ERD4	Early-responsive to dehydration stress protein (ERD4)	early-responsive to dehydration protein
Sapur.001G080400.1	272.0180405	-0.102507889	0.074638315	-2.58146	0.009868253	0.014293838	grey	-0.219370204	0.005456543	GO:0003824,GO:0005777	AT4G22200.1		Putative endonuclease or glycosyl hydrolase	nucleic acid binding protein, putative
Sapur.003G260800.2	2.341919434	-0.449475355	0.174117152	-2.58145	0.009883521	0.014293838	grey	-0.119124806	0.136161117	GO:0046872	AT3G21660.1		Zinc finger (CCCH-type) family protein	zinc finger CCCH domain protein
Sapur.006G042300.1	176.9914563	-0.152464164	0.05188745	-2.58021	0.009887112	0.014310268	grey	0.159529523	0.043823423		AT5G59320.1			transmembrane protein, putative
Sapur.013G113500.2	8.3851965	0.31727801	0.121243292	2.579681	0.009889163	0.014366152	grey	0.20999423	0.008298091		AT5G57130.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH protein
Sapur.016G255400.1	0.760217223	-0.721886407	0.278844037	-2.58147333	-2.57916	0.009904203	0.014387267	grey	-0.209153	0.015161622	AT2G20120.1		Plant protein of unknown function (DUF247)	NA
Sapur.010G071300.1	484.8783009	-0.102060785	0.039585256	-2.57825	0.009930104	0.014424413	grey	-0.223001189	0.006995732		AT1G74740.1		Protein of unknown function (DUF1423)	class I heat shock protein, putative
Sapur.005G150300.1	0.865357777	-0.367582377	0.1355119	-2.57817	0.009932407	0.014427073	grey	-0.223608654	0.010307778		AT3G58650.1		Ankyrin repeat family protein	NA
Sapur.015G072200.1	3.1659097	0.462805527	0.179607111	2.578025	0.009936681	0.014432647	grey	0.153717908	0.054529567	GO:0004648,GO:0005524,GO:0004672	AT4G11530.1	CRK34	cysteine-rich RLK (RECEPTOR-like protein kinase) 34	NA
Sapur.006G130000.1	4.224874556	-0.456058679	0.176933774	-2.576	0.009949017	0.014469929	grey	-0.206898128	0.009329988					NA
Sapur.005G180000.1	19.31166443	-0.317228884	0.123000147	-2.57525	0.010050016	0.014513734	grey	-0.208521203	0.008762203	GO:0030246,GO:0005975	AT5G56890.1		Sugar isomerase (SIS) family protein	NA
Sapur.018G067000.1	186.9728881	0.116091924	0.045410384	2.574696	0.010032825	0.014570372	grey	0.18063803	0.02376	GO:0004045	AT5G10700.1		Peptidyl-tRNA hydrolase II (PTH2) family protein	peptidyl-tRNA hydrolase PTH2
Sapur.008G291500.1	6037.878795	-0.142021225	0.054964872	-2.57392	0.01005	0.014601395	grey	0.159452918	0.046107369	GO:0009086,GO:0000476,GO:0005524	AT5G05340.1	AESAM1,MAT1,SAM-1,SAM1	S-adenosylmethionine synthetase	S-adenosylmethionine synthetase
Sapur.005G071100.3	1.432266139	-0.253302849	0.257584587	2.573247	0.010097368	0.014661531	grey	0.078585531	0.32814687	GO:0005515,GO:0016020	AT5G05460.1	SDE3	F-box/cyclophilin/tetratricopeptide hydrolases superfluoro family protein	hypothetical protein
Sapur.012G022300.2	0.742623133	0.909809542	0.353408975	2.573173	0.010100414	0.014665531	grey	0.192316126	0.015000197	GO:0005515,GO:0016020,GO:0051297,GO:0051328,GO:0006855	AT3G62670.1		MATE efflux family protein	MATE efflux family protein
Sapur.003G033800.1	0.528018803	-0.864371937	0.328282677	-2.57209	0.010108799	0.014676841	grey	-0.263780504	0.008494624	GO:0006351,GO:0003899	AT5G06790.1		RNA polymerase RpB7 N-terminal domain-containing protein	DNA-directed RNA polymerase III protein
Sapur.004G284400.1	1.794466613	-0.812321362	0.31506715	-2.57196	0.010126812	0.014702347	grey	-0.201132116	0.013166398		AT4G14960.1	ATRMI,FIM1	fimbrin 1	NA
Sapur.011G091700.1	3.329449407	0.00462669	0.190632334	-2.57124	0.010133376	0.014711231	grey	-0.174062594	0.029239614					NA
Sapur.005G170300.1	1051.104637	0.053839797	0.020916487	2.571008	0.010139136	0.014718946	grey	0.158488795	0.01662353	GO:0016887	AT2G32160.1		CCCH-type zinc finger family protein	zinc finger C-x8-C-x5-C-x3-H type family protein
Sapur.019G076000.1	25.8262251	0.195358048	0.075886955	2.57101	0.010140252	0.014719921	grey	0.192849358	0.015572076		AT2T17S.1		RING/U-box protein with domain of unknown function (DUF 1232)	C3HC4-type RING finger protein
Sapur.006G261500.1	157.0239838	0.340687303	0.132518813	2.570769	0.010149057	0.014732057	grey	0.190787851	0.016578487		AT1T19S.1,PTL1,TP3		lipid transfer protein 1	Non-specific lipid-transfer protein
Sapur.009G217001.1	829.3958561	0.104827755	0.040827755	2.570367	0.010150987	0.014745969	grey	0.215183811	0.014777141	GO:0003779	AT1G04120.2	ATVIN4,VIN4	villin 4	villin 4
Sapur.006G091100.1	2.270685579	-0.563766502	0.219369384	-2.56985	0.010174244	0.014767321	grey	-0.23078046	0.016638388		AT4G15580.1		Protein of unknown function (DUF567)	tubby C 2 protein
Sapur.T169500.1	11.34278844	0.507192227	0.199153666	-2.56974	0.010177466	0.014771349	grey	-0.203123996	0.015570714	GO:0006351,GO:0003899,GO:0003677,GO:0003249	AT3G18090.1	NRPD28	nuclear RNA polymerase D2	NA
Sapur.013G181500.1	1324.062172	-0.079010597	0.030760158	-2.56783	0.010218855	0.014851888	grey	-0.203413346	0.010613706		AT5G08310.1	ECT11	evolutionarily conserved C-terminal region 11	YTH domain protein
Sapur.T039700.1	3.870947147	0.224889147	0.110542516	2.56722	0.010231873	0.014876727

Sapur.005G120100.1	0.41428692	-0.03269861	0.409791754	-2.52004	0.01734283	0.016929725	grey	-0.245784231	-0.009170164				NA
Sapur.008G030900.4	1.038194535	-0.671879938	0.266617854	-2.52001	0.01173528	0.016930465	grey	-0.152526869	0.056513106	ATSG20060.1	UBC19	ubiquitin-conjugating enzyme19	ubiquitin-conjugating enzyme E2
Sapur.013G130900.1	141.7632691	-0.461420095	0.175204891	-2.5199	0.01172246	0.016954279	grey	-0.219791251	0.005675029	GO:0005528,GO:0004185	WCS2	serine carboxypeptidase-like 2	NA
Sapur.018G050100.1	3.232451734	-0.343777787	0.13645551	-2.51934	0.01175515	0.01696114	grey	-0.202089213	0.011140557				NA
Sapur.006G234100.1	10.12532809	-0.332253384	0.131915579	-2.51821	0.01178192	0.016984049	grey	-0.176788934	0.026764608				hypothetical protein
Sapur.004G123600.1	101.0919051	0.215152182	0.085585365	2.518564	0.01178461	0.016996345	grey	0.163421657	0.043413471	GO:0009733		SAUR-like auxin-responsive protein family	SAUR-like auxin-responsive protein
Sapur.002G132700.1	0.54453682	0.90006234	0.357400767	2.517701	0.01181302	0.017036545	grey	0.23469723	0.003895517	GO:0016757,GO:0047262	GALT1,LGT1	galactanosyltransferase	alpha-2h2ZK-galactanosyltransferase
Sapur.010G074400.2	0.357659321	0.187897091	0.471857666	2.51744	0.01185106	0.017048413	grey	0.243930009	0.002165863	GO:0016740,GO:0016020,GO:0006633	KCS20	3-ketoacyl-CoA synthase 20	3-ketoacyl-CoA synthase
Sapur.016G208800.1	2.990267904	0.490897089	0.195090029	2.517369	0.01183494	0.017051114	grey	0.180039784	0.024069649				NA
Sapur.010G013000.1	3.865045938	0.575984257	0.229000228	2.517062	0.01193782	0.017065221	grey	0.213413282	0.007276024	GO:0016758,GO:0008152	HYR1	UDP-glucose flavonoid 3-O-glucosyltransferase, putative	UDP-glucose flavonoid 3-O-glucosyltransferase
Sapur.018G091400.1	0.365162667	1.192400785	0.473802774	2.516661	0.01184728	0.017083939	grey	0.32654758	2.98E-05	GO:0005515	ARIP15,RLP15	receptor like protein 15	NA
Sapur.006G204600.3	0.709620794	0.777550097	0.30910968	2.516	0.01186621	0.017110027	grey	0.225129	0.004263646	GO:0005615,GO:0005576		Peptidase family M48 family protein	peptidase M48
Sapur.010G118400.1	40.57118805	0.198842368	0.079037547	2.515796	0.01187638	0.017124386	grey	-0.17545596	0.027961361				complex 1 LYR-like protein
Sapur.T020060.1	1.761291	0.461420095	0.175204891	2.5159	0.01188378	0.017129857	grey	-0.214163038	0.007173423	GO:0004689,GO:0004672	ATCAK1,CKA1	casein kinase alpha 1	NA
Sapur.015G236500.1	1.60048486	0.985664191	0.391838392	2.515512	0.01188956	0.017137671	grey	0.218556841	0.005958047	GO:0043565,GO:0003705,GO:0003700	ABF2,ABREB,ATRBF1	abscisic acid responsive elements-binding factor 2	NA
Sapur.005G078300.2	3.477275537	0.232023869	0.136213124	2.515041	0.01189909	0.017149986	grey	-0.214157184	0.005975678	GO:0005525		Translation factor family 2, small GTP-binding protein	translation initiation factor IF-2
Sapur.15WG143500.1	0.564028861	-1.112010071	0.442134206	-2.51517	0.01189735	0.017151642	grey	-0.218690905	0.005927129	GO:0005085,GO:0016020,GO:0012507,GO:0015138,GO:0006855		MATE efflux family protein	multidrug efflux protein
Sapur.009G086400.1	1938.568787	0.050426229	0.020049491	2.515088	0.01190026	0.017155111	grey	0.194511472	0.016462279				hypothetical protein
Sapur.003G313900.2	0.963819129	0.357113403	0.139429806	2.514746	0.01191237	0.017171014	grey	-0.042432207	0.597794945				monothiol glutaredoxin-S11 protein, putative
Sapur.016G082000.1	451.7460803	0.156232595	0.054227096	-2.51394	0.01193904	0.017209493	grey	-0.193277118	0.016521475	GO:0043565,GO:0006355,GO:0003700	ATCZF2,ATCZF-D1	WRKY transcription factor family protein	WRKY transcription factor
Sapur.005G093800.1	277.6008908	0.576984257	0.229000228	2.513863	0.01194246	0.017213508	grey	0.338842744	1.6E-05	GO:0055029,GO:0006488,GO:0005524,GO:0004671,GO:0003247	WAK2	wall-associated kinase 2	NA
Sapur.002G033400.1	10.00284162	0.29351291	0.116768582	2.513627	0.01194675	0.017223321	grey	0.187195190	0.026453764		PRA1,FL2,PRA7	PRA1 (Prenylated rab acceptor) family protein	NA
Sapur.010G044900.1	153.1547132	0.405756691	0.161835647	2.513425	0.01195129	0.017224449	grey	0.194093855	0.016892241	GO:0005515	ATGSTU7,GSTU5,GSTU17	glutathione S-transferase GST	glutathione S-transferase GST
Sapur.009G106700.2	7.571894806	0.280796038	0.111731244	2.513363	0.01195822	0.017234715	grey	0.21868664	0.005930015	GO:0055114,GO:0020037,GO:0006979,GO:0004601	APX3	ascorbate peroxidase 3	L-ascorbate peroxidase 3, peroxisomal protein
Sapur.006G268200.1	56.0838971	0.304817301	0.121389679	-2.51369	0.01196396	0.017245612	grey	-0.200060045	0.011995853	GO:0005515,GO:0048546,GO:0006468,GO:0004672		S-locus lectin protein kinase family protein	NA
Sapur.016G170100.4	28.20867204	0.177804713	0.070770115	2.512426	0.01199408	0.017279019	grey	0.215053513	0.006834402	GO:0005881,GO:0003398	MYB3R3	myb domain protein 3r-3r-like 15 snRNP	thioredoxin-like protein 4B
Sapur.016G135800.1	1.254396148	0.587391582	0.233976495	2.510479	0.01205749	0.017371864	grey	0.193839435	0.019740994	GO:0005515		Sterile alpha motif (SAM) domain-containing protein	downward leaf curling protein, putative
Sapur.T170081.1	199.0719481	0.223402202	0.101726101	2.509975	0.01207983	0.017397609	grey	0.176442248	0.027006395	GO:0005737,GO:0005524,GO:0016020		AAC-2 type transporter family protein	AAC-2 type transporter family protein
Sapur.010G075200.1	1.579188522	-0.010117935	0.243419194	-2.50911	0.01206807	0.017400669	grey	-0.221803034	0.004834483				hypothetical protein
Sapur.010G080800.1	1.862157247	0.455839941	0.181588884	2.509804	0.01210329	0.017447629	grey	0.212916655	0.007511869	GO:0005515,GO:0007165,GO:0043531		Disease resistance protein (TIR-NBS-LRR class) family	TIR-NBS-LRR resistance protein
Sapur.007G115300.1	0.956937838	-0.653659518	0.260488445	-2.50881	0.01211963	0.017653268	grey	-0.195372008	0.014201725	GO:0006351		Far-red impaired responsive (FAR1) family protein	Far-red impaired responsive family protein, putative
Sapur.002G074200.6	0.515588897	0.814161557	0.324530732	-2.50867	0.01213855	0.017659121	grey	-0.249397508	0.003904681	GO:0005515,GO:0006508,GO:0005524,GO:0004197	Eukarya	Eukarya protease family protein	cysteine proteinase like protein
Sapur.T163300.1	7.058823817	0.390919852	0.155852893	-2.50826	0.01216275	0.017678704	grey	-0.182926276	0.022307362		CLE25	CLAVATA3/ESR-RELATED 25	NA
Sapur.016G147300.1	1.529764645	0.509180426	0.230601731	-2.50743	0.01221242	0.017749096	grey	-0.173395864	0.033362211	GO:0016021,GO:0016020,GO:0022857		nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4, putative
Sapur.012G046900.1	1.530152663	0.627120694	0.250139874	2.50708	0.01217313	0.017357173	grey	0.177164808	0.026437858	GO:0008270,GO:0003676			NA
Sapur.005G243600.1	0.496019237	0.737828387	0.349160009	2.507264	0.01217576	0.017358396	grey	0.227126726	0.005049183				hypothetical protein
Sapur.007G086900.1	44.66876284	0.341696927	0.125426858	2.506677	0.01218719	0.017554006	grey	0.200332646	0.011879491	GO:0055114,GO:0020037,GO:0006979,GO:0004601		Peroxidase superfamily protein	peroxidase
Sapur.016G166100.2	0.776418396	0.863882093	0.344553468	2.506666	0.01218759	0.017554086	grey	0.185132876	0.030271895				CCT motif protein
Sapur.018G106000.2	1.470631372	0.549776737	0.242984658	2.506267	0.01220306	0.017575551	grey	-0.047009054	0.518858855	GO:0006468,GO:0004672		Protein kinase superfamily protein	Serine/Threonine-kinase Cx32, putative
Sapur.003G099300.1	2.462342911	-0.420082863	0.167618954	-2.50605	0.01220863	0.017581245	grey	-0.185719351	0.010871867			Protein of unknown function (DUF1191)	40p001, putative
Sapur.003G075100.1	13.87689157	0.291712581	0.113124124	2.505864	0.01221243	0.017591524	grey	0.40508854	1.00E-07			Sec14p-like phosphatidylinositol transfer family protein	SEC14 cytosolic factor family protein
Sapur.004G241500.2	6.183253861	-0.322079151	0.128915235	-2.50536	0.01222661	0.017615841	grey	-0.025005882	0.755901258	GO:0005992,GO:0003824		trehalose-phosphatase/synthase 7	trehalose-6-phosphate synthase
Sapur.006G072300.1	0.624868214	0.517884561	0.217184768	2.505251	0.01224872	0.017617269	grey	0.173972242	0.033264614			Eukaryotic translation initiation factor family protein	eukaryotic translation initiation factor 5
Sapur.009G135100.1	823.0224572	-0.132261633	0.052862188	-2.50526	0.01225125	0.017639455	grey	-0.208482897	0.008931089	GO:0005525		Ribosomal protein S5/Elongation factor G/III/V family protein	Ribosomal protein S5/Elongation factor G/III/V family protein
Sapur.003G027800.1	362.0797373	0.303894194	0.123447514	2.504664	0.01226811	0.017662215	grey	-0.176667671	0.024128658	GO:0005515,GO:0055114,GO:0016491		2-oxoglutarate-Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate-dependent dioxygenase
Sapur.016G249400.3	2.5705409	-0.488723302	0.195145852	-2.5044	0.01225884	0.017660299	grey	-0.025564987	0.750621062		ATGP1,GIP1	ASCFD1 interacting protein 1	mitotic-spindle organizing protein
Sapur.010G085200.1	2.396240469	-0.663266686	0.269866286	-2.50409	0.01228633	0.017692395	grey	-0.344164744	0.002055468				hypothetical protein
Sapur.003G111100.1	0.316278749	1.067372924	0.426239395	2.504163	0.01229147	0.017700968	grey	-0.237068839	0.002754803	GO:0004674,GO:0048544,GO:0006468,GO:0016772		protein serine/threonine kinases;protein kinases;ATP binding;sugar binding;kinases;carbohydrate binding	NA
Sapur.005G074100.2	2.509062635	-0.447882429	0.179005837	-2.50269	0.01233476	0.017763221	grey	0.018944306	0.818329975	GO:0016021,GO:0006630	ASPRT1,PPT1	polypeptide/phosphatase 1	4-hydroxybenzoate polypeptide/phosphatase
Sapur.016G090000.1	570.8576353	0.507374673	0.042984658	-2.5024	0.01237213	0.017840069	grey	0.195747215	0.014931391	GO:0005524,GO:0008270,GO:0005524,GO:0004222,GO:0006508	FTSH7	FTSH protease 7	ATP-dependent zinc metalloprotease family protein
Sapur.017G077900.1	592.3942099	0.220625246	0.088191373	2.501663	0.01238162	0.017923561	grey	-0.173909621	0.026102251	GO:0006508,GO:0004185	scpl25	serine carboxypeptidase-like 25	serine carboxypeptidase
Sapur.003G075100.1	23.11863383	0.385239365	0.153995115	2.5163	0.01239486	0.017936064	grey	-0.18215321	0.021381818	GO:0055114,GO:0016491,GO:0008270		Dehydrogenase, iron/zinc/polyol dehydrogenase family protein	quinone-oxidoreductase like protein
Sapur.016G217100.3	0.441127508	0.922104053	0.368634064	-2.50141	0.01233071	0.017803644	grey	-0.284236925	0.000388898	GO:0008168		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ribosomal RNA-processing protein
Sapur.007G050200.1	106.9040214	0.187598562	0.075000819	-2.50049	0.01238388	0.017939112	grey	-0.182526287	0.020197198	GO:0005524,GO:0003676		Helicase conserved C-terminal domain-containing protein	NA
Sapur.002G073200.1	10.06457042	0.352570169	0.140999444	2.500508	0.01240155	0.017947396	grey	0.11331265	0.162240674	GO:0045454,GO:0015035,GO:0009055,GO:0035556	EIF4A-III	electron carriers;protein disulfide oxidoreductases	electron transporter, putative
Sapur.006G005100.1	2.362835201	0.267539629	0.107139623	2.500465	0.01240117	0.017967598	grey	0.162153254	0.040439653				NA
Sapur.015G162600.1	27.40043519	-0.160885709	0.06435524	-2.49996	0.01242034	0.017972569	grey	-0.139595838	0.081205548	GO:0003676		RNA-binding (RRM/RBD/RNP motifs) family protein	polyadenylate-binding protein RBP45, putative
Sapur.012G269100.2	0.913806057	0.834386769	0.337015158	2.499949	0.01242131	0.017972659	grey	0.18391826	0.021128394				NA
Sapur.003G029705.1	224.1815076	0.145224056	0.058087019	2.499805	0.01242951	0.017972956	grey	0.183042853	0.02326116				histone acetyltransferase subunit Nua4
Sapur.001G034400.1	0.345432898	1.145835839	0.45834837	2.499923	0.01242014	0.017972659	grey	0.206503396	0.009464729			Protein of unknown function, DUF617	plant-specific domain TIGR01570 family protein, putative
Sapur.005G075000.1	744.3198023	0.150000254	0.060022322	2.499885	0.01242298	0.017973597	grey	0.151142298	0.058837316				SnRK1-interacting protein, putative
Sapur.019G005200.1	197.9420876	-0.557690801	0.223081699	-2.49964	0.01242913	0.017975079	grey	-0.247017131	0.010815521	GO:0005524,GO:0005515		NB-ARC domain-containing disease resistance protein	NA
Sapur.006G170400.1	0.403476562	0.910642543	0.364132897	2.498887	0.01245951	0.018175154	grey	-0.238041791	0.002603885			Domain of unknown function (DUF3123)	NA
Sapur.004G047200.1	153.774374	-0.085322037	0.034214528	-2.49885	0.01245825	0.018231375	grey	-0.200020602	0.010141485				NA
Sapur.006G173700.1	10.97327306	0.192219254	0.077064659	2.497966	0.01249068	0.018293216	grey	0.195747015	0.014931391	GO:0005515		F-box family protein	transcription regulation protein, putative
Sapur.019G064300.1	1.364528684	0.602261439	0.241561395	2.496428	0.01247564	0.017943104	grey	0.227858853	0.004103223	GO:0005515		F-box and associated interaction domains-containing protein	F-box protein interaction domain protein
Sapur.015G095700.1	965.6188888	0.157337769	0.063122948	2.496	0.01250629	0.018077027	grey	-0.207386668	0.005517719	GO:0004857,GO:0042545,GO:0030599,GO:0005618	ATMEMCPA,PMEPCRA	methylesterase PCR A	pectinesterase/pectinesterase inhibitor, putative
Sapur.015G072400.2	38.00638256	0.184273823	0.073792052	2.497265	0.01251553	0.018080462	grey	0.199345006	0.012315555		ATIDD15,SGR5	C2H2-like zinc finger protein	NA
Sapur.15WG022300.1	85.91394621	-0.162779014	0.065195454	-2.49684	0.01252708	0.018351417	grey	-0.225738839	0.004473899			Protein of unknown function (DUF761)	cotton fiber, putative
Sapur.005G157900.1	1.148.35467	0.239855671	0.095985553	-2.49692	0.01257562	0.018351417	grey	-0.224397612	0.003129276			Protein of unknown function, DUF338	NA
Sapur.003G099400.1	18.64709312	-0.087778644	0.035631912	-2.49689	0.01252888	0.018361534	grey	-0.204586663	0.000180481	GO:0003677		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ribosomal RNA-processing protein
Sapur.005G266700.1	3.464738391	0.230877832	0.093738819	-2.49687	0.01254988	0.018369151	grey	0.189274411	0.021347406			Amphoretic interchange chaperone family	cysteine synthase
Sapur.012G034300.1	101.9541489	0.230638214	0.092391371	-2.49622	0.01254905	0.018369151	grey	-0.211880396	0.007723804			electron carriers;protein disulfide oxidoreductases	electron transporter, putative
Sapur.003G051100.1	1.302833207	0.367807489	0.147186919	-2.49581	0.01256117	0.018367598	grey	0.192153254	0.040439653	GO:0008270,GO:0015151,GO:0046872		zinc finger (C2H2 type) /CSHCH-type RING finger) family protein	NA
Sapur.012G162600.1	2.694784	-0.446039278	0.178727727	-2.49564	0.01257169	0.018077073	grey	-0.139595838	0.081205548	GO:0003676	ATRBP4GC	RNA-binding (ERN/RBD/RNP motifs) family protein	polyadenylate-binding protein RBP45, putative
Sapur.009G106500.1	59.84352.2	0.180327767	0.082968176	2.495367	0.01258626	0.018080508	grey	0.221928279	0.004832365				NA
Sapur.012G061200.2	0.770220115	0.768184481	0.307884531	2.495043	0.01259499	0.018105736	grey	0.157047674	0.049497297	GO:0003676		RNA-binding (ERN/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein 27C, putative
Sapur.005G067000.1	1563.725612	0.095787027	0.038398733	2.494891	0.01259634	0.018107585	grey	0.17111984	0.032127345	GO:0009073,GO:0009234,GO:0008152,GO:0008324		fumarylacetoacetase family protein	fumarylacetoacetase
Sapur.016G055005.1	13.36604897	0.501463412	0.201081429	2.494612	0.01260948	0.018126164	grey	0.224827835	0.003075577	GO:0055114,GO:0047134		Cysteine/Histidine-rich C1 domain family protein	hypothetical protein
Sapur.003G193600.1	7.193319515	0.315691397	0.126538046	2.49444	0.01261521	0.018333378	grey	0.172508577	0.030735742			Protein of unknown function, DUF547	transcription factor, putative
Sapur.018G237700.1	46.21714282	0.211249169	0.084669105	-2.49427	0.01263017	0.018348824	grey	-0.242568783	0.002606633				hypothetical protein
Sapur.005G159800.1	2.308796653	0.411407661	0.164958769	2.494003	0.01263148	0.018154123	grey	0.198411169	0.012737148				hypothetical protein
Sapur.019G202300.1	1.015691884	0.668485498	0.268046679	2.49391	0.01263428	0.018157867	grey	-0.168592679	0.034786162				NA
Sapur.007G028700.1	20.94820732	-0.41481054	0.166330585	-2.49389	0.01265293	0.018158211	grey	-0.204661169	0.010210642			Protein of unknown function (DUF677)	NA
Sapur.003G113000.1	327.8192414	0.010270703	0.004386777	2.493665	0.01266149	0.018160027	grey	0.212210205	0.007842425	GO:0005085,GO:0016020,GO:0012599,GO:0006812	ATNHX7,ATSOS1,SOS1	sodium/potassium/hydrogen exchanger family (KEA) (SOS1)	Na+/H+ antiporter
Sapur.018G091100.1	11420.83448	0.108132071	0.04336895	2.493041	0.01266415	0.018200206	grey	0.197247165	0.011281655			beta-hydroxyisobutyryl-CoA hydrolase 1	NA
Sapur.004G099300.1	18.31101375	0.342027767	0.138298616	2.491763	0.01271848	0.018275114	grey	-0.344808051	0.003072369				NA
Sapur.013G241001.1	54.01135078	-0.612520352	0.245936356	-2.49049	0.01275654	0.018327335	grey	0.243163908	0.002150053		ATG14A60.1	LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.001G067600.1	0.958373833	0.634357943	0.254736709	2.490443	0.01275898	0.018329044	grey	0.15621168	0.050734895				hypothetical protein
Sapur.005G057001.1	8.925583638	0.245357316	0.114686601	2.4904	0.01276549	0.018330489	grey	0.192602316	0.015329335		ATG57540.2	Protein of unknown function (DUF506)	transmembrane protein, putative
Sapur.001G020600.1	143.0039439	0.107987441	0.043364073	2.490244	0.01276557	0.018337693	grey	0.186681855	0.019212084		ATG18780.1		transmembrane protein, putative
Sapur.009G108300.1	67.24602591	-0.291988286	0.120476828	-2.49066	0.01277508	0.018346294	grey	0.202185416	0.010138811	GO:0009955	UCC1	uclacyanin 1	plastocyanin-like domain protein
Sapur.009G082000.1	5.226679922	0.555218363	0.223121493	2.488413	0.01283472	0.018400823	grey	0.144517692	0.070946363	GO:0016787,GO:0008152	ATG47480.1	alpha/beta-Hydrolases superfamily protein	NA
Sapur.016G288100.1	0.333661884	-0.965349052	0.400020243	-2.48819	0.01283948	0.018401152	grey	-0.20705919	9.18E-05		ATG45260.2	Phosphoesterase family, metallophosphoesterase family protein	unusual positioning protein 1A, putative
Sapur.010G065500.3	1.46551134	0.954572722	0.389739823	2.488023	0.01284527	0.018449407	grey	-0.147008377	0.066167799	GO:0006629,GO:0005198,GO:0004190	ATG19330.1	APLA,ATAPA1	aspartic proteinase A1
Sapur.009G076100.1	-0.600867809	0.804021649	0.321417423	2.487948	0.01284632	0.018451227	grey	0.198524274	0.012685525	GO:0005515,GO:0050668,GO:0016491	ATG47961.1	FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.012G089400.1	0.329127775	1.397937674	0.561882266	2.487857	0.01285149	0.018455653	grey	0.266549029	0.000736677	GO:0004689,GO:0005524,GO:0004672	CRK29	cysteine-rich RLK (RECEPTOR-like protein kinase) 29	NA
Sapur.004G244800.1	67.63941224	0.115320649	0.046288322	2.487479	0.01286453	0.018474465	grey	0.185443909	0.020688888	GO:0016772,GO:0005524	ATRP5,BP1	PP2A regulatory subunit B' family	NA
Sapur.012G280800.3	1.061552153	0.714406208	0.287266893	-2.48665	0.01288295	0.018516065	grey	0.123943007	0.138158832	GO:0003723		RNA-binding CRS1 / YhbY (CRM) domain-containing protein	CRS2-associated factor 1
Sapur.002G013300.1	1283.956499	-0.083884775	0.033786092	-2.4865	0.01290677	0.018522987	grey	-0.203443857	0.015601774	GO:0046872		RING/FYVE/PHD zinc finger superfamily protein	zinc finger protein, putative
Sapur.005G093600.1	10.06615166	0.100200004	0.132838087	2.486258	0.01290945	0.018534765	grey	0.192721241	0.015032078			Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.15WG125800.1	0.58991922	-0.855451022	0.344180816	-2.48561	0.01292806	0.018587506	grey	-0.215658252	0.007553783	GO:0008270,GO:0003676			NA
Sapur.006G012300.1	4962.177222	-0.219462271	0.088273327	-2.48552	0.01293626	0.018751574	grey	-0.169897646	0.032070269		ATG10940.2	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/LTP family protein
Sapur.009G219300.1	247.3452002	0.270371883	0.108805548	2.484909	0.01295856	0.018801909	grey	0.208806528	0.008679524	GO:0003779	ATVLN4,VLN4	villin 4	NA
Sapur.009G261700.1	257.6005113	-0.560024134	0.225451563	-2.48469	0.01296906	0.018801977	grey	-0.184716557	0.025085265	GO:0016779,GO:0009058		transferases;nucleotidyltransferases	translation initiation factor eIF-2B subunit gamma
Sapur.017G019500.1	1.075442883	-0.653709944	0.263929271	-2.4834	0.01301394	0.018879498	grey	-0.216725348	0.006397315	GO:0005524,GO:0005515		cell division cycle protein 48-related / CDC48-related	bromodomain protein with A kinase anchoring domain
Sapur.015G000800.1	560.0255097	0.098456163	0.039650435	2.483047	0.01303605	0.018881457	grey	-0.198925419	0.015477773	GO:0005515	ABO4	armadillo repeat protein 4	ARM protein
Sapur.017G117300.1	2.482691521	-0.536191195	0.215977088	-2.48263	0.01304148	0.018718081	grey	0.185898361	0.019689941	GO:0005515,GO:0003824	BZO1	benzoyloxycoumarin/coumarin 1	acyl-CoA synthetase
Sapur.016G247400.1	0.341581823	1.510872644	0.608632637	2.482405	0.01306989	0.018726097	grey	0.32341793	3.82E-05	GO:0016829,GO:0003310,GO:0000287	ATS4G14540.1	Terpenoid cyclases/Protein prenyltransferases superfamily protein	NA
Sapur.012G067054.4	7.050971285	0.775834455	0.311355005	-2.48227	0.01309481	0.018751195	grey	-0.135054627	0.101770586		ATHSFA7,ATHSFA8,HSF13,HSF	heat stress factor 7	heat shock transcription factor 1, putative
Sapur.T041700.1	2.678833532	0.396355113	0.159694087	2.482317	0.01305789	0.01873668	grey	0.163123016	0.041222164		ATN6EIS,N6EIS	N/MA-related kinase 5	NA
Sapur.005G088900.1	57.86404693	0.202264472	0.081506164	2.481969	0.01306252	0.018756429	grey	0.15124656	0.052208449	GO:0006355,GO:0003700	ABR1	Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.005G085600.1	15.16037022	0.227793213	0.091691672	-2.48126	0.01306746	0.018758109	grey	-0.214002382	0.00711769	GO:0055114,GO:0016491		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	prolyl 4-hydroxylase alpha subunit, putative
Sapur.016G083100.1	0.406361003	0.948607928	0.382345119	2.481189	0.01308819	0.018825195	grey	-0.268092402	0.000886962	GO:0005515,GO:0016740,GO:0030390		Mitochondrial dihydrolipoamide succinyltransferase family protein	mTOR2 protein
Sapur.006G211200.1	178.161448	0.119208186	0.048033708	-2.48176	0.01307349	0.018758084	grey	-0.219721886	0.005692641		ATG22273.1	Nucleotide/sugar transporter family protein	UDP-sugar transporter, putative
Sapur.016G048800.1	281.6497976	0.102847104	0.041463164	2.481069	0.01309652	0.018872344	grey	0.192721241	0.015032078		ATG23130.1	polyprenol kinase family protein	DNA polymerase delta, putative
Sapur.016G032300.1	48.66993716	0.153653553	0.061937659	-2.48048	0.01310604	0.018824052	grey	-0.214973672	0.006990237		ATG60225.1		transmembrane protein, putative
Sapur.013G027500.1	0.866948070	0.720144565	0.290152578	2.480024	0.01313962	0.018904921	grey	-0.194036574	0.016425609	GO:0005515	ATG18730.1	DNA/RNA helicase family protein	Dna/Rna/B protein
Sapur.013G108700.1	154.5118732	-0.253581632	0.102331273	-2.47806	0.01320936	0.018950527	grey	-0.131491886	2.23E-05	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1	somatic embryogenesis receptor-like kinase
Sapur.013G185100.1	34.40617869	-0.301220502	0.122375721	-2.47775	0.01322134	0.018966387	grey	-0.19178299	0.016113379		ATG28710.1	C2H2-type zinc finger family protein	C2H2-type zinc finger protein
Sapur.009G077200.1	88.54551513	-0.200047381	0.081280656	-2.47665	0.01327206	0.018989931	grey	-0.191831212	0.016193108	GO:0005634	ATG18520.1	DNA binding	hypothetical protein
Sapur.003G135900.1	1.39477968	-0.59758206	0.24148889	-2.47468	0.01332455	0.019111613	grey	-0.141725614	0.076610477	GO:0005515	FY	Transducin/WD40 repeat-like superfamily protein	flowering time control protein FY, putative
Sapur.006G115700.1	0.572024674	0.337000197	0.136267149	2.474193	0.01333163	0.019113688	grey	-0.2777269334	0.002842022	GO:0005783,GO:0003779	ATG46490.1	cyclase associated protein 1	adenylyl cyclase-associated protein
Sapur.010G024200.1	0.089665096	-0.347027473	0.421757927	-2.47483	0.01333561	0.0191184	grey	0.201192264	0.009274322	GO:0006457,GO:0003755,GO:0004013	ROC2	rotamase cyclophilin 2	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.013G087500.1	7.098971884	0.439661164	0.177797717	2.474515	0.01334173	0.019133844	grey	0.19178799	0.016433164	GO:0008138,GO:0006470	ATG27232.1	dual specificity protein phosphatase family protein	dual specificity protein phosphatase
Sapur.006G017500.3	1.186560436	0.589401467	0.238236299	-2.47402	0.01336021	0.019195921	grey	-0.006681168	0.931794308		ATG22260.3	Cysteine proteinases superfamily protein	OTU-like cysteine protease
Sapur.009G008300.1	255.1454668	0.101018231	0.041000214	2.465766	0.01337938	0.019376574	grey	0.172681708	0.030449192		ATG6660.1	Scorpion toxin-like knottin superfamily protein	NA
Sapur.15WG114500.2	1.625383804	0.514338151	0.207577907	2.473451	0.01338159	0.019388382	grey	0.202118313	0.011133007		ATG53150.1	DNA/RNA helicase family protein	curved DNA-binding protein, putative
Sapur.005G283300.1	594.3013223	0.10251182	0.041768804	2.473214	0.01339048	0.019200033	grey	0.192382218	0.015783406		ATG54520.1		plant/F20D21-34 protein
Sapur.005G212500.1	0.372087991	1.446647739	0.585085647	2.472592	0.01340407	0.019211249	grey	0.246924207	0.001838519				transmembrane protein, putative
Sapur.T036200.1	0.441839433	-0.846014568	0.342135188	-2.47275	0.01340713	0.0192238

Sapur.15WG087600.8	3.09183381	1.36250387	0.46258677	2.42828	0.01570636	0.02164771	gene	0.06478107	0.42044227		GSZ42600.1	ARM-repeat superfamily protein	NA
Sapur.0146141000.1	2799.520482	-0.07456796	0.03086157	-2.42816	0.01517565	0.02164088	gene	-0.20927868	0.08525985	GO:0016779,GO:0009058	GSZ48300.1	ADGL.APS1	AGF glucose pyrophosphorylase 1	glucose-1-phosphate adenylyltransferase small subunit
Sapur.0053618000.1	0.10028522	-0.01575153	0.41804918	-2.42761	0.01519839	0.02167186	gene	-0.12814686	2.68E-05	GO:0004857	GSZ14130.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	plant invertase/pectin methylesterase inhibitor domain protein
Sapur.0010039100.1	228.4239544	1.41170185	0.58161362	2.427215	0.0151523	0.02169369	gene	0.29965968	0.00017513	GO:0016887,GO:0005524,GO:0016820	GSZ15520.1	ABCG40.ATABCG40.ATPDR1	pleiotropic drug resistance 12	transporter family ABC domain protein
Sapur.0053630000.1	20.92243938	0.57621883	0.07268082	2.426119	0.01526154	0.01758372	gene	-0.17573835	0.02766574		GSZ68930.1	IR	Chaperone Dnaj-domain superfamily protein	chaperone protein Dnaj
Sapur.0030113200.5	1.81164994	-0.51058232	0.21045591	-2.42608	0.01526093	0.02176056	gene	-0.20977096	0.00836821	GO:0006281,GO:0003684	GSZ44740.2	POLH	Y-family DNA polymerase H	DNA polymerase eta
Sapur.0096130300.1	24.88378658	-0.16978828	0.06968594	-2.42593	0.01528385	0.01760888	gene	-0.19823855	0.01277382	GO:0070176,GO:0007049,GO:0006251	GSZ46250.1		Integral membrane protein hemolysin-III homolog	hypothetical protein
Sapur.0192085400.1	9.77564351	-0.47408609	0.19178835	-2.42578	0.01575711	0.01776168	gene	-0.20587616	0.09487724	GO:0016021	GSZ09100.1			NA
Sapur.0196107000.1	1.79019428	-0.52357795	0.21589667	-2.42511	0.01503827	0.02185523	gene	-0.19002814	0.01713519		GSZ72280.1		Calcium-binding EF-hand family protein	Ae9/EFC-9 rapidly elicited protein, putative
Sapur.0146121900.1	0.37310811	-0.12018487	0.48167022	-2.425	0.01538277	0.02182071	gene	0.15388277	0.2735357	GO:0008033	GSZ10130.1	ATIPT3,IPT3	isopentenyltransferase 3	cytokinin biosynthetic isopentenyltransferase
Sapur.0061147000.1	200.978696	-0.09432855	0.04513925	-2.42468	0.01523918	0.02185228	gene	-0.21020046	0.08231647		GSZ06050.1	ORG4	OBP3-responsive gene 4	OBP3-responsive protein
Sapur.0042038000.1	16.85461474	0.30727234	0.12679212	2.424173	0.01524289	0.02168673	gene	-0.19981361	0.01208022		GSZ12110.1		Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.0110624000.1	13.97367072	0.36021903	0.10739563	2.423952	0.01526227	0.02181088	gene	0.10339441	0.01231909	GO:0055115	GSZ11080.1	ABRLP35,RLP35	receptor-like protein 35	NA
Sapur.0010268800.1	1.36115425	0.41521197	0.17190147	2.417318	0.01563287	0.02360045	gene	-0.19483318	0.03468387		GSZ46510.1		Ribonuclease H superfamily	NA
Sapur.0010950500.1	17.48103691	-0.30788840	0.12703897	-2.42356	0.01538349	0.02190345	gene	-0.18988249	0.01722655	GO:0006355,GO:0006289,GO:0000439	GSZ14240.1		Nucleotide excision repair, TFIIH, subunit TTDA	general transcription factor IIH subunit
Sapur.0061250000.1	41.95167073	0.29145631	0.12082729	2.412283	0.01576054	0.02387243	gene	-0.21233664	0.01922087		GSZ27010.1	AT-TCP20,ATTCP20,PCF1,TC	TEOSINTE BRANCHED 1, cycloidea, PCF (TCP)-domain family protein 20	TCP transcription factor
Sapur.7054200.1	43.9968199	0.32189555	0.13267173	2.420926	0.01548105	0.02258379	gene	-0.18887691	0.01785928					NA
Sapur.0161632300.1	1252.369411	0.78548884	0.32450303	2.420467	0.01500579	0.02385184	gene	0.30800462	8.70E-05		GSZ71950.1		Proteinase inhibitor, propeptide	peptidase inhibitor I9
Sapur.0070260000.1	887.0328976	-0.07609687	0.03113669	-2.41969	0.01867458	0.02398	gene	-0.18317809	0.01205503	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	GSZ37820.1	XTH7	xyloglucan endotransglycosylase/hydrolase 7	xyloglucan endotransglycosylase hydrolase
Sapur.0032601000.2	0.52070159	0.79501837	0.32858889	-2.41964	0.01535895	0.02233715	gene	0.14557801	0.08877907		GSZ51730.1			late embryogenesis abundant protein, putative
Sapur.0102079200.1	248.1610506	0.27238551	0.08903569	-2.4192	0.01573191	0.02394984	gene	-0.2207556	0.01256467	GO:0003677,GO:0043565,GO:0006355,GO:0003700	GSZ68780.1	ATHB13	Homeobox-leucine zipper protein family	homeobox leucine zipper protein
Sapur.0061145000.1	139.7543423	0.21507565	0.08927673	-2.418741	0.01574319	0.02218558	gene	0.16886504	0.03438077	GO:0008371,GO:0006486	GSZ08280.1		Glycosyltransferase family 29 (sialyltransferase) family protein	sialyltransferase-like protein
Sapur.0061231100.1	0.63438887	0.88263511	0.36468848	-2.41867	0.01577355	0.02188959	gene	-0.19614952	0.01815349		GSZ03370.1		Sec14p-like phosphatidylinositol transfer family	CRAL/TRIO domain protein
Sapur.1SWG0107300.1	2.43419399	-0.42458599	0.17537506	-2.41823	0.01559612	0.02214732	gene	-0.21304281	0.00738104	GO:0055114,GO:0020037,GO:0016705,GO:0005506	GSZ10080.1	CYP71B2	cytochrome P450, family 71, subfamily B, polypeptide 2	cytochrome P450 family protein
Sapur.0030150600.1	3.26090534	0.41557111	0.17189814	-2.417318	0.01563287	0.02360675	gene	-0.19326945	0.03437363	GO:0006270,GO:0005515	GSZ15130.1		RING/U-box superfamily gene	zinc finger protein
Sapur.0080253900.1	72.26921007	0.19491046	0.08064318	2.41699	0.01564432	0.02288748	gene	0.16625703	0.03747206		GSZ40080.1	ELF4	Protein of unknown function (DUF1313)	early flowering protein
Sapur.0010145700.5	1.62908211	0.52568849	0.21768555	-2.41689	0.01565628	0.02290764	gene	-0.22588921	0.09446318	GO:0005085,GO:0016021	GSZ79820.1	SGB1	Major facilitator superfamily protein	plastidic glucose transporter, putative
Sapur.0170581700.2	0.33767914	0.52348119	0.44521042	-2.41626	0.01568055	0.02316579	gene	-0.22608906	0.03363949		GSZ12830.1			hypothetical protein
Sapur.0170628800.1	147.6479867	0.23317529	0.09649145	-2.41584	0.01569659	0.02346913	gene	-0.20929276	0.00541924	GO:0016758,GO:0008152	GSZ12890.1		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase, putative
Sapur.0102609300.1	1.37606009	0.77155651	0.32973366	-2.41581	0.01550151	0.02356171	gene	-0.18172032	0.02398196		GSZ06190.1		Class I glutamine amidotransferase-like superfamily protein	NA
Sapur.0192027700.1	0.31294837	2.89912407	0.37238547	2.415148	0.01572882	0.02266044	gene	0.22762299	0.00417458	GO:0008270,GO:0003676	GSZ12180.1			NA
Sapur.0051121300.1	15.31638329	0.29150609	0.12069149	2.415076	0.01573191	0.02394984	gene	0.2358328	0.02023356					NA
Sapur.0010039600.1	43.35206648	0.33507807	0.13875182	2.414834	0.01572273	0.02413388	gene	0.16532278	0.03816427	GO:0016758,GO:0008152	GSZ22180.1	AtUGT85A1,UGT85A1	UDP-glucosyl transferase 85A3	NA
Sapur.0010620400.1	41.67812124	0.26358293	0.10917743	2.414267	0.01576347	0.02444889	gene	-0.16691027	0.01442689		GSZ46610.1			RXT2-like protein, putative
Sapur.0110287700.1	4.43916684	0.59602897	0.24685472	2.414466	0.01578289	0.02434128	gene	0.16528349	0.03578272		GSZ01400.1		ARM-repeat superfamily protein	NA
Sapur.7181200.1	1.62758798	0.69110254	0.28630455	2.414229	0.01578057	0.02434256	gene	-0.20850465	0.05872366	GO:0005515	GSZ12120.1	RPS5	Disease resistance protein (CC-NBS-LRR class) family	pollen coat protein
Sapur.0072640000.1	18.68173867	0.19180106	0.13762467	2.41426	0.01576749	0.02444889	gene	-0.18210895	0.02245145		GSZ15680.1		Calcium-binding EF-hand family protein	polycalcin Jun protein O, putative
Sapur.0102685800.1	93.17952544	0.13587878	0.05633897	2.412769	0.01582727	0.02534287	gene	0.17960883	0.02434145		GSZ28370.1		Uncharacterized protein family (UPF0497)	cytochrome P450 family protein
Sapur.0092678800.1	716.16597	0.04504363	0.4173837	-2.41283	0.01583858	0.02354962	gene	-0.22481618	3.32E-05	GO:0016758,GO:0008152	GSZ45180.1	UGT86A1	UDP-Glycosyltransferase superfamily	linoleoyl UDP-glucosyltransferase
Sapur.0021564000.2	22.08421276	0.20009012	0.08329212	2.412343	0.01585068	0.02357447	gene	0.18813999	0.01804125		GSZ27730.1	AATG1Bb	Transducin/WD40 repeat-like superfamily protein	WD repeat phosphoinositide-interacting protein
Sapur.0082650500.1	84.8626667	0.25307894	0.10424355	2.411306	0.01585949	0.02419734	gene	0.20273634	0.00398607		GSZ05520.1		sequence-specific DNA binding transcription factor	transcription factor
Sapur.0061150800.1	26.31479657	0.33704286	0.13908271	2.410746	0.01591914	0.02365487	gene	0.21227506	0.00706848		GSZ11600.1			hypothetical protein
Sapur.0010173800.1	13.26873675	0.24207889	0.11027269	2.41019	0.01594066	0.02381942	gene	-0.17783783	0.02584544		GSZ10760.1		ARM-repeat superfamily protein	Pa1 complex component
Sapur.0192049900.1	15.28421281	-0.21451898	0.08866608	-2.40981	0.01560703	0.02708608	gene	-0.18987695	0.01723148	GO:0043531	GSZ27220.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.0010637300.1	20.88864197	0.41605613	0.17262491	2.40967	0.01566855	0.02716384	gene	-0.19027918	0.01692211		GSZ14060.1	ATCYSD1,CYSD1	cysteine synthase 1	cysteine synthase
Sapur.0080243400.4	14.92912302	0.19857278	0.08241369	-2.40953	0.01597045	0.02724221	gene	-0.19679831	0.01497721		GSZ74310.1		Exostosin family protein	exostosin-like protein, putative
Sapur.0096282100.1	98.71939323	0.15852484	0.06581266	2.408361	0.01598136	0.02755073	gene	0.23469725	0.00388504					NA
Sapur.0061153400.1	9.78260819	0.31636799	0.13131711	2.409175	0.01588651	0.02744657	gene	-0.24625582	0.00201708		GSZ05170.1	ATCSA3,ATH-B,CSA3,CSV	Cellulose synthase family protein	cellulose synthase A, catalytic subunit
Sapur.0020678600.2	2.25285424	0.40847621	0.16953351	2.409136	0.01590343	0.02765887	gene	0.17519663	0.02839484	GO:0008168	GSZ78240.1	OSU1,QUA2,TSD2	S-adenosyl-L-methionine-dependent methyltransferases superfluorin protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.0170133900.1	5.72762645	0.51488964	0.21368808	2.409161	0.01604129	0.02778882	gene	0.17933881	0.02451743	GO:0003824	GSZ68880.1	BZO1	benzoylsynthase 1	NA
Sapur.0105161100.5	0.60574099	0.85918151	0.35674164	2.408359	0.01602498	0.02792369	gene	0.20894358	0.03938865	GO:0055114,GO:0016616,GO:0006694,GO:0003854	GSZ28760.3	UXS6	UDP-XYL synthase 6	UDP-glucuronate decarboxylase
Sapur.0010621500.1	5.72449517	0.36397128	0.15288385	2.4081	0.01602769	0.02797476	gene	-0.20738215	0.03916217					NA
Sapur.0130202700.1	69.92912219	0.16375489	0.07599402	2.408181	0.01602243	0.02800533	gene	0.16563086	0.03819106		GSZ26840.1		alpha/beta-Hydrolases superfamily protein	RNA binding family protein
Sapur.0092681600.1	15.17090616	0.22107889	0.10267269	2.408167	0.01602889	0.02800533	gene	-0.18050652	0.02836413		GSZ42740.1		RNA binding family protein	NA
Sapur.0020196800.1	2.07341683	-0.47029624	0.19528878	-2.40867	0.01602896	0.02800533	gene	-0.20582057	0.00978052		GSZ56500.1		Protein of unknown function (DUF1012)	serine-rich protein-related
Sapur.0161845000.1	35.95436283	0.18201874	0.08439889	2.40755	0.01603849	0.02832786	gene	-0.17809042	0.02460375		GSZ16465.1		Chaperone Dnaj-domain superfamily protein	heat shock protein-binding protein, putative
Sapur.0161130600.1	8.51599699	-0.32937188	0.13681238	-2.40747	0.01602486	0.02842071	gene	-0.16824035	0.03409596		GSZ28780.1			NA
Sapur.0070287100.4	1.38842692	0.59154529	0.24579339	2.407277	0.01607993	0.02852516	gene	0.25875276	0.00170357	GO:0005468,GO:0006672	GSZ33992.1	ATOST1,OST1,P44.SNRK2.6	Protein kinase superfamily protein	Serine/Threonine-kinase SAPK2
Sapur.0170082600.4	0.76766862	0.72353887	0.30214736	2.406956	0.01608611	0.02871292	gene	-0.16496912	0.16452574	GO:0005515	GSZ05080.1		SET domain-containing protein	rubisco-2\52C5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, putative
Sapur.0110252100.2	3.79948807	-0.4733457	0.19668184	-2.40666	0.01609291	0.02885049	gene	-0.15784438	0.04897629		GSZ26680.1	CAD1	MAC/Perforin domain-containing protein	MAC/perforin domain protein
Sapur.0180690000.1	92.45873997	0.09255164	0.03848166	2.405911	0.01608	0.02901557	gene	0.12888425	0.10708181					NA
Sapur.0061122300.1	41.23623092	0.17683768	0.07358515	2.405888	0.01613206	0.02905296	gene	0.14216564	0.07507784		GSZ19460.1		Protein of unknown function (DUF311)	DUF311 domain protein
Sapur.0061153400.1	206.7574034	0.36934476	0.15353183	2.405565	0.01614133	0.02948004	gene	-0.18102715	0.03230589	GO:0008233,GO:0005508	GSZ50940.1	ALPHA-VPE,AALPHAVPE	alpha-vacuolar processing enzyme	NA
Sapur.0180834800.1	1.61234135	-0.52735783	0.21090008	-2.40544	0.01615049	0.02960545	gene	-0.18185985	0.02638439	GO:0005739,GO:0004129	GSZ58005.2		Cytochrome c oxidase, subunit VIb family protein	NA
Sapur.0096280700.1	1.98916168	-0.60628674	0.2509431	-2.40504	0.01617202	0.02984684	gene	-0.19189238	0.03941078	GO:0016373,GO:0006511,GO:0005839,GO:0004298	GSZ21120.1	PAC1	20S proteasome subunit alpha type-4 protein	proteasome subunit alpha type-4 protein
Sapur.7025300.2	3.35608364	0.38616018	0.16059706	2.404918	0.01617523	0.02990087	gene	-0.18590809	0.01739745	GO:0055515,GO:0006488,GO:0004672	GSZ16270.2		Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain	Serine/Threonine-kinase domain protein
Sapur.0110616100.1	3.52798348	0.31341501	0.14004888	2.404888	0.01617773	0.02992347	gene	-0.17577773	0.02416673		GSZ18120.2		Kinase interacting (KIP1-like) family protein	kinase interacting (KIP1-like) family protein
Sapur.0061161600.1	11.19972936	-0.60108165	0.24970137	-2.40461	0.01618525	0.02300757	gene	-0.15371878	0.05456739		GSZ30880.2		Pleckstrin homology (PH) domain-containing protein	pleckstrin-like (PH) domain protein
Sapur.0130276800.1	3.59457024	0.46977461	0.18704675	-2.404613	0.01618602	0.02307557	gene	0.16442562	0.07228984					NA
Sapur.0110576200.1	81.9144225	-0.32168624	0.13376429	-2.40417	0.01619072	0.02316664	gene	-0.22756453	0.08263544		GSZ53400.1		Ubiquitin domain-containing protein	ubiquitin domain protein
Sapur.0140253800.5	1.40441887	-0.56224244	0.23388594	-2.40392	0.01620474	0.02369451	gene	-0.23539855	0.02999533	GO:0005515	GSZ02090.1	ATCSN7,COP15,CSN7,FUSS	Proteasome component (PCI) domain protein	COP9 complex subunit 7a
Sapur.0120684000.2	1.68608615	-0.47348801	0.19437161	-2.40338	0.01624426	0.02381274	gene	-0.18050652	0.02836413		GSZ66990.1		Drought-responsive family protein	stress-induced protein 15, carbosy-terminal protein
Sapur.0030287700.1	170.2685862	-0.92303667	0.08208459	-2.40319	0.01625278	0.02309552	gene	-0.18667181	0.01923975	GO:0004857	GSZ42360.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	pectin methylesterase inhibitor
Sapur.0165102092.1	6.46735546	-0.86047488	0.34980033	-2.4027	0.01627451	0.02321269	gene	-0.23542027	0.02091671		GSZ68970.1		Heavy metal transport/detoxification superfamily protein	copper-ion-binding protein, putative
Sapur.0061141300.1	19.09068227	0.55887437	0.23303976	2.402521	0.01629208	0.02331097	gene	0.13053821	0.10196551		GSZ59480.1		early nodulin-related	early nodulin 93
Sapur.0010261600.4	4.03456456	0.37022184	0.15397284	-2.402473	0.01629425	0.02333155	gene	0.15726169	0.04271612		GSZ60620.1	ATSNF6,SNF6	Homology of vacuolar nonfermenting 6	ARM-activated kinase, gamma regulatory subunit\52C putative
Sapur.7084700.1	0.78910147	0.97004258	0.40753348	-2.402428	0.01626648	0.02335532	gene	0.19864708	0.07262204		GSZ42881.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.0110253000.1	120.249299	0.10904319	0.04560127	-2.4022	0.01629605	0.02349188	gene	-0.20882197	0.08674664		GSZ45660.1			transmembrane protein, putative
Sapur.0051178200.1	11.06569014	-0.07268916	0.03038652	-2.40206	0.01630295	0.02349576	gene	-0.20692346	0.05652366	GO:0005622,GO:0003779,GO:0030042,GO:0015629	GSZ46120.1	ADF6,ATADF6	actin depolymerizing factor 6	actin-depolymerizing factor
Sapur.0051117500.1	3.38418309	0.37014387	0.15414863	-2.40132	0.01636117	0.02351818	gene	-0.17640373	0.02709983	GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	GSZ42510.1	ATNAC2,NACK2,TES	ATP binding microtubule motor family protein	NA
Sapur.1SWG0041100.1	4.99783931	0.38516262	0.16058186	2.400502	0.01637602	0.02352629	gene	0.16239384	0.04278388					NA
Sapur.7074800.1	3.75065574	0.3466008	0.14555026	2.400469	0.01637672	0.02353727	gene	0.19281606	0.01292606					NA
Sapur.0110567200.1	68.78608268	-0.62448832	0.26176745	-2.4004	0.01637637	0.02354691	gene	-0.19057608	0.01832581	GO:0055114,GO:0020037,GO:0016705,GO:0005506	GSZ14680.1	CYP71A15	cytochrome P450, family 71, subfamily A, polypeptide 15	cytochrome P450 family 72 monooxygenase
Sapur.0010609800.1	18.78072597	0.55039231	0.23061008	2.400302	0.01638165	0.02362371	gene	0.24819542	0.01723263		GSZ18600.1		Ubiquitin-conjugating enzyme family protein	Ubiquitin-conjugating enzyme family protein
Sapur.0110620400.1	1.70316479	-0.46502449	0.19450493	-2.39944	0.01639204	0.02391955	gene	-0.21422158	0.01088993		GSZ47750.1	DSPM2,2,PKS	DS protein kinase family	Serine/Threonine kinase domain protein
Sapur.0140203700.1	23.13465543	-0.29197064	0.12171422	-2.39887	0.01644545	0.02350218	gene	-0.15200948	0.05147743	GO:0043565,GO:0006355,GO:0003700	GSZ22850.2	AtBZIP60,bZIP6	basic leucine-zipper 6	BZIP transcription factor
Sapur.0170226800.3	10.38544777	0.26807424	0.11192113	2.398583	0.01645426	0.02360683	gene	0.18516545	6.31E-07	GO:0005515	GSZ13125.2		WW domain-containing protein	WW domain protein, putative
Sapur.0061260000.1	0.46401262	-0.94269279	0.39268338	-2.39846	0.01646051	0.02374486	gene	0.18042903	0.02741021					NA
Sapur.0180205300.1	331.9582937	0.07059582	0.02944701	-2.39737	0.01651235	0.02446288	gene	0.16445495	0.09583837	GO:0004108,GO:0000776	GSZ10733.2			centromere protein O
Sapur.0010622004.4	2.48068245	-0.30752283	0.1658969	-2.39675	0.01649386	0.02479059	gene	-0.20092406	0.01627076	GO:0005622,GO:0006741,GO:0003951	GSZ14640.1	ATNAD6Z,NAD6Z	NAD kinase	NAD kinase
Sapur.0061121800.1	59.2636453	0.26899828	0.12329781	2.395154	0.01661337	0.02581417	gene	0.17081486	0.03202457		GSZ58200.1			NA
Sapur.0010851000.1	1276.830651	0.07268796	0.02933245	2.394921	0.01662938	0.02595391	gene	0.18998824	0.01703063	GO:0005885,GO:0016020	GSZ18300.1	MSC5	MSC5-like 2	MsC5-like mechanosensitive ion channel MSC\52 protein
Sapur.0010689800.1	3.72581858	-0.42122665	0.17505201	-2.3949	0.01625115	0.02596063	gene	-0.17123686	0.03207927	GO:0016021,GO:0006506	GSZ63110.1		GPI transmembrane subunit PIG-U	GPI transmembrane subunit PIG-U
Sapur.0130202700.1	231.8242269	-0.10026204	-0.04186632	-2.39312	0.01670327	0.02707722	gene	-0.17928767	0.02401584		GSZ70552.1	TFIIIA	transcription factor IIIA	zinc finger protein
Sapur.0061105000.1	113.0625338	0.20334801	0.08498287	2.393056	0.01708699	0.02710624	gene	0.1503805	0.06103372		GSZ03230.1		Protein of unknown function, DUF584	NA
Sapur.0180214500.2	1.40070283	-0.54644234	0.22767447	-2.3926	0.01695195	0.02738224	gene	0.22316364	0.00842244	GO:0006351,GO:0005634,GO:0003700	GSZ14562.1		Homeodomain-like superfamily protein	trihelix transcription factor GT-1
Sapur.0080284800.1	24.24613638	0.30013632	0.12548281	-2.39232	0.01674246	0.02755171	gene	-0.18295673	0.02249736		GSZ06890.1	RTM2	HSP20-like chaperones superfamily protein	transmembrane protein, putative
Sapur.0130280600.1	1541.170744	0.30687421	0.07925765	2.391086	0.01678825	0.02833136	gene	0.16738502	0.03252877	GO:0005885,GO:0042626,GO:0016021,GO:0006810,GO:0005524,GO:0016887	GSZ80140.1	ATMRP14,MRP14	multidrug resistance-associated protein 14	multidrug resistance protein ABC transporter family protein, putative
Sapur.7128900.1	0.29900674	1.59335251	0.66534018	2.39047	0.01683625	0.02887108	gene	0.31789694	4.97E-05	GO:0003677				82 DNA-binding domain protein
Sapur.0010179300.1	9.56819605	-0.21306865	0.08959229	-2.39044	0.01682816	0.02872928	gene	-0.15750556	0.04883616		GSZ10760.1			transmembrane protein, putative
Sapur.0160577000.1	52.78514175	-0.26492133	0.11050835	-2.39087	0.01684499	0.02868277	gene	-0.20845499	0.03878564		GSZ10512.1	CPuDRF20	conserved peptide upstream open reading frame 20	NA
Sapur.1SWG0051000.1	0.26445857	1.38329307	0.57884939	2.389681	0.01688303	0.02919586	gene	0.23108863	2.21E-05		GSZ12180.1			NA
Sapur.0002656000.1	0.68891558	0.75858762	0.31757501	2.388541	0.01689458	0.02927654	gene	0.16687717	0.01105957	GO:0006355,GO:0003700	GSZ15620.1	SHN1,WIN1	Integrase-type DNA-binding superfamily protein	Integrase-type DNA-binding protein
Sapur.0042087400.1	216.0916168	0.17087965	0.07275144	2.389327	0.01687928	0.02940369	gene	0.16617006	0.0375295	GO:0006355,GO:0003677	GSZ39660.2	CDF2	cycling DOF factor 2	Dof zinc finger protein
Sapur.0061113300.1	944.5125547	0.07636544	0.03213046	2.38961	0.01688938	0.02960194	gene	0.20050831	0.01370723		GSZ42240.1		Protein of unknown function (DUF630 and DUF632)	bZIP transcription factor bZIPU07
Sapur.7072000.1	0.84329874	0.72682734	0.30735357	-2.38905	0.01689386	0.02965918	gene	-0.22607597	0.05481076		GSZ18670.1		Ankyrin repeat family protein	ankyrin repeat protein
Sapur.0080284600.1	15.21103796	0.25885454	0.10833829	2.388041	0.01690423	0.02985918	gene	0.15348681	0.05455547	GO:0006886	GSZ04640.1		ENTH/VHS family protein	NA
Sapur.0180217500.1	117.7323006	-0.57711456	0.24160623	-2.38866	0.01691045	0.02980026	gene	0.21853122	0.05968306	GO:0043531	GSZ14460.1		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.0070127100.1	80.68237369	-0.38049775	0.15926796	-2.38857	0.01695412	0.02984629	gene	-0.21041916	0.08165037	GO:0016758,GO:0008152	GSZ48820.1	ATSAG71-GT-SAG71-SGT1.U	UDP-glucosyltransferase 74F2	UDP-glucosyltransferase family
Sapur.0080264400.1	24.61847799	0.16759398	0.06107952	2.386668	0.01695799	0.02985675	gene	0.17085994	0.02393578	GO:0006508,GO:0004197	GSZ79140.1	AMAC4,MC4	metacaspase 4	NA
Sapur.0161611300.1	1.29708706	0.57908676	0.24297338	2.386842	0.01699785	0.02991483	gene	0.15760373	0.08676216	GO:0006468,GO:0005524,GO:0004672	GSZ79530.1	CRK3	cysteine-rich RLK (RECEPTOR-like protein kinase) 3	cysteine-rich receptor-like kinase
Sapur.0010681200.1	15.44232105	0.41586826	0.17502118	2.386665	0.01700218	0.02991664	gene	-0.17884504	0.02505892	GO:0005881,GO:0016021	GSZ26060.4		Major facilitator superfamily protein with SPC (SHS1/Pnb1/APE1) domain-containing protein	DPX domain membrane protein
Sapur.0042683000.1	3.32560003	0.66019917	0.27610194	2.385884	0.01703816	0.02415279	gene	0.19329665	0.01673471	GO:0006468,GO:0005524,GO:0004672	GSZ82820.1		Protein kinase superfamily protein	NA
Sapur.0062807000.1	0.42564394	-0.60308765	0.28613313	-2.38389	0.01710886	0.02491603	gene	-0.25249404	0.05456899		GSZ44640.1			nuclear fragile X mental retardation-interacting protein
Sapur.0080264400.1	29.72654166	-0.41417292	0.17261969	-2.3808	0.01713475	0.02486074	gene	-0.19356938	0.01513526		GSZ18670.1		Ankyrin repeat family protein	Copia-like polyprotein/retrotransposon
Sapur.0061153800.1	1612.331093	0.15603587	0.05895481	2.381513	0.01747243	0.02802846	gene	0.17232793	0.03215587		GSZ70370.1	PG2	polygalacturonase 2	polygalacturonase non-catalytic protein
Sapur.0161920200.1	18.14204047	0.19581823	0.07798583	2.38332	0.01757296	0.02410591	gene	0.21387631	0.0075249	GO:0006355	GSZ03120.1	SHL1	SHI2-like 1	paired amphipathic helix protein SIN1
Sapur.0030197000.2	12.53914806	0.21888722	0.09188545	2.382303	0.01730474	0.02481861	gene	0.08519234	0.28873858	GO:0005515	GSZ61090.1		UBX domain-containing protein	Fas-associated factor-like protein
Sapur.0140260400.1	5.56864981	0.32189604	0.13508492	2.382142	0.01731	0.02487737	gene	0.21217827	0.00765128	GO:0005515	GSZ48600.1	BSK3	BR-signaling kinase 3	receptor kinase, putative
Sapur.0010167700.1	61.91228816	-0.65798497	0.2809798	-2.38063	0.01728376	0.02488924	gene	0.17511558	0.02131385					NA
Sapur.0130102100.1	14.93021512	0.18478296	0.07761073	2.380227	0.01729819	0.02511739	gene	0.18116744	0.01632575	GO:0048359,GO:0016020	GSZ27700.1		Syntaxin/t-SNARE family protein	syntaxin 6, amino-terminal protein
Sapur.0092027700.2	0.6928418	1.01009917	0.42441772	2.379771	0.01723405	0.02545964	gene	0.19172674	0.01610723		GSZ02390.1		Protein of unknown function (DUF241)	Transducin/WD40 repeat-like superfamily protein
Sapur.0080282100.1	12.37796229	-0.60108224	0.25485627	-2.37864	0.01738509	0.02565126	gene	-0.19719664	0.01332657		GSZ79180.1		Transducin/WD40 repeat-like superfamily protein	E-phosphoglucosamine dehydrogenase family protein
Sapur.0010278800.1	143.6215275	0.12346394	0.05191814	2.378605	0.01740542	0.02565687	gene	0.18190018	0.02295529	GO:0055114,GO:0051287,GO:0046168,

Sapur.01G025200.1	5.739783396	-3.331456733	0.142626948	-2.32457	0.020695187	0.028310965	grey	-0.158998437	0.047405341					NA
Sapur.01G045400.1	2.012873446	-0.422850078	0.181912729	-2.32447	0.020100495	0.028317237	grey	-0.141438858	0.077235664	GO:0006468,GO:0006472	ATSG35980.1	YAK1	yeast YAK1-related gene 1	Serine/Threonine kinase domain protein
Sapur.05G121200.1	1.00247832	0.623667731	0.268075327	-2.32739	0.020139	0.028466612	grey	-0.132319267	0.023379869		ATSG27380.2			hypothetical protein
Sapur.01G062700.1	11.81010291	-0.227312461	0.097865831	-2.32369	0.020195562	0.028488743	grey	-0.205727045	0.009741744	GO:0045454,GO:0015035,GO:0009055	ATSG06470.1		Glutaredoxin family protein	NA
Sapur.03G130200.1	8.914414464	-0.658330806	0.283425837	-2.32353	0.0203043	0.028495881	grey	-0.219018371	0.055853008	GO:0071805,GO:0016020,GO:0015079	ATKT1,ATKT1P,ATKUP1,KT1	ATKT1	potassium transporter 1	potassium transporter
Sapur.7094S00.1	0.304204538	0.820406193	0.353305607	-2.32087	0.020282277	0.028492398	grey	-0.183485188	0.021432754					NA
Sapur.01G124800.1	4.546891554	0.345102799	0.148625889	-2.32363	0.020234934	0.028505563	grey	-0.158239132	0.047737742		ATSG78433.1		VQ motif-containing protein	AvrRPC9-9 rapidly elicited protein, putative
Sapur.05G145800.6	0.717666452	-0.719739202	0.310067293	-2.32124	0.020278128	0.028545455	grey	-0.136743598	0.087686106	GO:0008152,GO:0003824	ATGA07240.2	CERS1,ACS1	AMP-dependent synthetase and ligase family protein	long-chain-fatty-acid-CoA ligase
Sapur.01G085700.2	0.524092278	0.823863551	0.354943563	-2.321055	0.020283873	0.028567559	grey	-0.107730125	0.010303307	GO:0055114,GO:0016616,GO:0051287,GO:0000287	ATSG03290.1	IDH-V	Isocitrate dehydrogenase V	Isocitrate dehydrogenase (NAD+)
Sapur.01G052200.1	315.8508882	-0.103874849	0.044069231	-2.321001	0.020286766	0.028569972	grey	-0.11970261	0.013186104	GO:0005515	ATMG01360.1		RNA ligase/cyclic nucleotide phosphodiesterase family protein	cyclic phosphodiesterase
Sapur.03G158300.1	12.36738332	-0.428261156	0.185658133	-2.32047	0.020155599	0.028608087	grey	-0.18215882	0.022266388		ATSG19180.1			transmembrane protein, putative
Sapur.05G154600.1	891.4714113	-0.07850216	0.034754059	-2.32028	0.020202293	0.028613477	grey	-0.444239021	1.56E-08		ATG27770.1	FBL6I	gigantea protein (GI)	gigantea protein, putative
Sapur.01G028700.1	16.95026674	-0.421144131	0.181530872	-2.32009	0.020336197	0.028634653	grey	-0.176575647	0.026951711		ATSG68620.1		alpha/beta-Hydrolases superfamily protein	CXE carboxylesterase
Sapur.01G082200.1	147.6186645	-0.071084147	0.031456819	-2.31854	0.020839108	0.028723145	grey	-0.219039348	0.032315645	GO:0055114,GO:0016616,GO:0019752	ATSG47520.1	MDH	malate dehydrogenase	NAD-malate dehydrogenase
Sapur.01G028800.1	5.175552747	-0.525268797	0.2265159	-2.31851	0.020400029	0.028721476	grey	-0.215234445	0.006760421		ATSG07950.1			stellacyanin, putative
Sapur.01G058800.1	110.8273094	-0.08361892	0.036277509	-2.31846	0.020461346	0.028729239	grey	-0.18163331	0.020524548	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATSG08830.1	AtPSKR2,PSKR2	phytosulfokine-alpha receptor 2	phytosulfokine receptor, putative
Sapur.07G024000.1	21.32862496	-0.254874839	0.109934562	-2.318447	0.020425062	0.028752437	grey	-0.481847569	1.67E-10		ATSG13040.2		myb-like HTH transcriptional regulator family protein	transcription factor, putative
Sapur.09G069900.1	2.709042716	0.542935127	0.234214716	2.318109	0.020443424	0.02877766	grey	-0.15209672	0.020234216				S-locus lectin protein kinase family protein	hypothetical protein
Sapur.01G238400.1	-0.994681373	0.736388409	0.318004323	-2.31783	0.020587314	0.028797357	grey	-0.183273827	0.021058308	GO:0008544	ATSG27290.1		5-lipoxa lectin protein kinase family protein	NA
Sapur.01G118900.2	8.770509014	-0.223463463	0.096412402	-2.31779	0.020460871	0.028799168	grey	-0.154201661	0.05382428		ATSG64470.3	TBL12	Plant protein of unknown function (DUF828)	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.01G088100.1	12.80503287	-0.11184	0.048484	-2.31767	0.020484384	0.028816178	grey	-0.197182626	0.01331864		ATSG72120.1		Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.01G028200.1	84.3179456	-0.17385181	0.07762194	-2.31702	0.020502486	0.028855287	grey	-0.174251676	0.029057663		ATSG27670.1	HSP21	heat shock protein 21	NA
Sapur.7151S00.1	0.9891777	0.587387904	0.253715775	2.316826	0.020622471	0.029021684	grey	-0.213627187	0.037127813	GO:0016757,GO:0047262	ATSG02150.1	GALT9	galactosyltransferase family 9	NA
Sapur.07G075500.1	1056.214829	0.087740549	0.03792412	2.315582	0.020690581	0.029115187	grey	-0.142383361	0.075260309	GO:0006351,GO:0003899	ATSG09020.1	ATRPB1G,RNRPB4,RPB1,S	RNA polymerase II, RpB4, core protein	DNA-directed RNA polymerase II, putative
Sapur.7060S00.1	465.9215104	0.071084147	0.031102369	2.315125	0.020839219	0.029175258	grey	-0.176176065	0.024746446		ATSG19260.1		zinc finger (CCCH type) family protein / RNA recognition motif (RRM)-containing protein	RNA recognition motif (RRM) superfamily protein
Sapur.01G109600.1	57.23093667	0.302934388	0.130948715	2.313381	0.020703586	0.029228204	grey	-0.174258419	0.029365955		ATSG47890.1	ARLR7,RLP7	receptor like protein 7	NA
Sapur.01G082800.1	188.1771215	-0.234651348	0.101492569	-2.31186	0.020785457	0.029265585	grey	-0.18820962	0.019675449	GO:0016747	ATSG48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	NA
Sapur.01G005200.2	9.610005319	-0.093608504	0.041588554	-2.310238	0.020922616	0.029329506	grey	-0.163783672	0.040397006	GO:0007094	ATSG07030.1		mitotic checkpoint protein	mitotic spindle assembly checkpoint protein, putative
Sapur.01G055000.3	34.06023619	0.16602757	0.073332547	2.309037	0.020945123	0.029460652	grey	0.18936765	0.025513887	GO:0017069,GO:0000398	ATSG76940.1		RNA-binding (RRM/RBD/RNP motifs) family protein	hypothetical protein
Sapur.01G054100.1	57.52627481	0.182024015	0.080377599	2.307611	0.021004569	0.029547384	grey	-0.200609545	0.011848292	GO:0015124,GO:0006386,GO:0003676,GO:0000723	ATSG17320.1		PHD finger	NA
Sapur.7185S00.1	0.328554444	0.859769881	0.372647135	2.307172	0.021046242	0.029604046	grey	0.2103965	0.008173322		ATSG26880.1		Helicase/SNF2-associated, DNA binding protein	NA
Sapur.07G048000.1	8.73456798	-0.209069768	0.090550424	-2.30754	0.021264794	0.029804897	grey	-0.203073682	0.010510552		ATSG48185.1		FRIGIDA-like protein	frigida-like protein
Sapur.05W019300.1	109.6771152	-0.177329632	0.076861282	-2.30699	0.021505459	0.029615899	grey	-0.18803965	0.017855674		ATSG48845.1			cysteine-rich TM module stress tolerance protein
Sapur.01G028600.1	0.47839001	0.801195457	0.34903168	2.30683	0.021511	0.029618744	grey	-0.164873984	0.034452661	GO:0048871,GO:0000160	ATSG04180.1	AHP5	histidine-containing phosphotransfer factor 5	histidine phosphotransfer protein
Sapur.07G012900.1	696.1105885	0.055930267	0.024264527	2.306818	0.021620865	0.029624558	grey	-0.152030865	0.05721514	GO:0008236,GO:0006508	ATSG36195.1		Serine carboxypeptidase S28 family protein	serine carboxypeptidase S28
Sapur.01G000300.1	12.9453211	-0.054268864	0.023675888	2.306588	0.021694302	0.029634968	grey	-0.132916159	0.033101887					NA
Sapur.03G155900.1	749.0419389	-0.077625988	0.033657924	-2.30632	0.021692667	0.029663189	grey	-0.178267212	0.025499141		ATSG80890.3	UBP24	ubiquitin-specific protease 24	ubiquitin carboxyl-terminal hydrolase
Sapur.01G045100.1	3.281587113	0.330667789	0.143383447	2.306178	0.021930673	0.029673188	grey	-0.18906291	0.017716462	GO:0016021	ATSG19645.1		TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	plant/YDR623-12 protein
Sapur.07G044000.2	1.181474175	-0.125395762	0.054128859	-2.30577	0.021688	0.029706229	grey	-0.173938218	0.033109356	GO:0043565,GO:0006355,GO:0003700	ATWRKY7,WRKY7	ATWRKY7,WRKY7	WRKY DNA-binding protein 7	WRKY transcription factor
Sapur.01G117000.5	0.90122461	-0.675363187	0.294989664	-2.30385	0.021921296	0.0298518	grey	-0.158946136	0.045462842		ATSG25310.1		alpha/beta-hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.03G080200.1	22.12007577	-0.045693525	0.247285674	-2.30258	0.021934319	0.029905554	grey	-0.157613145	0.048675021	GO:0055114,GO:0006146,GO:0050663,GO:0006298	ATSG18670.1		6-phosphogluconate dehydrogenase family protein	decarboxylating 6-phosphogluconate dehydrogenase
Sapur.05G025700.2	6.648052519	0.378836466	0.164531372	2.302288	0.021921746	0.029976373	grey	-0.07667625	0.379090531		ATSG17680.1		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.05G139900.1	0.86888878	0.921245615	0.401294373	2.301225	0.022076171	0.029976371	grey	-0.174161994	0.028810888					NA
Sapur.7034S00.1	24.80369207	0.201078962	0.087386966	2.301479	0.021945191	0.030034109	grey	-0.21634528	0.006494635					NA
Sapur.04G074600.1	10.77053169	0.402067208	0.175119781	2.300475	0.021656466	0.030090545	grey	-0.214246461	0.005011078					NA
Sapur.15W026910.1	2.342304219	-0.415762332	0.180753511	-2.30005	0.021445135	0.030143796	grey	-0.180594377	0.023610923					NA
Sapur.01G028900.1	269.6288178	0.110309379	0.051831203	2.299954	0.021458829	0.030250315	grey	0.132654541	0.097689928		ATSG65320.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR protein
Sapur.7150S00.1	1.346060868	0.468976862	0.172560479	-2.29988	0.021649319	0.030354862	grey	-0.18738974	0.012151194	GO:0006468,GO:0005524,GO:0004672	ATSG05860.1		Protein kinase superfamily protein	NA
Sapur.04G046500.1	3.074552642	-0.407767414	0.177303828	-2.29862	0.021458253	0.030358807	grey	-0.19275129	0.014011237	GO:0006468,GO:0005524,GO:0004672	ATSG48480.1	RKL1	receptor-like kinase 1	receptor kinase
Sapur.01G036900.2	0.291547614	-1.125395762	0.489036569	-2.29593	0.021664	0.030416635	grey	-0.258817375	0.000601613	GO:0005515	ATSG56160.1		RING/U-box superfamily protein	NA
Sapur.09G181300.1	0.39016768	-0.168257757	0.073358737	-2.29948	0.021477642	0.03018252	grey	-0.105306206	0.189326828	GO:0016020	ATSG21920.1	ATYLMG2,YLMG2	YGGT family protein	YGGT family protein
Sapur.01G096200.1	15.91439999	-0.098267212	0.042813586	-2.2962	0.021535139	0.030283027	grey	-0.205456532	0.008829745	GO:0005789,GO:0005886	ATSG05170.1		Plant VAMP domain protein, conserved membrane protein) family protein	vesicle-associated membrane protein associated protein, putative
Sapur.09G087000.2	0.301611781	1.077718258	0.468957759	2.288114	0.021553118	0.030289357	grey	-0.279338452	0.000395715	GO:0006468,GO:0006672	ATSG60550.1	ATSNAK1,GRIK2	germinivirus rep interacting kinase 2	calcium/calmodulin-dependent kinase kinase
Sapur.05G205400.1	57.20179915	0.503881552	0.219557571	2.286027	0.021769417	0.030301635	grey	-0.171498612	0.031751684	GO:0055114,GO:0005515,GO:0006488,GO:0005524,GO:0004672	ATG88932.1		Leucine-rich repeat receptor-like protein kinase family protein	receptor kinase, putative
Sapur.03G116900.1	158.8257576	0.079708877	0.034699656	2.2943	0.021546645	0.030316688	grey	0.15936311	0.04621722		ATSG70570.1		RNA-like superfamily protein	F-box plant protein
Sapur.05G021900.1	2.46423813	-0.467340584	0.2034175	-2.29405	0.021693372	0.030389941	grey	-0.138838525	0.107802012		ATSG16447.1			hypothetical protein
Sapur.01G214100.4	4.491857655	-0.277772931	0.120905958	-2.29743	0.021594273	0.030389941	grey	-0.007746067	0.932295187					hypothetical protein
Sapur.09G225700.1	23.91485877	0.366356435	0.159475021	2.297302	0.021601546	0.030479884	grey	0.18228257	0.022423855					NA
Sapur.01G062800.1	1.604700166	-0.468014495	0.195431362	2.297245	0.021609778	0.030515112	grey	0.18966095	0.017202702	GO:0016758,GO:0008152	ATSG22590.1		UDP-Glycosyltransferase superfamily protein	UDP-glycosyltransferase family protein
Sapur.08G084900.1	1.091749891	0.57188824	0.248959543	2.266352	0.02165575	0.030421435	grey	-0.18227259	0.019508811		ATSG17000.1	UBC32	ubiquitin-conjugating enzyme 32	ubiquitin-conjugating enzyme E2
Sapur.05G124000.1	4.621458182	0.259127016	0.114264992	2.26068143	0.022082496	0.030455512	grey	0.179325	0.024117133	GO:0006468,GO:0005524,GO:0004672	ATSG39110.1		Malectin/receptor like protein kinase family protein	NA
Sapur.01G124500.1	6.076262686	0.259232309	0.112915302	2.259732	0.021691191	0.030468624	grey	0.153201906	0.037345301					hypothetical protein
Sapur.05G026100.1	17.40723234	0.188413106	0.082539661	2.282061	0.021737893	0.030514	grey	0.004969991	0.9814042		ATSG38620.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.01G058700.1	2528.176278	-0.219267655	0.095614897	-2.29488	0.021734257	0.030529941	grey	-0.221136055	0.005382104		ATSG24420.1		alpha/beta-Hydrolases superfamily protein	sigma factor sigb regulation protein rsbq protein, putative
Sapur.05G175400.3	16.29605849	0.070376205	0.031288329	2.084176988	-2.29329	0.021738124	0.030720884	0.164608208	0.072276501		ATSG07220.1		dentin sialophosphoprotein-related	hypothetical protein
Sapur.09G061100.1	24.79812661	-0.191367205	0.083415104	-2.29388	0.021795686	0.030601997	grey	-0.181152637	0.021071122		ATSG64480.1			hypothetical protein
Sapur.04G156600.1	1.111606457	-0.195353528	0.2356817	-2.2938	0.021783783	0.030613576	grey	-0.40021712	1.07E-07		ATSG07750.1		21-10/-exoribonuclease family protein	exosome complex exonuclease RRP42
Sapur.03G043200.1	0.66951979	0.826612652	0.360395286	2.293628	0.021811886	0.030257566	grey	-0.153512518	0.055015544					NA
Sapur.05G203000.1	767.5645599	0.08711348	0.037980776	-2.29382	0.021812216	0.030257566	grey	-0.179361688	0.024591914	GO:0016567,GO:0008842	ATSG76390.2		ARM repeat superfamily protein	ubiquitin-protein ligase, PUB43
Sapur.05G085005.1	2.681235014	-0.202421495	0.179404909	-2.29337	0.021835723	0.030445736	grey	-0.035675852	0.637341749		ATSG66341.1		zinc finger (C2H2 type) family protein	C2H2-type zinc-finger protein
Sapur.01G054400.1	4.337210758	-0.38448173	0.167649562	-2.29337	0.021836968	0.030463736	grey	-0.138724051	0.081148093	GO:0007165,GO:0005515	ATSG44630.3		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.7116T00.1	4.918839462	0.503881552	0.219557571	2.290577	0.021918913	0.030461457	grey	0.212607513	0.037670867					NA
Sapur.01G020500.2	9.613573887	-0.232354465	0.101324228	-2.29318	0.021837774	0.030563205	grey	0.07864835	0.32814697		ATSG36115.1		Pyridoxal-5'/-phosphate-dependent enzyme family protein	tryptophan synthase alpha subunit, putative
Sapur.05G020200.1	1038.616284	0.101010805	0.112638751	2.292264	0.021928207	0.030729754	grey	0.19413137	0.016851144	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	ATSG28160.1		MATE efflux family protein	MATE efflux family protein
Sapur.04G165900.1	429.0224812	-0.822462645	0.358736569	-2.29179	0.021931831	0.030763468	grey	-0.348670611	7.73E-06					NA
Sapur.01G052700.1	0.418616636	0.845266616	0.368704658	2.291549	0.021933186	0.030769958	grey	-0.420803134	1.52E-07		ATSG36630.1			hypothetical protein
Sapur.05G152300.4	66.69674515	-0.151229542	0.065909419	-2.29159	0.021939591	0.030777782	grey	-0.173622961	0.030623441	GO:0030256,GO:0016758,GO:000975,GO:0008152	ATG14320.2	TT11,LG-GT80B1	UDP-Glycosyltransferase superfamily protein	UDP-glycosyltransferase family protein
Sapur.08G054600.1	19.10364683	0.49902051	0.217768169	2.291542	0.021932088	0.030792635	grey	-0.228008806	0.003988488	GO:0001101	ATSG25180.1	ARR12,ARR12	response regulator 12	NA
Sapur.01G078300.1	41.3826611	-0.240569755	0.104987702	-2.29141	0.021939798	0.030797767	grey	-0.202103946	0.016194375	GO:0005525	ATSG07010.1		Translation initiation factor 2, small GTP-binding protein	translation initiation factor IF-2
Sapur.03G061500.2	0.70484195	0.685456604	0.299124269	2.291352	0.021940089	0.030791078	grey	0.16885857	0.034695602	GO:0016020	ATSG27280.1		Transmembrane proteins 14C	transmembrane protein 14C
Sapur.7189S00.1	0.923413524	0.424585948	0.2736268	2.291728	0.021928728	0.030796142	grey	-0.225255663	0.005819028	GO:0008270,GO:0003676	ATSG35620.1		zinc knuckle (CCHC-type) family protein	NA
Sapur.01G062100.1	162.1925324	-0.091510252	0.039949524	-2.29065	0.021938844	0.030844342	grey	-0.181665305	0.022935068	GO:0005515	ATSG30000.1	CDC27b,HBT	CDC27 family protein	cell division cycle protein-like protein B
Sapur.01G088000.1	120.3512924	-0.273819762	0.119561113	-2.29053	0.021945138	0.030894419	grey	-0.188062212	0.015015307		ATSG61060.1		Root hair defective 3 GTP-binding protein (RHD3)	ROOT HAIR defective-like protein
Sapur.01G078800.2	14.74490551	-0.29915959	0.130658897	-2.28966	0.022041159	0.030921133	grey	-0.206457548	0.009845053	GO:0005515	ATSG10840.1		Tetratricopeptide repeat (TPR)-like superfamily protein	kinesin light chain, putative
Sapur.01G025800.1	764.5089217	-0.003307949	0.004881837	-2.28964	0.022045119	0.030861292	grey	-0.191780645	0.010120309	GO:0055114,GO:0016491,GO:0016628	HMGL,HMGR1	HMGL,HMGR1	hydroxy methylglutaryl-coenzyme A reductase 1	3-hydroxy-3-methylglutaryl coenzyme A reductase, hydroxymethylglutaryl-CoA reductase
Sapur.05G192100.4	3.8935612	0.304245573	0.132952939	-2.28836	0.022131636	0.031055253	grey	0.01076531	0.893511678	GO:0006351,GO:0003677	ATSG30820.2	ANAC014,NAC014	NAC 014	NAC transcription factor
Sapur.05G026900.1	18.12558729	-0.251629553	0.110000267	-2.28829	0.022139124	0.031059667	grey	0.167497573	0.024803522	GO:0004518,GO:0030410	ATNAG3,NAG3	ATNAG3,NAG3	nicotinamine synthase 3	nicotinamine synthase
Sapur.03G036600.1	135.6270726	-0.102405364	0.044770168	-2.28786	0.022178986	0.031104605	grey	-0.178832128	0.026595279		ATSG16200.1			transmembrane protein, putative
Sapur.04G064800.1	1.202814797	0.610153661	0.266765352	-2.28723	0.022182418	0.031131711	grey	-0.173452025	0.029832923					hypothetical protein
Sapur.06G175450.1	107.0472307	-0.108937398	0.047606478	-2.28705	0.022195143	0.031159359	grey	-0.167863724	0.035015134		ATSG28330.1			hypothetical protein
Sapur.06G133200.1	21.62648711	-0.198666588	0.124198888	-2.28666	0.022215458	0.031156089	grey	-0.317810446	4.96E-05		ATSG68810.1		Zinc finger C-x8-C-x5-C-x3-H type family protein	hypothetical protein
Sapur.01G000500.1	1080.058849	0.075319386	0.033029731	2.286406	0.022235	0.031175814	grey	0.17387209	0.03180806		ATSG75810.1			transmembrane protein, putative
Sapur.01G060600.1	209.1554899	-0.132505091	0.058845573	-2.28547	0.022285397	0.0312502	grey	-0.195960878	0.013909347	GO:0016746,GO:0008152	ATGQ04010.1	AtGPAT8,GPAT8	glycerol-3-phosphate acyltransferase 8	glycerol-3-phosphate acyltransferase
Sapur.05G052500.1	28.90884701	-0.204076218	0.089523184	-2.28456	0.022338206	0.031364991	grey	-0.18873206	0.016031523		ATG11000.1	ATNAM3,NAK10	NAM/ATAF/CUC family protein	NAM10 subunit, NAC M14(alpha)-terminal acetyltransferase
Sapur.01G095100.4	3.522105233	-0.315176997	0.138026177	-2.28366	0.022403296	0.031431004	grey	-0.18450516	0.020651368	GO:0005515,GO:0016020	ATG12340.1		Cornichon family protein	cornichon protein
Sapur.01G000300.1	5.946208484	-0.223463463	0.097876376	-2.28266	0.022450457	0.031470321	grey	-0.142724608	0.074568898	GO:0016491,GO:0046872	ATSG04240.1	SNC4	suppressor of rps5-2 protein 4	NADH:ubiquinone oxidoreductase-like 1
Sapur.02G030300.1	5.408730741	0.770899669	0.337733589	2.282633	0.022451985	0.031471229	grey	-0.124041208	0.125675505	GO:0005515,GO:0003700	ATSG32230.1		Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor, putative
Sapur.07G030800.1	9.553353	0.74085377	0.324863277	2.281333	0.022461764	0.031496828	grey	0.176214668	0.023327783					NA
Sapur.02G018000.2	1.797749676	0.530726247	0.232584009	2.281912	0.022449535	0.031527771	grey	0.159865345	0.04552223		ATSG28305.1	ATLOG1,LOG1	Putative lysine decarboxylase family protein	cytokinin riboside 5'-monophosphate phosphoribohydrolase
Sapur.01G025500.1	0.530481027	-0.932865329	0.408805862	-2.28188	0.022466217	0.031531795	grey	-0.163373456	0.044811251	GO:0003677,GO:0046983	ATSG14920.1	GAI,RGA2	GRAS family transcription factor family protein	GRAS family transcription factor
Sapur.15W026480.2	8.7607203	-0.234565813	0.102849915	-2.28144	0.022522	0.031550927	grey	-0.056455726	0.551239453		ATG02080.1		2-oxoglutar ate (2OG) and Fe(II)-dependent oxygenase superfamily protein	transcription factor, putative
Sapur.01G239600.1	1673.3634	-0.090209188	0.039475329	-2.28075	0.022563324	0.03525318	grey	-0.178345335	0.027156672	GO:0005515,GO:0005524,GO:0003676	ATSG14630.2		DEAD box ATP-dependent RNA helicase	DEAD-box ATP-dependent RNA helicase
Sapur.09G089700.1	344.6659378	0.082522797	0.036276481	2.280424	0.022582287	0.031650822	grey	-0.188326556	0.019178558	GO:0046983	ATSG69010.1	BIM2	BES-interacting basic helix-loop-helix protein 2	transcription factor BIM2
Sapur.08G016100.2	28.8517982	0.188003349	0.081610004	2.279173	0.022616761	0.031754532	grey	0.200650674	0.011744419		ATSG55070.2		Lion1/CRR/RING-U-box domain-containing protein	macrophage erythroblast attacher
Sapur.01G264400.1	61.74454114	0.221663523	0.097403848	2.278661	0.022669029	0.031790854	grey	0.262546208	0.008194146		ATSG73900.1			transmembrane protein, putative
Sapur.04G115900.1	13.13515274	-0.219260993	0.096451858	-2.27845	0.022693678	0.031810904	grey	-0.172319326	0.014875842	GO:0003676	ATSG25680.1		RNA-binding (RRM/RBD/RNP motifs) family protein	nucleolar phosphoprotein, putative
Sapur.09G075500.2	0.85126208	-0.664857364	0.3818356	-2.27792	0.022704	0.031853845	grey	0.103308832	0.187677777	GO:0008152,GO:0022857,GO:0016021	ATSG17530.1	ZIFL1	zinc induced facilitator-like 1	carbohydrate transporter/sugar porter/transporter
Sapur.05G029200.1	27.67628828	0.254057099	0.111545133	2.277617	0.022749402	0.031877885	grey	0.163170241	0.041162964	GO:0004648,GO:0004672	ATSG58320.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.08G143300.1	2.776364386	-0.485485591	0.213209465	-2.27704	0.022790896	0.031927815	grey	-0.127205513	0.735195381	GO:0051603,GO:0008233,GO:0004298	ATSG36340.1		N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	proteasome subunit beta type-5 protein
Sapur.01G052400.1	0.425342994	0.985852758	0.433135281	-2.27609	0.022804917	0.031000698	grey	-0.476404602	2.78E-10	GO:0006883,GO:0003677,GO:0006355,GO:0005634,GO:0003700	ATG18960.1	AG	K-box region and MADS-box transcription factor family protein	MADS-box transcription factor
Sapur.04G164000.1	3.764875271	0.76088329	0.3349247	-2.27568	0.022840485	0.032018	grey	0.169197302	0.025002	GO:0005886,MYB86,MYB26,MYBCP/	ATG42470.2	AtMYB86,MYB86,MYBCP/	myb-like HTH DNA-binding family protein	MYB transcription factor
Sapur.05G011600.1	1.78419688	-0.195255884	0.147137002	-2.27554	0.022873575	0.032043738	grey	-0.192661874	0.015443579	GO:0031369,GO:0043603,GO:0005852,GO:0003743	ATSG56150.1	ATEIF1-A,ATTIF3C1,EIF3C	eukaryotic translation initiation factor 3C	eukaryotic translation initiation factor 3 subunit C
Sapur.01G000900.1	290.1274846	0.160899523	0.070714522	2.275355	0.022884227	0.032067863	grey	0.160851145	0.045072183	GO:0055114,GO:0016620,GO:0008152	ATSG62520.1	ALDH3H1	aldehyde dehydrogenase family 3	aldehyde dehydrogenase
Sapur.03G082000.1	5.517543803	-0.314358741	0.138202984	-2.27462	0.022928965	0.032118614	grey	-0.153205868	0.052262906	GO:0016020	ATSG29840.1		Sodium Bile acid symporter family	bile acid sodium symporter family protein
Sapur.01G027200.1	1.064663717	-0.182021482	0.080133197	-2.27449	0.022934	0.032132823	grey	-0.217820207	0.005133651	GO:0005975,GO:0004553	ATCHIA,CHIA	ATCHIA,CHIA	chitinase A	class III acidic chitinase
Sapur.05G005300.1	0.366160262	0.906896162	0.398789137	2.274125	0.022958498	0.032155898	grey	0.144473537	0.070353113	GO:0048046,GO:0016762,GO:0006073,GO:0005975,GO:0006553	ATX2G30.1	ATX2G,XTH6	xyloglucan endotransglycosylase 6	xyloglucan endotransglycosylase
Sapur.03G077100.1	0.263698016	0.81681762	0.3855487	2.271116	0.023021	0.032395668	grey	0.263698016	0.003462578		ATSG29500.1		ATP6/PDE domain superfamily protein	NA
Sapur.01G039800.9	0.46445288	0.939574116	0.41554568	-2.272	0.023086385	0.032322279	grey	-0.269742017	0.000365548	GO:0016787	ATSG10510.1	ATPAP16,PAP16	purple acid phosphatase 16	NA
Sapur.01G046300.1	183.9055625	0.455804127	0.200658545	2.271541	0.023142143	0.032409023	grey	0.19880788	0.012531066					NA
Sapur.03G111100.1	120.4770821	0.202574496	0.09092407	2.27114	0.023138152	0.032405564	grey	0.1585545	0.050973386					NA
Sapur.09G191300.1	1.573389292	0.531444895	0.234080793	2.270348	0.023186468	0.032483319	grey	0.13337321	0.095861279		ATSG33500.1	SRO2	similar to RCD one 2	inactive poly [ADP-ribose] polymerase SRO3, putative
Sapur.01G029200.1	2.031425489	0.275682254	0.121488257	2.270126	0.023196847	0.032481479	grey	0.10357676	7.33E-05	GO:0043531	ATG27170.2		transmembrane protein,ATP binding	NA
Sapur.01G092600.1	220.9979061	0.445431116	0.196239884	2.269991	0.023180	0.032500178	grey	0.23167508	0.003492625	GO:0006413,GO:0003743	ATSG71910.1		eukaryotic translation initiation factor 5G1L family protein	eukaryotic translation initiation factor 5G1L
Sapur.01G046900.1	0.323469041	0.118142403	0.054669163	2.269079	0.023202207	0.032511184	grey	0.208896276	0.000242203	GO:0007017	ATSG26170.1	NGA4	AP2/B3-

Sapur.008G000700.3	19.5816337	2.361547466	0.117905565	2.218279	0.0265358	0.036597	grey	0.189794396	0.01725537	ATSG23180.1	Plant protein of unknown function (DUF639)
Sapur.009G049900.1	100.6614601	6.165265172	0.074505898	2.218149	0.02654685	0.036970519	grey	0.215292888	0.00674099	GO:0006396;GO:0003723;GO:0003676	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D11/G-patch domain-containing protein
Sapur.T113300.1	1.896839971	-0.460478815	0.207239487	2.216682	0.02664599	0.037141867	grey	-1.124881817	0.019875025	PLA72 transcription factor family	PLA72 transcription factor family protein
Sapur.013G026400.1	740.4113366	10.10308621	0.045715272	2.216078	0.02684614	0.037364402	grey	0.175939072	0.027516155	GO:0006071;GO:0004371	Dihydroxyacetone kinase
Sapur.006G068300.1	15.83460213	0.161894337	0.072721212	2.215	0.02672548	0.037317924	grey	-0.132443387	0.008232569	GO:0016787	G2Ad1/2G28 nucleoside diphosphatase family protein
Sapur.15WG074700.1	0.964652147	-0.571561932	0.258116477	-2.21436	0.02680426	0.03725753	grey	-0.143039343	0.073912112		Protein of unknown function (DUF789)
Sapur.010G062700.3	0.568944968	-0.780208663	0.352369426	-2.21418	0.02683668	0.0373985	grey	-0.219873172	0.055363319	GO:0055085;GO:0016021	Major facilitator superfamily protein
Sapur.012G048800.2	1.279845452	0.516894381	0.24255882	2.213852	0.02684365	0.03737316	grey	0.185532025	0.020005159	GO:0055124	DNA2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing pr
Sapur.018G086300.1	20.71973854	0.519022156	0.234613359	2.212245	0.02694974	0.03752057	grey	0.158057107	0.04803377		
Sapur.013G118300.1	0.541055323	0.176224668	0.079611248	2.214149	0.02694798	0.03754141	grey	0.171733821	0.015363619		
Sapur.011G078600.1	2.63077511	-0.419751865	0.189794059	-2.21162	0.02693072	0.03759192	grey	-0.192461166	0.011748586	GO:0016758;GO:0008152	UDP-Glycosyltransferase superfamily protein
Sapur.003G208300.1	0.831837174	-0.184209359	0.3021666	-2.21139	0.02708556	0.03759166	grey	-0.112208955	0.016659168	GO:0008152;GO:0008150	CPC-B2 Cell Wall Protein
Sapur.006G044300.2	3.73565836	-0.362120947	0.16377563	-2.21115	0.02702555	0.03762188	grey	-0.122508735	0.126381742		ESS1-subunit of NADH:ubiquinone oxidoreductase (complex I) protein
Sapur.013G161600.1	9.952547132	-0.278468187	0.126248739	-2.21048	0.02708267	0.03768246	grey	-0.233610789	0.023121294		ankyrin repeat protein
Sapur.019G061100.1	35.69661753	0.169908286	0.076849589	2.210934	0.02704038	0.03768727	grey	0.184859502	0.020721526	GO:0008270;GO:0005515	RING/U-box superfamily protein
Sapur.T015100.1	2.983925514	-0.328325863	0.15	-2.20825	0.02738546	0.03809195	grey	-0.315453338	1.5-230-05		Cell differentiation
Sapur.016G049000.2	0.287084589	0.961579274	0.435139997	2.209816	0.02717966	0.03740534	grey	0.129103842	0.107073884	GO:0005085;GO:0016021;GO:0008324;GO:0006812	Cation efflux family protein
Sapur.016G046400.1	52.50510511	-0.223925	0.101104237	-2.20963	0.02731835	0.03760878	grey	-0.167327608	0.036262481		Chaperone DnaJ-domain superfamily protein
Sapur.004G050500.1	0.238146645	1.250405643	0.630017145	2.209287	0.02731429	0.03774599	grey	0.227327787	0.053747956	GO:0043565;GO:0008270;GO:0003700	BME3;BME3-2;GATA8	Plant-specific GATA/B GATA transcription factor family protein
Sapur.010G169000.1	4.202252329	-0.570466231	0.258196332	-2.20935	0.02715026	0.03776374	grey	-0.184187189	0.020931962		Protein of unknown function (DUF674)
Sapur.009G093900.9	0.154478275	-0.156621484	0.071387396	-2.20915	0.02734875	0.03816791	grey	-0.219030053	0.018183806		lactoylglutathione lyase family protein / glyoxalase I family protein
Sapur.001G109300.1	138.1114478	0.159019658	0.07180252	2.20912	0.02716629	0.03780824	grey	0.146298017	0.027503003		
Sapur.018G085400.1	18.7671205	0.185281615	0.084010192	2.20817	0.02717639	0.03781484	grey	0.192377772	0.017284613		
Sapur.012G098100.1	215.2985644	0.129660372	0.058703342	2.208777	0.02739167	0.03782881	grey	0.185677867	0.010899946	GO:0046983	bHLH005;LIL3	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.003G011300.1	9281.414655	0.566664181	0.257468739	2.208242	0.02731577	0.03786846	grey	0.227545145	0.018845997	GO:0016747	HXXXD-type acyl-transferase family protein
Sapur.007G076700.1	164.5996803	0.132300769	0.059934664	-2.20742	0.02738447	0.03795287	grey	0.333627662	1.96E-05		
Sapur.006G192600.2	3.021627545	-0.383168396	0.17377493	-2.20727	0.02729199	0.03797108	grey	-0.058573013	0.481682003		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.009G168800.2	2.610880976	-0.306374644	0.146168667	-2.20685	0.02731326	0.03805904	grey	-0.166815168	0.036785253	GO:0016773;GO:0016020;GO:0005524	mitogen-activated protein kinase 16	MAP kinase
Sapur.002G056600.1	23.45758876	-0.308002021	0.140023742	-2.20606	0.02738074	0.03808065	grey	-0.171537991	0.01702812		transmembrane protein, putative
Sapur.006G067050.1	0.280312127	0.566392266	0.257134647	2.204869	0.02743407	0.03814875	grey	-0.139826042	0.038188218	GO:0006412;GO:0005840;GO:0005622;GO:0003735	60S ribosomal protein L34, putative
Sapur.002G091500.1	10.79228074	-0.342027736	0.155503751	2.201299	0.02743135	0.03855683	grey	0.163475381	0.040780443	GO:0005085;GO:0022857;GO:0016021	phosphate transporter 1;9	inorganic phosphate transporter
Sapur.013G281300.1	97.78602204	-0.159624844	0.072387396	-2.20515	0.02744773	0.03856791	grey	-0.219030053	0.058183806		regulatory component of ABA receptor 3	abscisic acid receptor PYL8
Sapur.008G169700.1	880.5547097	0.08561033	0.040559727	2.20482	0.02746742	0.03860035	grey	0.217118255	0.006360478		Transducin/WD40 repeat-like superfamily protein	WD40 domain protein, putative
Sapur.009G132200.1	15.99465064	0.084406761	0.074027791	2.20373	0.02749869	0.03878673	grey	0.149869602	0.026736733			transmembrane protein
Sapur.017G047900.1	15.7889663	-0.238478752	0.108239317	-2.20357	0.02754745	0.03819204	grey	-0.153313599	0.055204263			EAP30/Vps36 family protein
Sapur.016G046400.1	7.572561337	-0.138165344	0.131568752	2.203317	0.02754938	0.03824156	grey	-0.101864183	0.066936017	GO:0016758;GO:0008152		UDP-Glycosyltransferase superfamily protein
Sapur.010G135700.1	2.016505838	-0.449590103	0.204575796	-2.20325	0.02750907	0.03836287	grey	-0.274513	0.005052281	GO:0005515;GO:0003755	ENB0135	RING/FYVE/PHD zinc finger superfamily protein	strawberry notch-like protein
Sapur.016G187400.1	1.003315325	0.691039393	0.313718341	2.202708	0.02753247	0.03835717	grey	0.193828208	0.05103683	GO:0016747	HXXXD-type acyl-transferase family protein	anthranilate N-benzoyltransferase, putative
Sapur.010G198500.1	4.746489329	-0.361197274	0.164384615	-2.20383	0.02757002	0.03841123	grey	-0.177308009	0.030164305	GO:0005737;GO:0016020;GO:0006629;GO:0005737	3-oxo-5-alpha-steroid 4-dehydrogenase (protein	3-oxo-5-alpha-steroid 4-dehydrogenase
Sapur.009G156300.1	11.54161316	-0.215827543	0.09688519	-2.20132	0.02771267	0.03828314	grey	-0.173491697	0.031765028	GO:0055114;GO:0016717;GO:0006629	FAD2	fatty acid desaturase 2	delta-12 fatty acid desaturase
Sapur.010G088600.1	4.796714852	-0.252391951	0.16051268	-2.2024	0.02773302	0.03832624	grey	-0.167318396	0.032767774				hypothetical protein
Sapur.005G125800.1	8.493971243	-0.285081532	0.12955662	-2.19976	0.02782864	0.03876353	grey	-0.147682671	0.064920387				NA
Sapur.006G296600.1	268.2848477	-0.135021225	0.058890341	-2.19975	0.02784238	0.03876352	grey	-0.211153241	0.007885215	GO:0003968	RDR6;SDE1;SGS2	RNA-dependent RNA polymerase 6	RNA-dependent RNA polymerase
Sapur.003G127500.1	253.1147834	0.209235185	0.091404341	2.199231	0.02786476	0.03726222	grey	-0.127158336	0.112511206			Protein of unknown function (DUF 3339)	
Sapur.004G042400.1	17527.24134	0.143192288	0.064118819	2.199125	0.02788008	0.03735062	grey	0.144887006	0.027350623	GO:0006396	ATHSP20;HSP70	heat shock protein 70	Non-cell-autonomous heat shock cognate protein
Sapur.019G060500.1	7.52248846	-0.244375968	0.11141061	-2.19879	0.02789298	0.03876648	grey	-0.190224968	0.017139136	GO:0016779	PAP/OAS1 substrate-binding domain superfamily	nucleic acid-binding protein, putative
Sapur.003G298600.1	0.423730312	-0.960824919	0.437041823	-2.19867	0.02791459	0.03879639	grey	-0.236837841	0.003463364				NA
Sapur.T164100.1	0.195250507	-0.738494937	0.5461829	-2.19853	0.02794346	0.03883027	grey	-0.359226609	3.88E-06				NA
Sapur.15WG021000.1	830.2028882	-0.344812517	0.111251293	-2.19684	0.02802667	0.03894687	grey	-0.18843387	0.018107452		NADPH-binding Rossmann-fold superfamily protein		short-chain dehydrogenase reductase
Sapur.005G207700.1	611.9655368	-0.192175104	0.087488223	-2.19683	0.02802923	0.03894142	grey	-0.225152176	0.004758653	ABA2;ATABA2;ATSDR1;GIN1	NADPH-binding Rossmann-fold superfamily protein	short-chain dehydrogenase reductase
Sapur.001G119900.1	1090.715573	0.200063043	0.091125824	2.195759	0.02810202	0.03905749	grey	-0.17609564	0.012603114	GO:0003676	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA-recognition motif 2 in yeast nucleolar protein 4 (Nop4p)-like protein
Sapur.013G099500.1	13.09729675	-0.234287587	0.11930422	-2.19647	0.02814224	0.03912234	grey	-0.160201712	0.016970477	GO:0005525	P-loop containing nucleoside triphosphate hydrolases superfamily protein	AIG1
Sapur.010G093300.1	14.02184423	-0.287229612	0.130887248	-2.19468	0.02820083	0.03918463	grey	-0.275438848	0.00647701		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase-like protein
Sapur.003G085200.1	10.88276669	-0.320004466	0.146148755	-2.19437	0.02822216	0.03920647	grey	-0.158549497	0.047333483	GO:0016392;GO:0006904	Sec1/munc18-like (SM) protein	SNARE-interacting protein KEU, putative
Sapur.T018900.1	0.31807918	1.292475898	0.589103576	2.193971	0.02823726	0.03922785	grey	0.146519276	0.080021185			MSF1-like family protein	
Sapur.003G156400.1	1355.199234	0.053164498	0.024245119	2.19324	0.02830562	0.03928858	grey	0.136425253	0.114615401	GO:0005524	RPT2a	regulatory particle AAA-ATPase 2A	26S proteasome regulatory subunit like protein
Sapur.018G022400.5	1.012577844	0.613300258	0.280337502	2.192007	0.02837909	0.0394072	grey	0.123523877	0.122450023	GO:0004648;GO:0004672		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.001G115700.1	294.4838635	0.059341324	0.048332386	-2.19196	0.02838268	0.03942463	grey	-0.204249515	0.010290954	GO:0016020		Transmembrane proteins 14C	transmembrane protein 14C
Sapur.006G193500.2	5.749842858	0.158185115	0.10208609	2.191638	0.02842728	0.03948326	grey	0.179121663	0.024793343			Cysteine proteinases superfamily protein	cysteine-type peptidase
Sapur.001G139300.1	38.77284646	0.244637583	0.111662924	2.190858	0.02846288	0.03959488	grey	0.16771814	0.015763069			Nucleotide-diphospho-sugar transferases superfamily protein	glycosyltransferase, putative
Sapur.016G188800.1	6.733378036	-0.268224966	0.122463	-2.19082	0.02853161	0.03960047	grey	0.18513953	0.020267453	GO:0004866	Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor KPI-A1
Sapur.016G099300.1	437.1922085	-0.169824919	0.077630075	-2.18956	0.02857132	0.03965524	grey	-0.171129423	0.011394196	GO:0055515;GO:0006488;GO:0005524;GO:0004672	Leucine-rich repeat protein kinase family protein	NA
Sapur.T164100.1	0.195250507	-0.738494937	0.5461829	-2.18953	0.02857349	0.03965524	grey	-0.192237976	0.033760827			senescence-associated gene 101	SAG101
Sapur.15WG021000.1	830.2028882	-0.344812517	0.111251293	-2.19684	0.02802667	0.03894687	grey	-0.18843387	0.018107452		NADPH-binding Rossmann-fold superfamily protein	xyloglucan endotransglucosylase/hydrolase 25	XTH25;XTR3
Sapur.005G207700.1	611.9655368	-0.192175104	0.087488223	-2.19683	0.02802923	0.03894142	grey	-0.225152176	0.004758653	ABA2;ATABA2;ATSDR1;GIN1	NADPH-binding Rossmann-fold superfamily protein	short-chain dehydrogenase reductase	
Sapur.001G119900.1	1090.715573	0.200063043	0.091125824	2.195759	0.02810202	0.03905749	grey	-0.17609564	0.012603114	GO:0003676	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA-recognition motif 2 in yeast nucleolar protein 4 (Nop4p)-like protein	
Sapur.013G099500.1	13.09729675	-0.234287587	0.11930422	-2.19647	0.02814224	0.03912234	grey	-0.160201712	0.016970477	GO:0005525	P-loop containing nucleoside triphosphate hydrolases superfamily protein	AIG1	
Sapur.010G093300.1	14.02184423	-0.287229612	0.130887248	-2.19468	0.02820083	0.03918463	grey	-0.275438848	0.00647701		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase-like protein	
Sapur.003G085200.1	10.88276669	-0.320004466	0.146148755	-2.19437	0.02822216	0.03920647	grey	-0.158549497	0.047333483	GO:0016392;GO:0006904	Sec1/munc18-like (SM) protein	SNARE-interacting protein KEU, putative	
Sapur.T018900.1	0.31807918	1.292475898	0.589103576	2.193971	0.02823726	0.03922785	grey	0.146519276	0.080021185			MSF1-like family protein	
Sapur.003G156400.1	1355.199234	0.053164498	0.024245119	2.19324	0.02830562	0.03928858	grey	0.136425253	0.114615401	GO:0005524	RPT2a	regulatory particle AAA-ATPase 2A	26S proteasome regulatory subunit like protein
Sapur.018G022400.5	1.012577844	0.613300258	0.280337502	2.192007	0.02837909	0.0394072	grey	0.123523877	0.122450023	GO:0004648;GO:0004672		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.001G115700.1	294.4838635	0.059341324	0.048332386	-2.19196	0.02838268	0.03942463	grey	-0.204249515	0.010290954	GO:0016020		Transmembrane proteins 14C	transmembrane protein 14C
Sapur.006G193500.2	5.749842858	0.158185115	0.10208609	2.191638	0.02842728	0.03948326	grey	0.179121663	0.024793343			Cysteine proteinases superfamily protein	cysteine-type peptidase
Sapur.001G139300.1	38.77284646	0.244637583	0.111662924	2.190858	0.02846288	0.03959488	grey	0.16771814	0.015763069			Nucleotide-diphospho-sugar transferases superfamily protein	glycosyltransferase, putative
Sapur.016G188800.1	6.733378036	-0.268224966	0.122463	-2.19082	0.02853161	0.03960047	grey	0.18513953	0.020267453	GO:0004866	Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor KPI-A1	
Sapur.016G099300.1	437.1922085	-0.169824919	0.077630075	-2.18956	0.02857132	0.03965524	grey	-0.171129423	0.011394196	GO:0055515;GO:0006488;GO:0005524;GO:0004672	Leucine-rich repeat protein kinase family protein	NA	
Sapur.T164100.1	0.195250507	-0.738494937	0.5461829	-2.18953	0.02857349	0.03965524	grey	-0.192237976	0.033760827			senescence-associated gene 101	SAG101
Sapur.15WG021000.1	830.2028882	-0.344812517	0.111251293	-2.19684	0.02802667	0.03894687	grey	-0.18843387	0.018107452		NADPH-binding Rossmann-fold superfamily protein	xyloglucan endotransglucosylase/hydrolase 25	XTH25;XTR3
Sapur.005G207700.1	611.9655368	-0.192175104	0.087488223	-2.19683	0.02802923	0.03894142	grey	-0.225152176	0.004758653	ABA2;ATABA2;ATSDR1;GIN1	NADPH-binding Rossmann-fold superfamily protein	short-chain dehydrogenase reductase	
Sapur.001G119900.1	1090.715573	0.200063043	0.091125824	2.195759	0.02810202	0.03905749	grey	-0.17609564	0.012603114	GO:0003676	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA-recognition motif 2 in yeast nucleolar protein 4 (Nop4p)-like protein	
Sapur.013G099500.1	13.09729675	-0.234287587	0.11930422	-2.19647	0.02814224	0.03912234	grey	-0.160201712	0.016970477	GO:0005525	P-loop containing nucleoside triphosphate hydrolases superfamily protein	AIG1	
Sapur.010G093300.1	14.02184423	-0.287229612	0.130887248	-2.19468	0.02820083	0.03918463	grey	-0.275438848	0.00647701		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase-like protein	
Sapur.003G085200.1	10.88276669	-0.320004466	0.146148755	-2.19437	0.02822216	0.03920647	grey	-0.158549497	0.047333483	GO:0016392;GO:0006904	Sec1/munc18-like (SM) protein	SNARE-interacting protein KEU, putative	
Sapur.T018900.1	0.31807918	1.292475898	0.589103576	2.193971	0.02823726	0.03922785	grey	0.146519276	0.080021185			MSF1-like family protein	
Sapur.003G156400.1	1355.199234	0.053164498	0.024245119	2.19324	0.02830562	0.03928858	grey	0.136425253	0.114615401	GO:0005524	RPT2a	regulatory particle AAA-ATPase 2A	26S proteasome regulatory subunit like protein
Sapur.018G022400.5	1.012577844	0.613300258	0.280337502	2.192007	0.02837909	0.0394072	grey	0.123523877	0.122450023	GO:0004648;GO:0004672		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.001G115700.1	294.4838635	0.059341324	0.048332386	-2.19196	0.02838268	0.03942463	grey	-0.204249515	0.010290954	GO:0016020		Transmembrane proteins 14C	transmembrane protein 14C
Sapur.006G193500.2	5.749842858	0.158185115	0.10208609	2.191638	0.02842728	0.03948326	grey	0.179121663	0.024793343			Cysteine proteinases superfamily protein	cysteine-type peptidase
Sapur.001G139300.1	38.77284646	0.244637583	0.111662924	2.190858	0.02846288	0.03959488	grey	0.16771814	0.015763069			Nucleotide-diphospho-sugar transferases superfamily protein	glycosyltransferase, putative
Sapur.016G188800.1	6.733378036	-0.268224966	0.122463	-2.19082	0.02853161	0.03960047	grey	0.18513953	0.020267453	GO:0004866	Kunitz family trypsin and protease inhibitor protein	kunitz-type protease inhibitor KPI-A1	
Sapur.016G099300.1	437.1922085	-0.169824919	0.077630075	-2.18956	0.02857132	0.03965524	grey	-0.171129423	0.011394196	GO:0055515;GO:0006488;GO:0005524;GO:0004672	Leucine-rich repeat protein kinase family protein	NA	
Sapur.T164100.1	0.195250507	-0.738494937	0.5461829	-2.18953	0.02857349	0.03965524	grey	-0.192237976	0.033760827			senescence-associated gene 101	SAG101
Sapur.015G055900.1	2.180283641	-0.718003324	0.328005378	-2.188999	0.02856939	0.03970766	grey	0.148607629	0.002240602	GO:0005975;GO:0004553	XTH25;XTR3	xyloglucan endotransglucosylase/hydrolase 25	
Sapur.008G000700.3	0.831837174	-0.184209359	0.3021666	-2.21139	0.02708556	0.03759166	grey	-0.112208955	0.016659168				NA
Sapur.T113300.1	1.896839971	-0.460478815	0.207239487	2.216682	0.02664599	0.037141867	grey	-0.124881817	0.019875025		PLA72 transcription factor family	PLA72 transcription factor family protein	
Sapur.013G026400.1	740.4113366	10.10308621	0.045715272	2.216078	0.02684614	0.037364402	grey	0.175939072	0.027516155	GO:0006071;GO:0004371		Dihydroxyacetone kinase	2h2c4-dihydroxy-2-butanone kinase, putative
Sapur.006G068300.1	15.83460213	0.161894337	0.072721212	2.215	0.02672548	0.037317924	grey	-0.132443387	0.008232569	GO:0016787		G2Ad1/2G28 nucleoside diphosphatase family protein	nucleoside diphosphatase
Sapur.15WG074700.1	0.964652147	-0.571561932	0.258116477	-2.21436	0.02680426	0.03725753	grey	-0.143039343	0.073912112			Protein of unknown function (DUF789)	NA
Sapur.010G062700.3	0.568944968	-0.780208663	0.352369426	-2.21418	0.02683668	0.0373985	grey	-0.219873172	0.055363319	GO:0055085;GO:0016021		Major facilitator superfamily protein	folate/biopterin transporter
Sapur.012G048800.2	1.279845452	0.516894381	0.24255882	2.213852	0.02684365	0.03737316	grey	0.185532025	0.020005159	GO:0055124	DNA2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing pr	DNA2 domain protein	
Sapur.018G086300.1	20.71973854	0.519022156	0.234613359	2.212245	0.02694974	0.03752057	grey	0.158057107	0.04803377				NA
Sapur.013G118300.1	0.541055323	0.176224668	0.079611248	2.214149	0.02694798	0.03754141	grey	0.171733821	0.015363619				NA
Sapur.011G078600.1	2.63077511	-0.419751865	0.189794059	-2.21162	0.02693072	0.03759192	grey	-0.192461166	0.011748586	GO:0016758;GO:0008152		UDP-Glycosyltransferase superfamily protein	NA
Sapur.003G208300.1	0.831837174	-0.184209359	0.3021666	-2.21139	0.02708556	0.03759166	grey	-0.112208955	0.016659168	GO:0008152;GO:0008150	CPC-B2 Cell Wall Protein	acyl-CoA synthetase	
Sapur.006G044300.2	3.73565836	-0.362120947	0.16377563	-2.21115	0.02702555	0.03762188	grey	-0.122508735	0.126381742			ESS1-subunit of NADH:ubiquinone oxidoreductase (complex I) protein	NA
Sapur.013G161600.1	9.952547132	-0.278468187	0.126248739	-2.21048	0.02708267	0.03768246	grey	-0.233610789	0.023121294			ankyrin repeat protein	
Sapur.019G061100.1	35.69661753	0.169908286	0.076849589	2.210934	0.02704038	0.03768727	grey	0.184859502	0.020721526	GO:0008270;GO:0005515		RING/U-box superfamily protein	RING-H2 finger protein ATL5H
Sapur.T015100.1	2.983925514	-0.328325863	0.15	-2.20825	0.02738546	0.03809195	grey	-0.315453338	1.5-230-05			Cell differentiation	NA
Sapur.016G046400.2	0.287084589	0.961579274	0.435139997	2.209816	0.02717966	0.03740534	grey	0.129103842	0.107073884	GO:0005085;GO:0016021;GO:0008324;GO:0006812		Cation efflux family protein	metal tolerance protein
Sapur.016G046400.1	52.50510511	-0.223925	0.101104237	-2.20963	0.02731835	0.03760878	grey	-0.167327608	0.036262481			Chaperone DnaJ-domain superfamily protein	chaperone protein DnaJ
Sapur.004G050500.1	0.238146645	1.250405643	0.630017145	2.209287	0.02731429	0.03774599	grey	0.227327787	0.053747956	GO:0043565;GO:0008270;GO:0003700	BME3;BME3-2;GATA8	Plant-specific GATA/B GATA transcription factor family protein	GATA zinc finger protein
Sapur.010G169000.1	4.202252329	-0.570466231	0.258196332	-2.20935	0.02715026	0.03776374	grey	-0.184187189	0.020931962			Protein of unknown function (DUF674)	NA
Sapur.009G093900.9	0.154478275	-0.156621484	0.071387396	-2.20915	0.02734875	0.03816791	grey	-0.219030053	0.018183806			lactoylglutathione lyase family protein / glyoxalase I family protein	glyoxalase I
Sapur.001G109300.1	138.1114478	0.159019658	0.07180252	2.20912	0.02716629	0.03780824	grey	0.146298017	0.027503003				
Sapur.018G085400.1	18.7671205	0.185281615	0.084010192	2.20817	0.02717639	0.03781484	grey	0.192377772	0.017284613				
Sapur.012G098100.1	215.2985644	0.129660372	0.058703342	2.208777	0.02739167	0.03782881	grey	0.185677867	0.010899946	GO:0046983	bHLH005;LIL3	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	bHLH transcription factor
Sapur.003G011300.1	9281.414655	0.566664181	0.257468739	2.208242	0.02731577	0.03786846	grey	0.227545145	0.018845997	GO:0016747	HXXXD-type acyl-transferase family protein	HXXXD-type acyl-transferase family protein	
Sapur.007G076700.1	164.5996803	0.132300769	0.059934664	-2.20742	0.02738447	0.03795287	grey	0.333627662	1.96E-05				NA
Sapur.006G192600.2	3.021627545	-0.383168396	0.17377493	-2.20727	0.02729199	0.03797108	grey	-0.058573013	0.481682003			Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.009G168800.2	2.610880976	-0.306374644	0.146168667	-2.20685	0.02731326	0.03805904	grey	-0.166815168	0.036785253	GO:0016773;GO:0016020;GO:0005524	MPK16	mitogen-activated protein kinase 16	MAP kinase
Sapur.002G056600.1	23.45758876	-0.308002021	0.140023742	-2.20606	0.02738074	0.03808065	grey	-0.171537991	0.01702812			transmembrane protein, putative	
Sapur.006G067050.1	0.280312127	0.566392266	0.257134647	2.204869	0.02743407	0.03814875	grey	-0.139826042	0.038188218	GO:0006412;GO:0005840;GO:0005622;GO:0003735		60S ribosomal protein L34, putative	60S ribosomal protein L34
Sapur.002G091500.1	10.79228074	-0.342027736	0.155503751	2.201299	0.02743135	0.03855683	grey	0.163475381	0.040780443	GO:0005085;GO:0022857;GO:0016021		phosphate transporter 1;9	inorganic phosphate transporter
Sapur.013G281300.1	97.78602204	-0.159624844	0.072387396	-2.20515	0.02744773	0.03856791	grey	-0.219030053	0.058183806			regulatory component of ABA receptor 3	abscisic acid receptor PYL8
Sapur.008G169700.1	880.5547097	0.08561033	0.040559727	2.20482	0.02746742	0.03860035	grey	0.217118255	0.006360478			Transducin/WD40 repeat-like superfamily protein	WD40 domain protein, putative
Sapur.009G132200.1	15.99465064	0.084406761	0.074027791	2.20373	0.02749869	0.03878673	grey	0.149869602	0.026736733				transmembrane protein
Sapur.017G047900.1	15.7889663	-0.238478752	0.108239317	-2.20357	0.02754745	0.03819204	grey	-0.153313599	0.055204263				EAP30/Vps36 family protein
Sapur.016G046400.1	7.572561337	-0.138165344	0.131568752	2.203317	0.02754938	0.03824156	grey	-0.101864183	0.066936017	GO:0016758;GO:0008152		UDP-Glycosyltransferase superfamily protein	UDP-glycosyltransferase, putative
Sapur.010G135700.1	2.016505838	-0.449590103	0.204575796	-2.20325	0.02750907	0.03836287	grey	-0.274513	0.005052281	GO:0005515;GO:0003755	ENB0135	RING/FYVE/PHD zinc finger superfamily protein	strawberry notch-like protein
Sapur.016G187400.1	1.003315325	0.691039393	0.313718341	2.202708	0.02753247	0.03835717	grey	0.193828208	0.05103683	GO:0016747	HXXXD-type acyl-transferase family protein	anthranilate N-benzoyltransferase, putative	
Sapur.010G198500.1	4.746489329	-0.361197274	0.164384615	-2.20383	0.02757002	0.03841123	grey	-0.177308009	0.030164305	GO:0005737;GO:0016020;GO:0006629;GO:0005737		3-oxo-5-alpha-steroid 4-dehydrogenase (protein	3-oxo-5-alpha-steroid 4-dehydrogenase
Sapur.009G156300.1	11.54161316	-0.215827543	0.09688519	-2.20132	0.02771267	0.03828314	grey	-0.173491697	0.031765028	GO:0055114;GO:0016717;GO:0006629	FAD2	fatty acid desaturase 2	delta-12 fatty acid desaturase
Sapur.010G088600.1	4.796714852	-0.252391951	0.16051268	-2.2024	0.02773302	0.03832624	grey	-0.167318396	0.032767774				hypothetical protein
Sapur.005G125800.1	8.493971243	-0.285081532	0.12955662	-2.19976	0.02782864	0.03876353	grey	-0.147682671	0.064920387				NA
Sapur.006G296600.1	268.2848477	-0.135021225	0.058890341	-2.19975	0.02784238	0.03876352	grey	-0.211153241	0.007885215	GO:0003968	RDR6;SDE1;SGS2	RNA-dependent RNA polymerase

Sapur.014G127800.3	0.38667931	-0.86781538	0.409934976	-2.11696	0.03463136	0.047168632	grey	-0.30689386	9.25E-05	GO:0016755,GO:0016117		lycopene beta/epsilon cyclase
Sapur.006G031000.1	1.04667872	-0.40527539	0.191549844	-2.11575	0.03436211	0.047308251	grey	-0.21449051	0.00698269		AT5G50510.1	lycopene beta/epsilon cyclase
Sapur.005G076600.1	2.90024268	-0.41297787	0.195122825	-2.11539	0.03436157	0.047348054	grey	-0.18861401	0.01799274	GO:0008270,GO:0005515	BRH1	transmembrane protein, putative
Sapur.010G170300.1	13.78181097	-0.21743708	0.102871374	-2.11472	0.03445187	0.047425411	grey	-0.2042927	0.03274305			brassinosteroid-responsive RING-H2
Sapur.004G079600.1	25.38869007	-0.17318738	0.08200265	-2.11381	0.03463146	0.047620777	grey	-0.19914709	0.01243248		AT5G61600.1	RING/U-box superfamily family protein
Sapur.008G072600.2	0.36691271	-0.83732734	0.396133561	-2.11375	0.03463595	0.047534887	grey	-0.20357669	0.0155192		AT5G61600.1	cerulenin-resistant RMD1
Sapur.001G238500.1	46.8987934	0.25339478	0.120837292	-2.11354	0.03465439	0.047557331	grey	-0.17828065	0.02548334		AT5G69180.1	Protein of unknown function (DUF1263)
Sapur.001G188300.1	0.65431553	-0.76296706	0.361079035	-2.11303	0.03469913	0.047616995	grey	-0.12682671	0.11335456	GO:0003676	AT2G47720.1	protein of unknown function (DUF151)
Sapur.003G125300.1	281.704374	-0.09602488	0.045466149	-2.11201	0.03480881	0.047734399	grey	-0.17263561	0.03061593		AT5G13100.1	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.004G030000.2	0.68807815	-0.55455984	0.2947935	-2.11183	0.0347007	0.047752864	grey	-0.04206645	0.59687943		AT3G26200.2	plant/T19L91-60 protein
Sapur.012G038200.1	5.66017288	-0.21583012	0.102106729	-2.11174	0.03470847	0.047761439	grey	-0.21660723	0.05729028	GO:0005515	AT4G18790.1	Telomerase activating protein Est1
Sapur.010G218100.1	1978.080004	-0.07774552	0.036815572	-2.11159	0.03472899	0.047776627	grey	-0.13367516	0.09120022	GO:0003677	AT5G62160.1	Est1 DNA/RNA-binding domain protein
Sapur.012G044400.1	20.24594034	-0.37089633	0.175427005	-2.11135	0.03474456	0.047802289	grey	-0.15597785	0.04617639	GO:0003700,GO:0009058	AT5G12150.2	AMSH-like ubiquitin thioesterase
Sapur.003G030800.1	2.77861188	-0.59207197	0.279806479	-2.11132	0.03474649	0.047802205	grey	-0.17260679	0.11133202	GO:0004872,GO:0030001	AT4G28710.1	tubulin beta chain
Sapur.009G064100.1	430.6162603	0.12512349	0.059230337	-2.11125	0.03476136	0.047824564	grey	0.15854599	0.04803782	GO:0005515,GO:0006468,GO:0015234,GO:0004672	AT5G09570.1	Heavy metal transport/detoxification superfamily protein
Sapur.010G053800.1	153.3231813	-0.03973984	0.19543441	-2.11074	0.03485243	0.047947643	grey	-0.15122041	0.05858261	GO:0005262,GO:0003887,GO:0003677	AT2G47620.1	leucine-rich receptor-like protein kinase family protein
Sapur.15WG055900.1	18.2542444	0.15647015	0.07451558	-2.11025	0.03485217	0.047950858	grey	-0.14320255	0.07816373		AT4G18510.1	DNA polymerase alpha 2
Sapur.010G081500.2	25.0168188	0.14705618	0.06970975	2.109549	0.03489179	0.04835211	grey	0.14879776	0.06293304		AT5G61660.2	Vacuolar protein sorting-associated protein 26
Sapur.15WG138300.1	175.7988642	-0.12802187	0.05859575	-2.10947	0.03491215	0.048491285	grey	-0.16481019	0.0495		AT5G15451.1	plasmodesmata-located protein 6
Sapur.006G067300.8	1.07853201	0.54135661	0.256660829	2.109238	0.03492082	0.04838223	grey	0.16809403	0.03134543		AT5G13640.1	LPA2
Sapur.006G111100.1	251.189976	0.14585589	0.069267	2.109035	0.03496067	0.04844112	grey	0.1508582	0.06481112	GO:0006468,GO:0004672	AT4G36670.1	low psii accessory4
Sapur.010G103500.1	43.19195066	0.33976681	0.161172138	2.108222	0.03511773	0.04852835	grey	0.17462961	0.02871563	GO:0005515	AT5G65316.1	DNA-binding protein, putative
Sapur.009G287800.1	267.6317661	0.10224844	0.04320335	2.108051	0.03512703	0.04859342	grey	0.12052128	0.10960242	GO:0045454,GO:0010535,GO:0006662	AT5G65230.1	ARF/RHO family proteins
Sapur.010G051300.3	15.37183649	-0.18516134	0.087696786	-2.1066	0.0515125	0.04834282	grey	-0.15423168	0.05193092		AT5G18530.1	tyrosine kinase domain
Sapur.012G022600.1	2.10945677	-0.47388252	0.224694704	-2.10623	0.03517931	0.04863578	grey	-0.18875017	0.03793032		AT4G24240.1	Protein kinase superfamily protein
Sapur.010G137400.1	14.1904477	0.26819671	0.127343258	2.106092	0.03519635	0.04869605	grey	-0.14319305	0.07359084		AT5G18550.1	Thioredoxin superfamily protein
Sapur.004G090400.1	108.072396	-0.00782069	0.28869795	-2.10538	0.03525848	0.04881973	grey	-0.21437667	0.00702683		AT1G11800.1	Protein of unknown function (DUF707)
Sapur.010G084200.4	-0.49561279	0.76274042	0.37168193	2.104988	0.03528324	0.04885671	grey	0.19738432	0.03216876		AT5G03250.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.012G058300.1	0.36412081	0.96787446	0.459813591	2.104924	0.03529966	0.04852319	grey	0.16467193	0.07254863	GO:0055114,GO:0016491,GO:0008152	AT4G38000.1	endonuclease/exonuclease/phosphatase family protein
Sapur.003G079200.1	167.2922168	0.27232731	0.129828152	2.104625	0.03539967	0.04856665	grey	0.16499586	0.06418619		AT4G21440.1	aldehyde dehydrogenase 2B4
Sapur.010G101900.1	198.9269674	0.14196456	0.067476118	2.104014	0.03537267	0.04865286	grey	0.13840913	0.08357101		AT5G15560.1	copper ion binding
Sapur.001G031300.1	0.23171264	0.44819892	0.68871283	2.103757	0.03540504	0.04878162	grey	0.15108562	1.64E-04	GO:0005634	AT2G22520.1	hypothetical protein
Sapur.010G028500.1	5.98947781	-0.25432639	0.120915563	-2.1026	0.03550048	0.04875695	grey	-0.16016188	0.04508632	GO:0006355,GO:0005739,GO:0003690	AT5G07900.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Sapur.010G088300.1	-0.01741386	0.48147942	0.23008865	2.101981	0.03559349	0.04887454	grey	-0.13419193	0.09406396	GO:0016604,GO:0005634,GO:0006412	AT5G07090.1	Mitochondrial transcription termination factor family protein
Sapur.003G028200.1	62.05833773	-0.14352004	0.068299616	-2.10133	0.03561997	0.04895778	grey	-0.17047056	0.03279142	GO:0005515	AT5G36310.1	S-locus lectin protein kinase family protein
Sapur.010G100300.1	7065.6301	0.15611	0.074353837	2.101069	0.03562575	0.04895723	grey	0.15239411	0.05408463	GO:0006468,GO:0004672	AT3G54960.1	switch subunit 3
Sapur.15WG072200.1	1.25487739	0.50569584	0.24082947	-2.10029	0.03570046	0.04906839	grey	-0.20328629	0.03062209		AT5G18650.1	transmembrane protein, putative
Sapur.013G077000.1	4.47612945	0.27229659	0.12962488	-2.10013	0.03571928	0.04908454	grey	-0.13684011	0.08787528		PDC83	transmembrane kinase family protein
Sapur.15WG051880.1	0.36598076	0.78883748	0.37573874	2.099426	0.03579391	0.04916531	grey	-0.20528316	0.03969334		AT5G18550.1	phosphoglycerate/bisphosphoglycerate phosphatase, putative
Sapur.014G020500.1	1.08813632	0.52735497	0.251653383	2.098955	0.03582842	0.04920045	grey	0.15104376	0.05898627	GO:0005509	CML37,CML39	calmodulin-like 37
Sapur.013G091700.1	33.21343807	0.17795495	0.08521167	2.098675	0.03585379	0.04924041	grey	-0.15664449	0.05092034		AT3G49910.1	EF hand protein
Sapur.009G076400.2	0.46215984	-0.7835172	0.36674756	-2.09822	0.03585782	0.04935681	grey	-0.28155673	0.00294727		AT5G18890.1	cytoplasmic membrane protein
Sapur.010G085800.1	2.88215154	-0.49833882	0.238376404	-2.09786	0.03589	0.04940204	grey	-0.18815016	0.03264596	GO:0055114,GO:0016491,GO:0016209,GO:0006979,GO:0004602	AT2G41480.1	NADP(+)-binding Rossmann-fold superfamily protein
Sapur.013G087800.4	0.58184937	-0.68835157	0.328209721	-2.09724	0.03597076	0.04942014	grey	-0.19197411	0.05693874	GO:0055115	AT2G36400.1	glutaredoxin family protein
Sapur.010G029900.1	-0.80533786	0.50772648	0.237524388	2.09661	0.03602820	0.04953127	grey	-0.16829377	0.03512513		AT5G55400.1	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.010G051500.1	26.5642904	0.37690254	0.176812184	2.09609	0.03607199	0.04956324	grey	-0.17072557	0.02653068	GO:0070018,GO:0005875,GO:0003777	AT3G11310.1	Endosomal protein P24 family protein
Sapur.010G075500.2	47.18528772	0.07608889	0.035636	2.095963	0.03607419	0.04958688	grey	0.20647292	0.00475016	GO:0003674	AT5G27520.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.013G023000.1	4.16964396	-0.45898628	0.218981698	-2.09601	0.03608162	0.04956165	grey	-0.10874284	0.17520175		AT5G22660.2	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.010G080800.1	786.583425	-0.46439471	0.221603324	-2.09563	0.03611599	0.04965778	grey	-0.18677629	0.01795942		AT5G12190.1	Disease resistance protein (CC-NBS-LRR class) family
Sapur.004G117700.1	2.39404866	-0.76883567	0.367267	-2.09538	0.03612975	0.04968689	grey	-0.18508802	0.03946669		AT5G52610.1	BURP domain-containing protein
Sapur.001G192600.2	0.47437999	-0.96769596	0.452385214	2.094829	0.03618261	0.04969975	grey	-0.18369718	0.03946569	GO:0005515,GO:0003723	AT1G72310.1	Protein of unknown function (DUF630 and DUF632)
Sapur.006G067300.1	1.36205487	0.72383229	0.3001731	-2.09477	0.03620197	0.04970581	grey	-0.18307917	0.03470578		AT4G32540.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.011G075100.1	32.14562049	0.17096799	0.081610202	-2.09466	0.03620501	0.04976748	grey	-0.20765353	0.00918852		AT1G16916.1	2-phosphoglycerate kinase, putative
Sapur.005G188800.4	9.1709084	0.09880076	0.047164255	2.093969	0.03623519	0.04980076	grey	-0.21523277	0.00678175	GO:0005524	AT2G20080.2	transmembrane protein
Sapur.15WG041100.1	35.95402487	0.21010185	0.100483789	2.092976	0.03631273	0.04991218	grey	0.14119138	0.07775945		AT5G17030.1	MECA	methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonoyl-CoA carboxylase 1 (MECA)
Sapur.015G139100.1	4.36299008	0.27665303	0.132104388	2.09463	0.03633112	0.04997651	grey	0.16373673	0.04044184	GO:0055114,GO:0050660,GO:0016491	AT4G37670.1	cysteine and histidine-rich domain protein RAR1
Sapur.018G046500.1	3.06049789	-0.35005391	0.171564165	-2.09272	0.03637439	0.04994757	grey	-0.20600684	0.01176816		AT4G38020.1	FAD-binding Berberine family
Sapur.012G084000.1	25.70983561	0.14303601	0.068469788	-2.09206	0.03642398	0.05002192	grey	-0.17615102	0.02723876		WAV2	alpha/beta-hydrolases superfamily protein
Sapur.003G075900.1	24.44316569	0.17550052	0.08551443	2.091918	0.03644601	0.05005121	grey	-0.15148602	0.05897827		AT5G58320.1	Transport protein particle (TRAPP) component
Sapur.011G141200.1	0.4901676	0.92495463	0.442337291	2.091064	0.03652254	0.05018649	grey	-0.17526109	0.02831409	GO:0005975,GO:0004553	AT5G49310.1	putative-beta-glucosidase-glucosidase/cellulase-related
Sapur.001G175500.2	5.87348322	-0.35188277	0.172000886	-2.09026	0.03653	0.05020662	grey	-0.14445101	0.07075642		AT1G72160.1	Glycosyl hydrolases family 31 protein
Sapur.013G209900.4	15.85209514	-0.16425527	0.078450691	-2.09008	0.03659278	0.05034681	grey	-0.12226454	0.12714521		AT5G62160.1	T-complex protein 10
Sapur.015G132600.1	451.6714864	-0.12903936	0.061711899	-2.09003	0.03659537	0.05030154	grey	-0.10874284	0.17520175		AT5G12290.1	Transport protein particle (TRAPP) component
Sapur.013G093500.1	5247.912534	-0.12005365	0.057420088	-2.09079	0.03664674	0.05036343	grey	-0.18317618	0.02170607	GO:0006556,GO:0004679,GO:0005524	AT2G22930.1	AT2G22930.2
Sapur.010G045200.1	161.3940934	0.07738804	0.036921207	-2.09066	0.03671524	0.05046604	grey	-0.18852404	0.03946469	GO:0006413,GO:0005737,GO:0003743	AT3G12310.1	Eukaryotic translation initiation factor 1a/2B
Sapur.019G101100.1	143.4742813	0.87213829	0.417373285	2.089769	0.03683539	0.05208527	grey	-0.26392639	0.00087701		AT4G03500.1	Ankyrin repeat family protein
Sapur.015G084000.1	202.2539914	0.05364001	0.025588323	2.089365	0.03685236	0.05209195	grey	-0.13968045	0.09310621	GO:0005085,GO:0004673,GO:0003001,GO:0016020	AT2G01260.1	ZIP family protein
Sapur.011G054200.1	1814.293826	-0.07752947	0.037010466	-2.08955	0.03686428	0.05208749	grey	-0.17662843	0.03259823	GO:0007275,GO:0005634	AT4G27520.1	ZIP metal ion transporter family
Sapur.15WG142700.1	6.51146227	-0.28319893	0.13800895	-2.08899	0.03708272	0.05275563	grey	-0.14891719	0.06262343	GO:0017704,GO:0016868,GO:0005975	AT1G51820.1	IAP-like protein 1
Sapur.017G125200.1	0.42180936	-0.78703227	0.418096923	2.088546	0.03709747	0.05245598	grey	0.19221416	0.03127468	GO:0016021	AT2G07690.1	PTPMT1
Sapur.15WG074600.1	1.54912606	-0.41054389	0.196571868	-2.0865	0.03752735	0.05331895	grey	-0.18806475	0.01717346		AT5G03630.1	phosphoglycerate mutase family protein
Sapur.001G051700.5	0.36825152	-0.96355933	0.461377389	-2.08844	0.03758089	0.05347146	grey	-0.21693027	0.0052524	GO:0006355,GO:0005634,GO:0009725,GO:0003677	AT5G62020.1	Protein of unknown function (DUF789)
Sapur.006G171300.1	103.3885286	-0.14037937	0.067171462	-2.08838	0.03763	0.05346892	grey	-0.16079528	0.04424348		AR5-1-BP,ARF2,HS5,DRE14	auxin response factor 2
Sapur.001G242000.1	1.55046424	-0.64437574	0.307061133	-2.08243	0.03807927	0.05407428	grey	-0.10796912	0.17882257			
Sapur.004G021500.2	5.78827952	-0.28447145	0.136129207	-2.08819	0.03780913	0.05362188	grey	-0.17326685	0.02997876	GO:0008184,GO:0005975	AT4G29170.1	alpha-glucan phosphorylase 2
Sapur.010G039100.1	42.76808019	-0.28707663	0.137014511	-2.08753	0.03784028	0.05359426	grey	-0.14452067	0.07009142	GO:0016758,GO:0008152	AT4G18250.1	AGUSTIBA,LUCTISA3
Sapur.015G185900.1	4034.042249	0.11402859	0.055013465	2.087288	0.03788205	0.05367558	grey	-0.11644872	0.1463943	GO:0055114,GO:0016491,GO:0016209,GO:0046354,GO:0015035,GO:0006662	AT1G10130.1	ATTRX H1,ATTRX1,TRX1
Sapur.007G107100.1	95.09258888	0.12876568	0.061729157	-2.08647	0.03808479	0.05266721	grey	-0.15830925	0.04767197			thioredoxin H-type 1
Sapur.010G238800.1	1.50462479	0.41497966	0.20752969	2.085888	0.03809766	0.05755596	grey	-0.10543604	0.26265618	GO:0008152,GO:0003824	AAE12	AAE14
Sapur.001G090500.1	93.16717183	0.61078246	0.293015161	2.084487	0.03715956	0.05090703	grey	0.21507672	0.00829163	GO:0055114,GO:0051537,GO:0016491,GO:0010277	ACD1-LIKE,PTC52,TIC55-IV	acyl activating enzyme 12
Sapur.003G030900.1	0.26857625	0.97885221	0.4900657	2.084047	0.03719364	0.05095695	grey	0.21351824	0.00720259	GO:0009570,GO:0009576	ACD1-LIKE,PTC52,TIC55-IV	ACD1-like
Sapur.006G114700.1	677.026381	0.09806659	0.04708007	2.0828	0.03728479	0.05113389	grey	0.13545617	0.09079196		AT5G20700.1	Protein of unknown function (DUF581)
Sapur.006G171100.1	0.66878589	0.91760183	0.44063259	2.082152	0.03731669	0.05115591	grey	0.16631917	0.03470578			
Sapur.001G194000.1	198.2199664	0.12548286	0.06027563	2.081841	0.03735021	0.05122017	grey	0.17521185	0.02817272		AT5G13130.1	RING/U-box superfamily family protein
Sapur.003G087500.1	23.27599017	0.16506015	0.079321	2.081665	0.03737419	0.05124862	grey	-0.17983925	0.02483883	GO:0008270,GO:0003676	AT5G15160.1	zinc knuckle (CCHC-type) family protein
Sapur.010G084700.1	689.4859628	0.28050955	0.13485934	2.080018	0.03753841	0.05146047	grey	0.14269809	0.07461087	GO:0016021,GO:0055114,GO:0008272,GO:0055085,GO:0016020,GO:0008271	AST91,SULTR3;5	sulfate transporter 91
Sapur.003G075300.1	88.09535563	0.20466127	0.10386925	2.079867	0.03762567	0.05159788	grey	0.16486649	0.03653023			
Sapur.009G007700.1	2.27979043	0.32661842	0.157063879	2.075526	0.03756918	0.05149858	grey	0.18944996	0.01718538		AT5G35481.1	HSP20-like chaperones superfamily protein
Sapur.010G080800.6	0.62844229	0.71184399	0.342406248	-2.07894	0.03762448	0.05160682	grey	-0.21001566	0.00839141	GO:0006355	FRS10	FARS-related sequence 10
Sapur.006G172200.2	271.9848904	-0.2813113	0.137217598	-2.07844	0.03768504	0.05165222	grey	-0.17410156	0.02620618		AtcwINV2,CWINV2	cell wall invertase 2
Sapur.010G053600.1	93.42512175	-0.16612728	0.079691907	-2.07811	0.03769691	0.05166953	grey	-0.14906145	0.06242517		ACD1-LIKE,PTC52,TIC55-IV	ACD1-like
Sapur.003G160200.1	2.40087832	0.50758188	0.24396187	2.078007	0.03773159	0.05169225	grey	0.14998124	0.06581111	GO:0055114,GO:0003727		
Sapur.006G049600.5	20.11785583	0.16316097	0.07030323	-2.07795	0.03773136	0.05181963	grey	0.07648531	0.3281467	GO:0006396,GO:0003723	AT5G21120.2	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein
Sapur.010G177000.1	1011.129317	0.06680169	0.03254087	-2.07757	0.03774848	0.05172687	grey	-0.12168844	0.09288344	GO:0009507,GO:0009570	EMB1144	chloroplast-localized protein family protein
Sapur.011G195900.1	613.1262679	-0.07628884	0.03677564	-2.07742	0.03776297	0.05176585	grey	-0.23914717	0.00257654		AT4G13990.1	Exostosin family protein
Sapur.010G238300.1	0.86328888	0.65340769	0.31452581	-2.07736	0.03777483	0.05180454	grey	-0.18964643	0.01413163			
Sapur.014G105200.1	0.22508836	1.07021312	0.61181767	2.075997	0.03784252	0.05192073	grey	0.33072317	2.32E-05		AT3G21045.1	Rhodanese/Cell cycle control phosphatase superfamily protein
Sapur.006G017900.1	52.80310649	0.15906762	0.076631583	2.075587	0.03785238	0.05188768	grey	0.15116456	0.05878583		AT4G27140.1	Transmembrane amino acid transporter family protein
Sapur.006G200300.1	2.50453211	-0.39141382	0.192335109	-2.07535	0.03795365	0.05198786	grey	-0.20739345	0.00915153	GO:0051603,GO:0005839,GO:0004298	PBG1	20S proteasome beta subunit G1
Sapur.001G091100.1	3.37992625	-0.35276059	0.169993139	-2.07532	0.03795616	0.05199714	grey	-0.17792436	0.02578798	GO:0055085,GO:0016020,GO:0008510,GO:0015171,GO:0003333	AT4G13620.1	Amino acid permease family protein
Sapur.7092880.1	4.50861147	0.10407161	0.05127436	2.075202	0.03796762	0.05201967	grey	0.17416944	0.03156318			
Sapur.014G019200.1	5.73522904	-0.18031873	0.18403997	-2.07495	0.03799157	0.05204724	grey	-0.15939732	0.04146541	GO:0005509	CML38	calmodulin-like 38
Sapur.007G101100.1	0.72246513	0.27331387	0.34746144	2.074609	0.03799439	0.05206778	grey	0.13895915	0.08202385		AT4G34570.1	dicarboxylate carrier 2
Sapur.012G067200.1	15.07223977	-0.38046118	0.183401905	-2.07447	0.03803592	0.05209764	grey	-0.16920273	0.03418929		AT3G01680.1	sieve element occlusion protein
Sapur.005G113600.1	18.52463616	0.07202973	0.10016767	-2.07443	0.03804672	0.05211274	grey	-0.12263743	0.0421885	GO:0055114,GO:0016616,GO:0051287,GO:0000287	AT3G17130.1	isocitrate dehydrogenase subunit 2
Sapur.002G146700.3	22.78356329	-0.15673497	0.07556377	-2.07421	0.03808028	0.05214374	grey	-0.09408014	0.23706601		AT4G01540.1	alpha/beta-Hydrolases superfamily protein
Sapur.006G160500.1	1.25166447	0.53089795	0.25678647	2.073589	0.03808742	0.05215909	grey	0.14506065	0.07281287			
Sapur.010G025200.1	2.6070561	0.51583709	0.24877183	2.073527	0.03813282	0.05206419	grey	0.15819097	0.04784218		AT1G72700.1	ATP binding;nucleic acid binding;helicases
Sapur.010G014000.5	2.34018198	-0.38958693	0.187934385	-2.07301	0.03817142	0.05270192	grey	-0.07513932	0.37349362	GO:0005515	AT5G55130.3	Calcium-dependent lipid-binding (CALB domain) family protein
Sapur.011G082300.1	671.1212207	0.06667224	0.04860965	2.072488	0.03821925	0.05316429	grey	0.09704937	0.23636792		AT3G46140.1	BIRCH4, putative
Sapur.010G180800.1	1.06632122	-0.53028693	0.255963453	-2.07257	0.03824129	0.05272249	grey	-0.18982509	0.0172565		AR5A15,ATAR5A1E	ADP-ribosylation factor A1E
Sapur.010G076100.1	0.90873628	0.45364491	0.2189	2.072193	0.03826183	0.05243886	grey	-0.10962203	0.17126368			
Sapur.017G061700.1	74.91041172	-0.27801785	0.13907384	-2.07144	0.03831805	0.05266231	grey	-0.13728192	0.08418919	GO:0006468,GO:0005524,GO:0004672	AP4M4,ATPK12,PEX12	pertein-12
Sapur.011G144500.2	17.98616563	0.15812613	0.076577125	2.071187	0.03833138	0.05491987	grey	0.06007879	0.45982022	GO:0007186,GO:0005834,GO:0004871	AGC2	G-protein gamma subunit 2
Sapur.007G047000.1	9.31442026	0.52608649	0.25404114	2.070792	0.03837838	0.05245029	grey	0.19016536	0.01697348		AT4G18680.1	BSD domain-containing protein
Sapur.010G027100.1	12.3707666	0.15812542	0.07636	2.070688	0.03840214	0.05252262	grey	0.17404934	0.03156318		AT5G18180.1	ARR12,RR12
Sapur.001G005900.1	20.48885109	0.71040364	0.34332362	2.069889	0.03846256	0.05261678	grey	-0.20680319	0.00850026			
Sapur.010G139400.1	1.18161994	-0.59604561	0.288174	2.069545	0.03848545	0.05280553	grey	-0.17404707	0.03852481	GO:0016887,GO:0005524,GO:0016020	AT5G34480.1	ABC2GT,ATPDRB-PDRB-PIS1
Sapur.016G040900.1	10.02091578	0.23435498	0.11331612	2.068143	0.03863545	0.05287152	grey	-0.23026751	0.00254386	GO:0005085,GO:0016021,GO:0008324,GO:0006812	AT3G12100.1	pleiotropic drug resistance 9
Sapur.006G097000.9	0.92627963	0.56004461	0.275180195	2.067898	0.03864603	0.05290086	grey	0.15783047	0.04835192	GO:0016021	AT5G19420.1	Cation efflux family protein
Sapur.007G129900.1	286.3520733	0.11489331	0.05577575	2.067838	0.03867148	0.05291809	grey	0.16219064	0.03747748		AT4G27650.1	Sulfite exporter TauE/SafE family protein
Sapur.016G277200.1	5.06095363	0.27698826	0.18243363	2.066495	0.03878124	0.05307133	grey	0.13210182	0.09051119		AT4G02725.2	plastid transcriptionally active 2
Sapur.015G082100.1	1.82164467	0.52189012	0.25684875	2.0664	0.03879449	0.05303419	grey	-0.17949462	0.02705051		AT1G01720.1	PPR containing protein
Sapur.015G113800.1	382.6836698	-0.08803393	0.04293786	-2.06587	0.03884113	0.05347614	grey	-0.17246008	0.03077625	GO:0006355,GO:0006468,GO:0004672	AT3G06320.1	cullin-associated and neddylation dissociated
Sapur.011G144900.1	12.11949115	-0.22628235	0.10957547	-2.06518	0.03886147	0.05350364	grey	-0.17728928	0.02833122		AT5G61250.1	PAS domain-containing protein tyrosine kinase family protein
Sapur.004G082500.1	0.28963074	-0.90266198	0.437150791	-2.06488	0.03894777	0.05364759	grey	-0.3479288	7.97E-06		AT4G27520.1	Plant protein of unknown function (DUF827)
Sapur.006G108400.1	245.5682602	0.10277537	0.05249817	2.064197	0.03906611	0.05372205	grey	0.17006571	0.03234092	GO:0016021,GO:0006605,GO:0004348	AT5G49900.1	Beta-glucosidase, GBA2 type family protein
Sapur.006G111800.5	935.0420635	0.08268388	0.04068628	2.06364	0.03905181	0.05420476	grey	0.17720256	0.02955193	GO:0003677	AT4G32240.1	ARID/BRIGHT DNA-binding domain-containing protein
Sapur.002G077800.3	0.45538808	0.72878815	0.35232199	-2.06321	0.03908082	0.05437322	grey	-0.24772936	0.00179724		AT3G19120.1	cytochrome b5 family protein
Sapur.003G080600.1	12.54718845	0.35242081	0.17076127	2.06319	0.03909545	0.05437232	grey	0.11484045	0.09203688		AT5G52120.1	DUF740 family protein
Sapur.006G035100.1	763.9781106	-0.12470749	0.060492111	-2.06321	0.03911423	0.05369143	grey	-0.19020811	0.01929765		AT5G58220.1	zinc finger (ECCH-type) family protein
Sapur.004G160600.1	83.77887275	0.09708325	0.04741237	2.06282	0.03923741	0.05315984	grey	0.16770409	0.03573668		AT3G07780.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase family protein
Sapur.007G039600.1	0.23521882	1.09697855	0.53189969	2.06264	0.03916829	0.05337143	grey	0.26432159	0.0008221		AT4G37030.1	CCR1,CCR1L1
Sapur.010G088200.1	14.44820263	0.07308753	0.03567	2.062514	0.03921	0.05351147	grey	-0.08524142	0.38353118	GO:0005524	XCT	XAPS family protein
Sapur.010G084600.1	2.15178843	0.36318601	0.176240019	-2.06093	0.03930976	0.05375495	grey	-0.13128871	0.10123393	GO:0006418,GO:0000166,GO:0005524,GO:0004812,GO:0002161,GO:0006429,GO:0004812	EMB2369	leucyl-tRNA synthetase
Sapur.004G160600.1	3.36429348	0.70776838	0.3823623	2.060264	0.03937281	0.05388349	grey	0.20482469	0.01007388		AT4G13180.1	Homeodomain-like protein
Sapur.008G122200.3	1.7254445	0.49132793	0.238490445	2.060158	0.03938466	0.05385189	grey	0.15281117	0.05262885	GO:0005085,GO:0016021	AT5G26340.1	Major facilitator superfamily protein
Sapur.004G084000.1	0.99833963	0.65269863	0.3171618	2.058887	0.03963088	0.05387128	grey	-0.23637028	0.00387593	GO:0005515,GO:0008152	AT5G65230.2	ARF/RHO family proteins
Sapur.010G190900.1	2.48250738	-0.52432232	0.24498263	-2.05924	0.03967154	0.05390587	grey	0.16534287	0.03850454	GO:0055114,GO:0020037,GO:0016679,GO:0046910	AT5G14550.1	UGT85A2
Sapur.012G086800.1	49.48854166	0.30384429	0.147386372	2.

Sapur.01BG091100.1	0.90083205	0.57796883	0.28727573	2.011918	0.04022859	0.06017068	grey	0.14510087	0.06908806	GO:0005515	AtSEB190.2	AtRLP9;RLP9	receptor like protein 9	NA
Sapur.01G6241200.1	569.1715457	-0.06244926	0.03104527	-2.01143	0.04420063	0.06023516	grey	-0.19488469	0.01445032	GO:0003676;GO:0006351;GO:0003899	AtSG9180.1	NRP87	DNA-directed RNA polymerase II	DNA-directed RNA polymerase II subunit Rpb7
Sapur.01G6284100.2	1.50667748	0.55376123	0.27635185	-2.01122	0.04420273	0.06036388	grey	-0.15814428	0.03240713		AtSG9200.2		Iron-sulphur cluster biosynthesis family protein	transmembrane protein, putative
Sapur.01G6268000.1	1.55726912	0.44404293	0.22078497	2.011183	0.04436109	0.06268992	grey	0.15078557	0.05943317	GO:0004674;GO:0006468;GO:0006470	AtSG7300.1		S-locus lectin protein kinase family protein	NA
Sapur.01G6289300.1	1.46819819	0.4620183	0.23078643	2.010808	0.04456725	0.06310398	grey	-0.20736177	0.09836469		AtSG6835.1	ARG1	Chaperonin Dnaj-domain superfamily protein	chaperone protein Dnaj
Sapur.01G6213300.2	1.06587701	0.50435155	0.24894536	2.01022	0.04497884	0.06402465	grey	-0.10419651	0.1926584		AtCZS2580.1			AmmeMemoRadiSam system protein B
Sapur.01G0280080.1	864.2807864	0.08073124	0.04015361	2.010046	0.04466289	0.06425015	grey	0.14228157	0.07597465	GO:0006950	AtSG11360.4		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.01G0501100.1	0.63491664	0.60435725	0.30068954	2.009569	0.04479788	0.06549121	grey	-0.17891727	0.03458728	GO:0016021;GO:0016020;GO:0022857	AtSG18200.1		nodulin MtN21 /EamA-like transporter family protein	NA
Sapur.15W0G01700.1	52.1821918	0.19588349	0.09747921	-2.00942	0.04492292	0.06550911	grey	-0.13810283	0.0845206	GO:0004683;GO:0005524;GO:0004672	AtSG68920.2		Protein kinase superfamily protein	receptor Serine/Threonine kinase, putative
Sapur.7J1900G0.1	0.27504843	0.72369379	0.36166239	2.009512	0.04513287	0.06564068	grey	-0.17228927	0.02980598		AtSG16890.1		Excision repair protein	NA
Sapur.09G0190800.1	1.36568833	-0.46240642	0.23019551	-2.00899	0.04538624	0.06595635	grey	-0.17200324	0.01232997		AtSG15880.2	HMGB1;NFD1	high mobility group B1	NA
Sapur.01G0255700.1	11.13027968	0.26455765	0.13214663	2.00895	0.04562921	0.06556875	grey	-0.19909983	0.01242678		AtSG24104.4		Vacuolar protein sorting 55 (VPS55) family protein	vacuolar protein sorting-associated-like protein
Sapur.05G0091100.1	0.36199703	0.94265969	-0.46936014	2.008818	0.04656445	0.06598602	grey	0.20099665	0.01159756		AtSG26805.1			hypothetical protein
Sapur.01G6139000.3	0.97761153	0.37896152	0.18872008	2.00787	0.04681727	0.06607147	grey	0.05667277	0.48076417	GO:0005975;GO:0004553	AtSG6860.1	BGLU42	beta glucosidase 42	beta-glucosidase
Sapur.01G6303700.1	27.24727255	0.31025057	0.15468979	2.008358	0.04685325	0.06604559	grey	0.12689426	0.11236121		AtSG18470.1		Curculin-like (mannose-binding) lectin family protein	NA
Sapur.09G0340400.1	148.0125366	0.30142484	0.15148968	2.008139	0.04682742	0.06608387	grey	0.17249491	0.03922347	GO:0003779	AtSG8160.2	ATVIN4;VIN4	villin 4	villin 4
Sapur.02G0278200.2	14.05025711	0.16368757	0.08157227	2.007547	0.04695428	0.06775654	grey	0.18950365	0.01745187	GO:0045454	AtSG4780.1	APR6;ATAPR1;4	APR-like 4	5'-adenylylsulfate reductase-like protein
Sapur.01G0372600.1	0.46307987	0.72306517	0.36019728	2.007502	0.04698267	0.06775737	grey	0.13329782	0.09581847		AtSG4290.2	KAS;LKAS1	3-ketoacyl-acyl carrier protein synthase I	3-ketoacyl-acyl carrier protein synthase I
Sapur.01G0501700.2	0.54057659	0.37389594	0.18528664	-2.00701	0.04734578	0.06792561	grey	-0.17636564	0.07105227		AtSG8290.1		SAC2/SAC4 family protein	SAC2/SAC4 family protein
Sapur.01G6134800.3	10.35793805	-0.12787682	0.06374352	-2.00614	0.04845159	0.06904168	grey	-0.13687333	0.0878829	GO:0005515;GO:0003676	AtSG16280.2	ICA	RNA binding;abscisic acid binding	RNA recognition motif 1 in plant flowering time control FCA-like protein, putative
Sapur.09G0128300.1	4.53576203	0.35185829	0.17545231	2.005819	0.04918396	0.06980027	grey	-0.04770561	0.52657717	GO:0005515	AtSG7600.1	ATVLP1;TLP1	tubby like protein 1	tubby-like F-box protein
Sapur.07G0649000.1	66.08940372	-0.29273228	0.14603128	-2.00472	0.04960659	0.06154254	grey	-0.18884701	0.01881313	GO:0019205;GO:0006139;GO:0005524	AtSG26667.1	PYR6	P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.09G0131300.1	4.91853567	0.30349663	0.15141212	2.00466	0.04502099	0.06137654	grey	-0.16226955	0.06872228		AtSG20100.1		Homeodomain-like superfamily protein	Myb-like transcription factor family protein
Sapur.7D0I000.1	0.98523159	0.58587904	0.29233291	2.004172	0.04501625	0.06137644	grey	0.17177876	0.03146328					NA
Sapur.01G0278700.1	62.16564692	0.27809052	0.13877208	2.003977	0.04509172	0.06187162	grey	-0.12422529	0.17267747	GO:0016747	AtSG9580.1	ATSWAT	HXXXD-type acyl-transferase family protein	anthocyanin 5-O-glucoside 6-O-malonyltransferase, putative
Sapur.02G0164600.1	40.09199513	0.16706892	0.08337983	2.003595	0.04513348	0.06129451	grey	0.13613403	0.08822617		AtSG8660.1		Pathogenesis-related thaumatin superfamily protein	thaumatin-like protein
Sapur.01G6262400.1	14.28064707	0.34087028	0.17009223	-2.00329	0.04546553	0.06134035	grey	-0.17728354	0.03151128	GO:0043531	AtSG3450.1		Disease resistance protein (CC-NBS-LRR class) family	NA
Sapur.7D5G300.1	2.28847861	0.41387164	0.20653524	2.003804	0.04538292	0.06158209	grey	0.14564509	0.08740868		AtSG8600.1	ATNIES;NIES	NIMIN-interacting protein 5	NIMIN-interacting protein 1
Sapur.01G0280800.1	0.35411841	-0.77663712	0.38695935	-2.00272	0.04520759	0.06141843	grey	-0.24041868	0.02421527	GO:0006412;GO:0005840;GO:0005622;GO:0003735	AtSG4950.1	ATBBC;BBC1;RSU2	breast basic conserved 1	60S ribosomal protein L13
Sapur.01G3202500.1	13.04983124	0.37301372	0.18610197	2.000337	0.04520664	0.06463177	grey	-0.11821485	0.16320657	GO:0005886;GO:0006629;GO:0006825	AtSG2630.1		MATE efflux family protein	MATE efflux family protein
Sapur.09G0106500.1	370.4173732	0.14329943	0.07193357	-2.00173	0.04531679	0.06158445	grey	-0.15307161	0.05476157		AtSG38620.1	ATMYB48;MYB48	myb domain protein 48	MFR transcription factor
Sapur.05G0135200.6	0.30258874	0.85176257	0.41752919	-2.00169	0.04543936	0.06152124	grey	-0.29627271	0.00164867		AtSG27720.1	PPK1	putative protein kinase 1	Serine/Threonine kinase domain protein
Sapur.01G0261000.3	23.33734532	-0.21684376	0.10834571	-2.00157	0.04531069	0.06150707	grey	-0.15490702	0.05258381		AtSG4180.1	MPL1	Mytus persicae-induced lipase 1	lipase
Sapur.01G0236200.1	16.84705164	0.16580799	0.08286503	2.000977	0.04534922	0.06161063	grey	-0.14001306	0.08206634					NA
Sapur.01G6093600.1	2.25039969	-0.42079306	0.21029404	-2.00081	0.04542419	0.06167429	grey	-0.16348876	0.04390635					hypothetical protein
Sapur.01G0280300.1	54.16138886	-0.21277583	0.10635201	-2.00001	0.04569812	0.06178987	grey	-0.09664514	0.20208386		AtSG3400.1	DFL2;GH3-10	Auxin-responsive GH3 family protein	indole-3-acetic acid amido synthetase GH3.5 protein, putative
Sapur.01G0210100.1	5.68994593	-0.31426797	0.15714954	-1.99969	0.04534171	0.06183287	grey	-0.13417612	1.85E-05		AtSG3750.1		Ankyrin repeat family protein	ankyrin-like protein
Sapur.05G0641000.1	0.34447748	0.87856025	0.43953874	1.999527	0.04535132	0.06185445	grey	0.24559988	0.00392966	GO:0043565;GO:0003700;GO:0045893	AtSG5210.5	TGA1	bZIP transcription factor family protein	transcription factor TGA
Sapur.01G0881000.1	0.40787224	-0.75737282	0.37904564	-1.99906	0.04582107	0.06169989	grey	-0.22203701	0.00455571	GO:0006355;GO:0005634;GO:0003677;GO:0009725	AtSG2600.1	ATHB-2	auxin response factor 2	auxin response factor, putative
Sapur.05G1360600.1	53.82757179	-0.17983784	0.08959738	-1.99871	0.04639364	0.06196185	grey	-0.16060761	0.0446576		AtSG7680.1	Ribosomal;ribosomal protein family	Ribosomal;ribosomal protein family	60S ribosomal protein L6
Sapur.01G0425400.1	1.06734926	0.34117501	0.24246144	1.988708	0.04583997	0.06166185	grey	0.21770221	0.07759615		AtSG7140.1	SWEETIE	HEAT repeat-containing protein	NA
Sapur.05G1608000.1	0.57695989	0.7751705	0.38784329	1.99865	0.04564271	0.0619723	grey	0.16322969	0.04107767		AtSG23440.1			transmembrane protein, putative
Sapur.01G0280500.1	12.4604043	0.20208164	0.10116168	1.998466	0.04626781	0.06206469	grey	0.16167066	0.04208502		AtSG3100.1		Ribonuclease H protein family protein	RNA-dimers recognition kinase 42.2; putative
Sapur.04G0687300.1	476.1398852	0.05470631	0.02740921	1.997968	0.04657102	0.06267371	grey	0.11307708	0.15878291	GO:0042545;GO:0035599;GO:0005618	AtSG2690.1	ATPME31;PME31	pectin methylesterase 31	pectinesterase
Sapur.01G0139000.1	2.40562713	0.19375771	0.19709658	1.997588	0.0670263	0.06319363	grey	-0.15483606	0.05224165	GO:0004683;GO:0004602;GO:0006623	AtSG2680.1	PRX62	phosphoenolpyruvate carboxylase-related kinase 2	phosphoenolpyruvate carboxylase kinase
Sapur.01G0255400.1	271.0662611	0.36631379	0.18345459	1.996748	0.04585298	0.06239536	grey	0.12167751	0.12893687	GO:0055114;GO:0020037;GO:0006979;GO:0004601	AtSG6730.1	ATPA2;PA2	peroxidase 2	peroxidase
Sapur.01G6132500.1	7927.029099	0.1184841	0.05928227	1.995277	0.04681266	0.06263281	grey	0.12853703	0.10877982	GO:0006810	AtSG9390.1	ATMT-1;ATMT-4;MT2A	metallothionein 2A	metallothionein-like protein type 2
Sapur.15W0G14200.1	19.81332882	0.40170531	0.21080416	1.995027	0.04691849	0.06245301	grey	-0.18519555	0.02028189		AtSG7560.1		Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator repeat protein
Sapur.01G6092200.5	4.59245088	-0.30587464	0.13111326	-1.99523	0.04601803	0.06245376	grey	-0.12490875	0.19082835		AtSG2475.1		Polyketide cyclase/dehydrase and lipid transport superfamily protein	polyketide cyclase/dehydrase and lipid transport
Sapur.01G0280200.1	7.025892	0.57337164	0.29609223	-1.99469	0.04605507	0.06204088	grey	-0.16332008	0.04097839	GO:0016020	AtSG2240.1		Sodium bile acid symporter family protein	bile acid sodium symporter family protein
Sapur.05G0550600.3	1.96639092	-0.79120043	0.39680256	-1.99424	0.04625536	0.06297171	grey	-0.07827647	0.72836642	GO:0006412;GO:0005840;GO:0005622;GO:0003735	AtSG3160.1	EMB3010;RPS6B	Ribosomal protein S6e	40S ribosomal protein S6
Sapur.01G0364700.1	12.36565014	0.27610047	0.09924848	-1.99409	0.04641618	0.06261797	grey	-0.24481448	0.01899969	GO:0016491;GO:0050660	AtSG5520.1	Gln1;Ns;Lpt12	N-acetylglucosamine-6-phosphate uridylyltransferase 2	UDP-N-acetylglucosamine pyrophosphorylase, putative
Sapur.01G6201500.1	211.4722364	0.15461564	0.07754119	1.993984	0.04651275	0.06263062	grey	-0.14287703	0.07425615	GO:0008725;GO:0006284	AtSG7590.1		DNA glycosylase superfamily protein	DNA-3-methyladenine glycosylase I
Sapur.01G6140100.1	0.88055171	0.26274798	0.13174381	1.99321	0.0462851	0.06274778	grey	0.10201185	0.18667276					NA
Sapur.01G0254200.5	2.89643457	0.33532321	0.18338509	-1.99315	0.04625466	0.06274643	grey	-0.11695349	0.14664103		AtSG4720.1			transmembrane protein, putative
Sapur.7D8A001.1	88.34313004	0.16577469	0.08317676	1.992043	0.04652143	0.06285157	grey	-0.20308667	0.01606474		AtSG24880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.09G0091100.1	12.61259836	0.14679927	0.07369293	1.991758	0.04639572	0.06290868	grey	-0.17395769	0.02933989					NA
Sapur.01G0275700.1	429.8957345	0.09021204	0.04931428	1.991669	0.04640738	0.06296192	grey	0.13809552	0.10216173	GO:0005515	AtSG0740.1	FIS;FIS1;FIS3	Transducin/WD40 repeat-like superfamily protein	fertilization-independent endosperm protein
Sapur.01G0280800.1	197.9054572	0.09225341	0.04605341	1.990154	0.03255326	-0.19161	grey	-0.15624243	0.05263366		AtSG7360.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing protein, putative
Sapur.01B0135900.1	21.52975338	0.47134472	0.23668309	1.990614	0.04623325	0.06311528	grey	0.18127884	0.02308262	GO:0006468;GO:0005524;GO:0004672	AtSG6730.1		Wall-associated kinase family protein	wall-associated receptor kinase-like protein, putative
Sapur.01G0280100.1	1.30021138	0.56113108	0.28186221	1.990267	0.04623619	0.06311528	grey	0.16143042	0.04306618		AtSG4760.1		Transmembrane amino acid transporter family protein	amino acid transporter, putative
Sapur.01G0353500.1	6.93055758	0.20177228	0.10137627	1.99033	0.04655542	0.06315087	grey	0.27167163	0.00579389	GO:0005515	AtSG5590.1	LRS1	Transducin/WD40 repeat-like superfamily protein	salt-induced WD protein
Sapur.01G0280400.1	1.91192223	0.56328873	0.28316143	1.990157	0.04657264	0.06316554	grey	0.16607024	0.03848871	GO:0006412;GO:0005525;GO:0005840	AtSG2660.1		Leucine-rich repeat family protein	NA
Sapur.01G0209300.1	320.6957788	0.24826169	0.12476395	-1.98985	0.04660747	0.0621373	grey	-0.14481767	0.07031904		AtSG6680.1			sieve element occlusion protein
Sapur.01G0280900.1	1.20794817	0.29487572	0.14806451	-1.98962	0.04663502	0.06290787	grey	-0.15298428	0.05195922	GO:0008270;GO:0003676	AtSG7560.1		zinc knuckle (CCHC-type) family protein	kinesin light chain
Sapur.01B0247000.2	0.61004533	0.70239403	0.35209251	1.989236	0.04675214	0.06304192	grey	-0.11474034	0.16457497	GO:0005515	AtSG5160.1		Tetratricopeptide repeat (TPR)-like superfamily protein	nodulin MtN21 /EamA-like transporter family protein
Sapur.01G0280600.1	0.95114304	0.50513703	0.25388671	1.988863	0.04688332	0.06381869	grey	-0.15802364	0.06139486	GO:0016021;GO:0016020;GO:0022857	AtSG6180.2	KUP10	K+ uptake permease 10	potassium transporter 11
Sapur.01G0275100.1	0.46767264	-0.71795175	0.36814676	-1.98778	0.04683651	0.06351764	grey	-0.16390473	0.03388956	GO:0071805;GO:0016020;GO:0015079	AtSG3120.1	ACD1-LIKE;PTC52;TIC55-IV	ACD1-like	phosphoinositide A-oxygenase
Sapur.01G0269700.1	788.5968507	0.07638426	0.03841149	1.987657	0.04689662	0.06332074	grey	0.15292293	0.05261634	GO:0055114;GO:0051537;GO:0016491;GO:0010277	AtSG2650.2		Chalcone-flavanone isomerase family protein, putative	chalcone-flavanone isomerase family protein, putative
Sapur.7J4I000.1	446.3631279	0.07606047	0.03826798	1.987389	0.04687617	0.06360628	grey	-0.22884096	0.00595346		AtSG6230.1		Protein of unknown function (DUF247)	NA
Sapur.01G0255500.1	9.00255993	0.39106825	0.14185423	1.9873	0.04689203	0.06381383	grey	0.13183291	0.10753253		AtSG15140.1		Polynucleotidyl transferase, ribonuclease-H-like superfamily protein	exonuclease
Sapur.01G6160400.1	7.95172398	0.52803837	0.26604512	1.98687	0.04694823	0.06360227	grey	0.18731376	0.01863469		AtSG6500.1		Ankyrin repeat family protein	ankyrin repeat protein
Sapur.15W0G07100.1	2.72485821	0.26238253	0.18238452	1.986496	0.04697839	0.06369321	grey	0.12490334	0.11907128	GO:0016887;GO:0005524;GO:0005085;GO:0042626;GO:0016021;GO:0006810	AtSG3940.1	ALS3;ATRA2;TAP2	transporter associated with antigen processing protein 2	transporter associated with antigen processing protein 2
Sapur.01G0255200.1	172.2774864	-0.07705433	0.03877166	-1.98612	0.04700703	0.06374739	grey	-0.19703275	0.01291882		AtSG9240.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.01G0251100.1	0.2375873	1.46030249	0.73512427	1.985395	0.04700567	0.0638549	grey	0.12135258	4.07E-05		AtSG1480.1		S-locus lectin protein kinase family protein	NA
Sapur.01G0280700.1	17.87366466	0.15209704	0.08419124	1.985207	0.04707621	0.06381466	grey	-0.14726289	0.08001207	GO:0006468;GO:0004672	AtSG8280.1	PBSK	PBS-like receptor kinase	NA
Sapur.01G1511300.1	3.00977881	0.41704005	0.20690421	1.985168	0.0471258	0.06380087	grey	0.09650192	0.23924591		AtSG6700.1			NA
Sapur.01G1849400.1	171.2344652	0.11245798	0.06679405	1.985162	0.04726415	0.06380587	grey	0.15329664	0.05488975	GO:0018894	AtSG9420.1	ATTOC64-V;ATTOM64;TOC6	translocon at the outer membrane of chloroplasts 64-V	amidase
Sapur.01G7014000.5	1.99068828	0.45429453	0.24719955	1.983633	0.04736076	0.06407791	grey	-0.10692546	0.17083894	GO:0003676	AtSG9120.1	SUA	suppressor of abi3-1	nucleic acid-binding protein
Sapur.01G0693500.2	1.15846076	-0.6457906	0.32677489	-1.98325	0.04739191	0.06455997	grey	-0.22423758	0.00511267		AtSG8830.1		Cysteinyl-tRNA synthetase, class Ia family protein	cysteinyl-tRNA synthetase
Sapur.01G0280600.1	0.30905781	1.87389343	0.94662269	1.983186	0.04746677	0.06487513	grey	0.24482245	0.00200885		AtSG2280.1			NA
Sapur.01G1119200.1	369.721289	0.17337353	0.08742784	-1.98303	0.04736912	0.06488341	grey	-0.14304619	0.07190135	GO:0006355;GO:0003700	AtSG5190.1		Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.7D8H000.1	88.24114641	0.19167325	0.09664618	1.9829	0.04739524	0.06505166	grey	0.16182916	0.07928868	GO:0005515;GO:0016491	AtSG6600.1		2-oxoglutarate (OGD) and Fe(II)-dependent 2-oxoglutarate superfamily protein	NA
Sapur.01T0G01300.1	8.47299386	-0.46286455	0.20695522	-1.98281	0.04738481	0.06416085	grey	-0.18346037	0.02148374		AtSG6470.1		Plant protein of unknown function (DUF247)	NA
Sapur.01G0280700.1	15.52158893	0.07193333	0.03627157	1.982167	0.04738889	0.06427882	grey	0.14716445	0.06595487	GO:0006355;GO:0005515;GO:0003677	AtSG7370.1		GC-rich sequence DNA binding factor-like protein with Tuftelin interacting domain	tuftelin-interacting like protein
Sapur.09G0964500.1	5.07700839	0.24369216	0.12281934	1.981983	0.04748114	0.06433653	grey	0.17003919	0.03246123	GO:0031179;GO:0015991;GO:0015078	AtSG9080.1	VHA-a3	vacuolar protein ATPase a3	vacuolar protein ATPase a3
Sapur.09G0628800.1	17.72191125	0.15701709	0.08117329	1.981966	0.04750175	0.06461692	grey	0.15238188	0.06446802	GO:0007165	AtSG2080.1	APG	ATP sulfurylase 1	NA
Sapur.08G0150200.1	44.06141003	-0.22491857	0.11363274	-1.98055	0.04764812	0.06459039	grey	-0.14057968	0.07907616	GO:0016020;GO:0008417;GO:0005315	AtSG6570.2	ORFQ2;PHT2;1	phosphate transporter 2;1	inorganic phosphate transporter 2-1
Sapur.09G0115500.1	838.1362728	-0.07470472	0.03748555	-1.9799	0.04774568	0.06462265	grey	-0.19529035	0.0147563		AtSG4950.1		Pectin lyase-like superfamily protein	glycoside hydrolase family 28 protein
Sapur.01G6160100.1	39.23287977	-0.56078384	0.28124955	-1.97986	0.04791804	0.06476622	grey	-0.24484787	0.00497096		AtSG9120.1		Protein of unknown function (DUF674)	NA
Sapur.01B0261200.1	4.36326185	0.50017205	0.25263076	1.979794	0.04779719	0.0645343	grey	0.10747263	0.18016222	GO:0005085;GO:0005231	AtSG6530.1	PINS	Auxin efflux carrier family protein	auxin efflux carrier protein
Sapur.01G0280200.1	0.67864356	1.87389343	0.94662269	1.978186	0.04786269	0.06490471	grey	-0.18973664	0.01789092	GO:0006355;GO:0008990;GO:0003677;GO:0003249	AtSG4540.2	NRM2	nuclear RNA polymerase	DNA-directed RNA polymerase
Sapur.02G1175600.1	75.06015672	0.13700856	0.06945826	1.976792	0.04805117	0.06510884	grey	-0.23491569	0.03121595		AtSG6720.1		dentin sialophosphoprotein-related	hypothetical protein
Sapur.01G6102000.5	2.27060425	-0.10268156	0.05206455	-1.97685	0.04809727	0.06544873	grey	0.01281249	0.82602487	GO:0007165	AtSG5420.1	ATSDS2;CIPK24;SNRK3;11.5	Protein kinase superfamily protein	CBL-interacting kinase
Sapur.01G1654500.1	7.24137607	0.20187422	0.10200729	-1.97598	0.04815695	0.06520158	grey	-0.17390749	0.0034565		AtSG2330.1		Zinc knuckle (CCHC-type) family protein	nucleic acid-binding protein, putative
Sapur.01G1648000.2	0.30057807	0.92922818	0.47033836	-1.97567	0.04818239	0.06535421	grey	-0.27642074	0.00047569	GO:0005524;GO:0003676	AtSG8600.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.01G0260900.1	231.2776431	0.16819725	0.08509169	-1.9755	0.04821229	0.06288384	grey	-0.17297906	0.03452848	GO:0009378;GO:0006310;GO:0006281;GO:0006508;GO:0005524;GO:0004222	AtSG16290.1	EMB2083	AAA-type ATPase family protein	cell division protein FtsH, putative
Sapur.01G6174000.1	7.34264673	0.21388427	0.10830116	1.974724	0.04829964	0.06545184	grey	-0.1350853	0.06067874	GO:0016021	AtSG4470.1		NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.01G0899500.1	233.8706794	0.12295947	0.06227052	1.974643	0.04832588	0.06544744	grey	-0.13412283	0.09396883	GO:0016757	AtSG13250.1	GATL3	galacturonosyltransferase like 3	CAZy family GT8 glycosyltransferase
Sapur.01G6252300.1	10.39439828	0.29768342	0.15090523	1.974409	0.04835289	0.06548348	grey	-0.17130816	0.03193502	GO:0043531	AtSG2550.1		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.01T0G601000.1	2258.210994	0.21068431	0.10676283	-1.97351	0.04843933	0.06570524	grey	-0.16303555	0.04055515	GO:0008152	AtSG2360.1	AtUGT85A2;UGT85A2	UDP-glucosyl transferase 85A2	UDP-glucosyl transferase family protein
Sapur.01G0711000.1	7.17293068	0.29466333	0.14920103	1.973369	0.04854531	0.06559753	grey	-0.17531165	0.03612671	GO:0005524	AtSG4280.1	ATBTAF1;BTAF1;CHR18;CHR	DNA binding;ATP binding;nucleic acid binding;binding;helicases;ATP binding;DNA binding;helicases	TATA-binding protein associated factor
Sapur.09G0511400.1	475.8589844	0.07022553	0.03556855	-1.97317	0.04867573	0.06582282	grey	-0.17924176	0.02468944	GO:0005515;GO:0008270;GO:0005515;GO:0003700;GO:0005515	AtSG4470.1	GATA25;TIFY;ZIM	GATA type zinc finger protein with TIFY domain	GATA transcription factor, putative
Sapur.01G6257600.1	15.17425786	-0.76805463	0.38937591	-1.97255	0.04854656	0.06575581	grey	-0.15908816	0.04662842	GO:0005885;GO:0016021;GO:0016020;GO:0006810;GO:0005215	AtSG2450.1	NRT1.5	nitrate transporter 1.5	peptide transporter, putative
Sapur.09G6114400.1	0.20072979	1.20310971	0.60997687	-1.97246	0.04856855	0.06570882	grey	-0.3042193	3.24E-07	GO:0008033	AtTYR5;PTS	tuzyenkinase;PTS	tuzyenkinase;PTS	cytokinin biosynthesis enzyme;phosphotransferase
Sapur.15W0G17000.4	3.05663619	-0.31112556	0.15775899	-1.97222	0.04864479	0.06758706	grey	-0.14894162	0.06261197	GO:0006511	AtSG4135.1	ASG1;SG21	SKP1-like 21	ubiquitin-protein ligase, putative
Sapur.01G0280300.1	0.38743973	0.53202195	0.30806343	-1.97109	0.04868243	0.06860985	grey	-0.12758007	0.11506385		AtSG5540.1		alpha/beta-Hydrolases superfamily protein	esterase/lipase domain protein, putative
Sapur.01G0152800.1	12.16638623	-0.23974307	0.12161849	-1.97128	0.04882242	0.06589035	grey	-0.16769232	0.03581835		AtSG5840.1		Protein of unknown function (DUF620)	lipase, putative
Sapur.01G6287900.1	1314.15818	0.07835861	0.03988543	1.970546	0.04877816	0.0660701	grey	-0.09513131	0.23994591	GO:0005525	AtUBA5;AT;AABA1F	RAB GTPase homolog A1F	RAB GTPase homolog A1F	Rab-related GTPase family
Sapur.01G0280900.1	15.67945938	0.40452519	0.17488785	-1.97022	0.04882964	0.06645579	grey	-0.17452348	0.03796129	GO:0006425;GO:0005737;GO:0055114;GO:0004819;GO:0000166;GO:0004818;GO:0004831	AtSG3520.1	OVA9	glutamine-tRNA ligase / glutamyl-tRNA synthetase, putative / GlnRS, putative	glutamyl-tRNA synthetase
Sapur.09G0239800.1	20.10566863	-0.81761874	0.08232191	-1.96978	0.0488639	0.06618897	grey	-0.17212543	0.03117331	GO:0016567;GO:0006842	AtSG6920.1		ARM repeat superfamily protein	E3 ubiquitin ligase PUB14, putative
Sapur.01G0147300.1	141.5287921	-0.22008183	0.11178264	-1.96967	0.04888458	0.06621729	grey	-0.12741926	0.17075518		AtSG7040.1	ATBPM6;BPM4	BTB-POZ and MATH domain 4	BTB-POZ and MATH domain 4
Sapur.01B0269800.1	7.6764001	-0.21603103	0.10682391	-1.96866	0.04880679	0.06630127	grey	-0.13718557	0.0863872					NA
Sapur.01G6169700.1	42.58337006	0.15450774	0.07924728	1.963207	0.04894145	0.06721247	grey	-0.14434455	0.08447517		AtSG1591.1			transmembrane protein, putative
Sapur.09G0875200.1	14.21417508	0.16907831	0.08168072	1.960608	0.04884231	0.06214603	grey	-0.13937509	0.08164916	GO:0016567;GO:0006842	AtSG16090.1	ARI2;ATARI2	RING/U-box superfamily protein	E3 ubiquitin-protein ligase ARI2, putative
Sapur.01G1127000.1	0.35242141	0.61665922	0.31662011	1.96824	0.04888903	0.06224464	grey	-0.22766847	0.00812017					hypothetical protein
Sapur.01G0920200.1	6.41008065	-0.33641281	0.17094053	-1.96808	0.04905854	0.06362411	grey	-0.22366487	0.00818517		AtSG12030.1		Disease resistance protein (TIR-NBS-LRR class) family	TIR-NBS-LRR resistance protein
Sapur.09G0801300.1	301.4684014	0.07160854	0.03638433	-1.96723	0.04915638	0.06401005	grey	-0.20973075	0.01299213	GO:0005515	AtMC1;UEV1A	MMZ;EMB3 homologue 1	MMZ;EMB3 homologue 1	ubiquitin-conjugating enzyme E2
Sapur.01G6290300.1	23.32876518	-0.15751243	0.07985429	-1.96698	0.04918595	0.06529261	grey	-0.19131685	0.01638947		AtSG7960.2	UB

Sapur.007G130900.2	0.324667054	-0.80700183	0.422117191	-1.9118	0.055803152	0.075183571	grey	-0.221559086	0.055292301			EMB0674	kinase interacting family protein	SANTA [SANT associated] protein
Sapur.010G293800.3	0.225229862	0.942754871	0.493173363	1.911528	0.055936716	0.07126728	grey	0.275262624	0.00484605			AT5G15140.1	Galactose oxidase/kelch repeat superfamily protein	kelch motif protein
Sapur.002G355800.1	0.538276622	0.553579397	0.368205597	-1.9121	0.055970048	0.07127906	grey	-0.219277115	0.00376564	GO:0005585,GO:0016020,GO:0008810,GO:0005215		AT5G17010.1	Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.012G293400.2	2.120533839	-0.336075484	0.175837215	-1.9109	0.056017204	0.07132884	grey	-0.139923357	0.08049283	GO:0016021		AT4G10430.1	TMPIT-like protein	TMPIT-like protein
Sapur.006G298800.1	6.6L78287	-0.352775385	0.027620214	-1.9107	0.056026899	0.07132283	grey	-0.15392563	0.05424304	GO:0006396,GO:0006334,GO:0000287,GO:0000015		AT5G39160.1	CN-DC	endosc
Sapur.012G258300.1	24.21938738	-0.209286327	0.109535137	-1.91068	0.056046299	0.07136182	grey	-0.145975972	0.07926602			AT5G46295.1		transmembrane protein, putative
Sapur.002G023200.1	3.58485263	0.353391451	0.184970272	1.910531	0.056064868	0.07138748	grey	0.143887049	0.07199344	GO:0006355,GO:0003677		AT1G14680.1	BLH7	BELL-like homeodomain 7
Sapur.019G117100.1	84.32553964	-0.224163071	0.117331713	-1.91006	0.056135752	0.07146409	grey	-0.15128145	0.05214696	GO:0005515		AT5G26570.1		DNA-binding bromodomain-containing protein
Sapur.004G160600.1	0.424888669	0.704361001	0.368865156	1.9095	0.056197046	0.07149991	grey	0.12011932	0.13622569					NA
Sapur.013G092300.1	0.383045534	0.558882019	0.292966405	0.918588314	-0.056217199	0.07153788	grey	-0.29017199	0.00237588			AT5G21280.1		NA
Sapur.010G026000.3	2.364143104	1.012534597	0.530414768	1.908949	0.056287706	0.07163975	grey	0.25885789	0.00166804	GO:0016787,GO:0005975,GO:0004134		AT4G40840.1	DPE2	disproportionating enzyme 2
Sapur.004G151100.1	1.541651517	0.7107628E5	0.394798894	1.908592	0.056314696	0.07166812	grey	-0.15131004	0.05328819			AT1G31200.1		mitotic checkpoint protein
Sapur.003G038500.1	5.934675587	-0.247277793	0.129620763	-1.90847	0.056339908	0.07171491	grey	-0.15388704	0.05188276			AT5G21280.1		NA
Sapur.010G141000.1	7.698812785	0.952868499	0.501298849	1.900736	0.056362324	0.07174254	grey	-0.14329734	0.07292191	GO:0006351,GO:0005634,GO:0003700		AT5G58190.1		Homeodomain-like superfamily protein
Sapur.006G040400.1	17.01242851	-0.257378296	0.133002748	1.908068	0.056382449	0.07179954	grey	0.143284729	0.06203622			AtSFP2_SFP2	seed inhibitor 2	raffinose synthase or seed inhibitor protein, putative
Sapur.011G083900.1	1.888884347	-0.223811325	0.132602771	1.907756	0.056423916	0.07183117	grey	0.132146638	0.04856253			GRI	Sigma-specific Sig1 family protein	Sig1 sigma-specific protein
Sapur.017G027700.1	4.65957511	-0.334989128	0.175624278	-1.90722	0.056491898	0.07192087	grey	-0.15125164	0.05851008?			AT5G40390.1	SIP1	Raffinose synthase family protein	galactinol-sucrose galactosyltransferase
Sapur.159G085500.1	165.3674144	0.112068314	0.058762696	1.907134	0.056552284	0.07203104	grey	0.163925264	0.03396584	GO:0004648,GO:0004672		AT4G26740.1	ATCPK20,CDPK14,CPK30	calcium-dependent protein kinase 30	calcium-dependent kinase
Sapur.008G171100.1	1274.613127	0.750665264	0.393692264	1.906592	0.056572625	0.07206054	grey	-0.12238826	0.17382217			AT4G14570.1		Bax inhibitor-1 family protein	transmembrane BAX inhibitor motif protein
Sapur.010G202000.4	7.46882283	0.216228889	0.113453712	1.906759	0.056551801	0.07209129	grey	-0.18202119	0.08432492	GO:0003676		AT5G13190.1	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif (RRM) superfamily protein
Sapur.7S04880.1	1.011082804	0.458880215	0.241868148	1.90602	0.056611441	0.07217135	grey	-0.19464151	0.05753115	GO:0003277,GO:0046983		AT4G21751.1	BED zinc finger ,MAT family dimerization domain	BED zinc finger ,MAT family dimerization domain
Sapur.019G041700.1	173.8727179	0.275210201	0.039688834	1.905882	0.056665547	0.07231687	grey	0.109609024	0.17182339			AT5G16660.1		transmembrane protein, putative
Sapur.006G045600.1	159.7507554	0.260448939	0.135684724	1.90416	0.056889081	0.07243042	grey	0.111881873	0.09718022			AT3G04860.1	ATPGIP1,PGIP1	polygalacturonase inhibiting protein 1	polygalacturonase-inhibiting protein
Sapur.007G065700.10	1.404440807	0.44660842	0.236121068	1.904144	0.056895485	0.07243163	grey	0.164099971	0.04000759			AT5G50120.1			retrotrans
Sapur.013G081100.1	305.197353	0.854863293	0.450872219	1.903968	0.056907218	0.07245767	grey	0.154342236	0.05362039	GO:0046872,GO:0030001		AT4G19520.1		Heavy metal transport/detoxification superfamily protein	heavy metal associated domain protein
Sapur.010G178500.1	20.14542009	-0.360741907	0.189517628	-1.90347	0.056978703	0.07247123	grey	-0.15454583	0.05232852	GO:0003677,GO:0009725,GO:0006355,GO:0005634		AT4G30080.1	ARF16	auxin response factor 16	auxin response factor, putative
Sapur.006G147900.1	37.31316738	0.318949258	0.192230541	1.90341	0.056989719	0.07255532	grey	0.17421159	0.02908895	GO:0006413,GO:0003743		AT3G24060.1		Translation initiation factor 3 protein	translation initiation factor if-3
Sapur.016G012900.1	0.275931767	0.502427471	0.261154061	1.903135	0.057029239	0.07269521	grey	-0.27182035	0.00557886						NA
Sapur.003G060800.1	3.131410198	-0.317164623	0.166654772	-1.90312	0.057029425	0.07269213	grey	-0.11842107	0.13691159			AT3G14940.1	GRAS family transcription factor	GRAS family transcription factor	nodulation signaling pathway-like protein
Sapur.017G038900.1	2.39802019	0.346122942	0.164483309	-1.90307	0.057030531	0.07268581	grey	-0.11881138	0.08286344			AT3G04330.1			hypothetical protein
Sapur.001G100600.1	0.6021053	-0.932069142	0.489782684	-1.90299	0.057042497	0.07271285	grey	-0.12679833	0.11368389			AT3G22142.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein		hydrophobic seed protein
Sapur.002G300900.1	135.7124964	0.115684888	0.060809845	-1.90241	0.057174151	0.07314776	grey	-0.13944936	0.08153856			AT5T5462.1	STH2	salt tolerance homolog 2 family protein	salt-tolerance protein, putative
Sapur.018G046200.1	8.569953448	-0.221082349	0.116230757	-1.90227	0.057153578	0.07316458	grey	-0.13227509	0.08656431	GO:0016567,GO:0008842		AT5G36080.1		RING/U-box superfamily family protein	zinc finger protein, putative
Sapur.004G144500.15	1.232249914	-0.679406612	0.351864683	-1.90221	0.057243232	0.07318404	grey	-0.14092828	0.07829682			AT5G45160.1	SIR02	zinc finger (C3HC4-type RING finger) family protein	ubiquitin-activating protein-like protein
Sapur.007G063300.1	0.264616057	0.704475921	0.370343439	-1.90222	0.057314967	0.07278404	grey	-0.31706763	5.21E-05						NA
Sapur.016G179700.1	1027.949659	0.651297900	0.322202097	0.904257175	0.057337168	0.07285025	grey	-0.18093118	0.03368447	GO:0055114,GO:0016491,GO:0008270		AT3G19450.1	ATCAD4,CAD,CAD_C,CAD4	GroES-like zinc-binding alcohol dehydrogenase family protein	cinnamyl alcohol dehydrogenase
Sapur.013G304600.1	0.26683774	1.164585811	0.613184687	1.90071	0.057340024	0.07295005	grey	0.25439161	0.00103731			AT5G27620.1		glycosyl hydrolase-related protein	galactose oxidase
Sapur.014G276900.4	3.890218649	0.273051561	0.143573801	1.900548	0.057362236	0.07301828	grey	0.13432505	0.09409435	GO:0005515		AT4G17480.2	ATX3,SDG14	SET domain protein 14	histone-lysine N-methyltransferase ATX3, putative
Sapur.003G187000.1	1.491954182	0.404876306	0.212609776	-1.89994	0.057412291	0.07321591	grey	-0.11849114	0.18882741			AT5G59570.1		C2H2 and C3HC4-type RING finger family protein	zinc finger protein
Sapur.017G018200.2	1.03317581	-0.471881512	0.248435543	-1.89988	0.057489905	0.07329682	grey	0.12545681	0.11742347	GO:0006355		AT5G59470.1		Fer-red impaired response (FAR1) family protein	Fer-red impaired responsive family protein
Sapur.002G133800.1	1.984727171	-0.304488891	0.18987522	-1.89979	0.057512537	0.07347985	grey	-0.14319739B	0.07609113	GO:0003968		AT3G19910.1		RNA-dependent RNA polymerase family protein	RNA-dependent RNA polymerase
Sapur.012G052500.1	23.30782311	0.326553211	0.1715124	1.896829	0.057580566	0.07265519	grey	0.18547142	0.01990413						NA
Sapur.005G201300.1	30.13787670	-0.347388884	0.183064184	1.89685	0.057727234	0.07387204	grey	-0.22997216	0.02732148	GO:0004648,GO:0005524,GO:0004672		AT5G08680.1	RLK1	receptor-like protein kinase 1	leucine-rich repeat transmembrane protein kinase
Sapur.018G093500.1	0.560257576	0.692565133	0.365188366	1.89647	0.057897871	0.07709365	grey	0.130102213	0.09318412	GO:0005515		AT4G27190.1	ARIA,P15,RLP15	receptor-like protein 15	receptor-like protein kinase
Sapur.004G081600.1	0.331932969	0.464783016	0.261956683	1.896164	0.057897237	0.07760264	grey	0.17367707	0.03604174	GO:0017179,GO:0009058		AT4G29120.1	APL3	Glucose-1-phosphate adenylyltransferase family protein	glucose-1-phosphate adenylyltransferase
Sapur.017G027300.1	0.237836539	1.175053639	0.619937204	1.89544	0.058034162	0.07885972	grey	0.27725893	0.00439166			AT2G24670.1		Domain of unknown function (DUF213)	DUF213 domain protein
Sapur.018G073100.1	18.13211565	0.895809164	0.4728474	-1.8945	0.058182249	0.07896938	grey	-0.2237573?	0.00846296			AT2G04130.1	ATOSM34,OSM34	osmotin 34	pathogenesis-related thaumatin-like protein, putative
Sapur.010G050500.1	-0.056203909	0.495457363	0.262291656	-1.89418	0.058255005	0.07935468	grey	-0.16455074	0.03969964	GO:0016887,GO:0005524		AT1G10080.1	ATMRP3,MRP3	multidrug resistance-associated protein 3	multidrug resistance protein ABC transporter family protein
Sapur.018G051100.1	1258.359447	-0.661796465	0.332460569	-1.89327	0.058321968	0.0263527	grey	-0.15341895	0.05267996	GO:0005096		AT5G13150.1	NIG	NSP (nuclear shuttle protein)-interacting GTPase	Arf-GTPase activating protein, putative
Sapur.001G194000.1	98.12131888	0.205159756	0.104275221	-1.89317	0.058331665	0.078277	grey	-0.15918884	0.04628016	GO:0005768,GO:0008152		AT5G46690.1		U19-Glycosylation enzyme family protein	NA
Sapur.T174400.1	0.36810989	-1.775730409	0.902137381	-1.89309	0.058345519	0.07829755	grey	-0.21995702	0.05539325						NA
Sapur.002G178200.2	2.82367809	0.3255145	0.171696961	1.893368	0.058375415	0.07832487	grey	-0.17835264	0.02516415	GO:0006629		AT4G10955.1		alpha/beta-hydrolases superfamily protein	triacylglycerol lipase
Sapur.001G122600.1	1.06479665	0.632862882	0.334352656	1.892801	0.058384402	0.07833768	grey	0.13945773	0.08145667	GO:0008270,GO:0006355,GO:0005634,GO:0004402,GO:0003712		AT5G05690.1	BT3	BTB and TAZ domain protein 3	BTB and TAZ domain protein
Sapur.018G069600.1	86.06423293	0.268109888	0.142000429	1.892648	0.058397203	0.07847201	grey	-0.18488816	0.03054569	GO:0005524,GO:0016553		AT2G27480.1		6-hexo-oxotetrahydrobiopterin triphosphate hydrolases superfamily protein	AAA-type ATPase family protein
Sapur.001G122200.9	0.363995655	0.760782348	0.402335563	-1.89092	0.058435445	0.07866157	grey	-0.16301042	0.0432396	GO:0003676		AT4G03110.1	AtRBP-DR1,RBP-DR1	RNA-binding protein-defense related 1	RNA recognition motif 3 in CUGBP etav-like protein CELF-1
Sapur.003G194900.1	0.327926394	0.553429401	0.293159031	1.89048	0.058439975	0.07870357	grey	-0.15801501	0.06809075	GO:0016020,GO:0004970		AT2G17720.1	GLR2.7,GLR2.7	glutamate receptor 2.7	glutamate-gated kainate-type ion channel receptor subunit gluR; protein
Sapur.002G102000.1	6.233415892	-0.263101843	0.139200458	-1.89009	0.058545493	0.07880223	grey	-0.14397593	0.07797778			AT4G25207.2		Remorin family protein	remorin
Sapur.001G081600.1	226.8852717	0.190018971	0.100874644	-1.89006	0.058570195	0.07882033	grey	-0.17681506	0.03687959			AT4G39310.1,MYB101D	myb domain protein 103	myb domain protein 103	
Sapur.018G118500.1	-4.020410515	0.314884476	0.166341189	-1.89006	0.058572769	0.07882109	grey	-0.17857957	0.02575088			AT3G25290.1			hypothetical protein
Sapur.012G048400.1	589.665685	0.131111294	0.069371171	-1.89	0.058578381	0.07890955	grey	-0.13226413	0.09872092	GO:0046872,GO:0006508,GO:0004176		AT5G18660.1		zinc finger (C3HC4-type RING finger) family protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.001G141600.5	1.468955123	0.776000217	0.411068163	-1.8985	0.058637908	0.07907021	grey	-0.16491297	0.03008761			AT4G27340.1			transglutaminase family protein
Sapur.002G009400.2	2.302609847	0.356957607	0.190081139	1.889084	0.058805138	0.07896089	grey	0.15342871	0.05059315			AT5G02590.1			hypothetical protein
Sapur.018G040800.2	0.112727477	0.624224413	0.332457622	-1.88803	0.058884754	0.07936887	grey	-0.12958215	0.11595056	GO:0016020,GO:0008810,GO:0015215		AT5G18910.1	ATNIM2,NIP1;2,NIUM2	NOD26-like intrinsic protein 1;2	aquaporin NIP1;2, putative
Sapur.018G085500.1	5.691928859	-0.278308665	0.147363754	-1.88854	0.058853928	0.07950988	grey	-0.16398873	0.04062485			AT5G03150.1	JKD	C2H2-like zinc finger protein	zinc finger protein
Sapur.018G080500.1	6.453864043	-0.275236274	0.146056417	-1.88847	0.058907018	0.07951461	grey	-0.17602856	0.02740379			AT5G02120.1		Homeobox protein 2 family protein	zinc finger (C2H2 type) protein, putative
Sapur.004G067000.2	9.003957567	0.518955613	0.274601679	1.886965	0.059164908	0.07932044	grey	0.15392851	0.01837068	GO:0030976,GO:0003824,GO:0003287		AT1G73880.1		Thiamine pyrophosphate dependent pyruvate decarboxylase family protein	2-hydroxyphytanoyl-CoA lyase
Sapur.018G066300.1	0.249464153	0.696236301	0.368772886	1.886328	0.059216882	0.07963888	grey	0.09298531	0.07030864	GO:0055114,GO:0016740,GO:0005634,GO:0003677		AT2G35170.1	CHD3,CHR5,GYM,PKL,SSL2	chromatin remodeling factor CHD3 (PICKLE)	chromatin-remodeling factor CHD3
Sapur.005G113900.2	1.697763044	-0.419892882	0.222684686	-1.88573	0.059331204	0.07919553	grey	-0.09541667	0.23455637	GO:0051082,GO:0031072		AT1G[illegible]	ATJ1	DNAJ heat shock family protein	chaperone protein DnaJ
Sapur.013G008800.2	0.316541071	-0.802320188	0.453636724	-1.88496	0.059463961	0.07927188	grey	-0.09463408	0.23977635	GO:0003787		AT5G55910.1		Pectinacetylesterase family protein	pectin acetylesterase, putative
Sapur.017G031800.1	106.7898134	0.204855156	0.102956647	-1.88484	0.059488006	0.07947064	grey	-0.11827243	0.08724403	GO:0003723		AT4G34590.1	HEN4	RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein K, putative
Sapur.007G130200.1	7.559315589	0.586688892	0.311378841	1.884743	0.059646587	0.07970461	grey	0.16527876	0.03580624						transmembrane protein, putative
Sapur.016G192600.1	155.7928854	0.166027846	0.088125271	-1.88443	0.059537075	0.07976101	grey	-0.16002147	0.04601784			AC14	ALC-interacting protein 1	ALC-interacting protein 1	
Sapur.003G054000.6	1.824773635	-0.403804087	0.214348884	1.88443	0.059542991	0.07980464	grey	-0.03127554	0.60026792	GO:0005634		AT1G74380.1	NDF1		NA
Sapur.003G191600.1	28.28026272	0.170028927	0.090264272	1.884649	0.059622478	0.07989354	grey	0.15302102	0.05707791			AT3G22120.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.017G110200.1	0.241158071	0.932382717	0.495100539	1.883219	0.059670702	0.07966751	grey	0.209457092	0.08848719	GO:0006629		AT2G26580.1	PLA IIA,PLA2A,PLP2	phospholipase A 2A	patatin-like phospholipase
Sapur.003G060800.2	0.217564693	0.772963151	0.566678564	1.883002	0.059680641	0.07992266	grey	0.07984818	0.12017619	GO:0016020,GO:0004970		AT4G18[illegible]	ATGLR3.1,GLR3.1	glutamate receptor	glutamate receptor
Sapur.016G221700.1	344.0094692	-0.152925257	0.084063044	-1.88305	0.059683041	0.07990226	grey	-0.13580197	0.08991264			AT3G59980.1	EDA7	embryo sac development arrest 7	NA
Sapur.004G201700.1	87.72581691	0.165082256	0.087750738	1.883326	0.059767777	0.08021271	grey	0.13286607	0.15938388	GO:0005635,GO:0003700		AT4G24210.1	ATERF-6,ATERF9,ERF9	erf domain protein 9	ethylene-responsive element-binding protein
Sapur.T038400.1	431.6413865	0.152609563	0.11207662	1.882008	0.059834968	0.0801759	grey	0.18469327	0.03775575	GO:0016773,GO:0005515		AT5G44190.1		Phosphatidylinositol 3- and 4-kinase family protein with FAT domain	NA
Sapur.006G199000.1	2.852817012	0.318895573	0.169545136	1.881524	0.059900663	0.08260676	grey	0.12128424	0.13244852	GO:0005515		AT2G18160.1	ATPRIA,A ATPRTASE,RPA1A	replication protein A 1A	DUF829 domain protein
Sapur.005G140200.1	7.585292097	0.243520327	0.129464679	1.88107	0.059922112	0.08319754	grey	0.19266171	0.01466125	GO:0016567,GO:0004842		AT3G27310.1		plant U-box 26	ubiquitin-protein ligase, putative
Sapur.159G011800.1	59.74217987	-0.625024803	0.332628874	-1.87905	0.06023832	0.08096755	grey	-0.20717163	0.09234961			AT5G55150.1	ATPP2-A10,PP2-A10	phloem protein 2-A10	phloem protein
Sapur.016G080300.6	4.403718172	-0.267861123	0.142607422	-1.87849	0.060293032	0.08204445	grey	0.28765532	0.00205862			AT5G60620.1		Homeobox-leucine zipper superfamily protein	MYB transcription factor
Sapur.019G070000.2	1.5290478	-0.421891067	0.210845112	-1.8781	0.060347511	0.08263272	grey	-0.07884648	0.37697178	GO:0016597,GO:0005515,GO:0055114,GO:0005829,GO:0050661,GO:0016491		AT4G19730.2	AK-HSDH,AK-HSDH II	aspartokinase/homoserine dehydrogenase II	aspartokinase/homoserine dehydrogenase
Sapur.018G038300.1	24.21128875	-0.182464661	0.07261155	-1.87806	0.060372749	0.08366675	grey	0.18187245	0.03320286			AT1G07240.1			hypothetical protein
Sapur.004G090900.1	77.31774904	-0.12615524	0.067179905	-1.87796	0.060385957	0.08381429	grey	-0.16306659	0.04129118			AT3G15760.1		Protein of unknown function (DUF3445)	AR781, yeast pheromone receptor-like protein5,N2C protein
Sapur.003G173000.1	16.9423739	-0.350270001	0.187	-1.87711	0.060469953	0.08503687	grey	-0.15543855	0.05982441	GO:0055114,GO:0016614,GO:0050660		AT3G09360.1		Glucose-methanol-choline dehydrogenase family protein	NA
Sapur.013G072300.1	531.4223836	0.051157896	0.027225541	1.877179	0.060493575	0.08510731	grey	0.13815119	0.13988886	GO:0055114,GO:0016491		AT4G17420.1	ATNTRA,NTR2,NTRA	NADPH-dependent thioredoxin reductase A	thioredoxin-disulfide reductase
Sapur.007G115100.1	0.690667977	0.441759456	0.341920473	-1.87693	0.060528225	0.08528854	grey	-0.12954518	0.15586454	GO:0006355		AT4G32280.1		Far-red impaired responsive (FAR1) family protein	Far-red impaired responsive-like protein, putative
Sapur.006G148700.1	5.413015254	-0.225764486	0.120332466	-1.87623	0.060533936	0.08538234	grey	-0.10613316	0.18548778			AT5G44190.1		Leucine-rich repeat protein family protein	NA
Sapur.004G089700.2	3.118873536	0.323195863	0.172261447	1.876194	0.06062867	0.08186795	grey	0.11777486	0.14181027			AT5G16595.1		Protein of unknown function DUF829, transmembrane S3	DUF829 domain protein
Sapur.004G147000.1	117.1557666	0.087809285	0.04680905	-1.8759	0.060683879	0.08213334	grey	-0.16098955	0.04398787			AT3G04310.1			NA
Sapur.002G027700.3	14.26872208	0.176817757	0.094276832	1.875517	0.060731697	0.08310149	grey	-0.00634368	0.93695887	GO:0007034		AT5G35910.1	VPS2.3	vacuolar protein sorting-associated protein 2.3	charged multivesicular body protein 2a, putative
Sapur.004G054500.1	25.38637819	0.168241142	0.08971687	-1.87525	0.060732128	0.08347912	grey	-0.11657577	0.09734197			AT2G25120.1		dentin sialophosphoprotein-related	NA
Sapur.016G227700.4	1.446584554	-0.464844717	0.237281258	-1.87476	0.060826151	0.08431456	grey	-0.09057612	0.24120387	GO:0006468,GO:0005524,GO:0004672,GO:0005515		AT5G15344.1	SPK1	SPK1-related 3	ubiquitin ligase cop1, putative
Sapur.004G182300.1	3.860282617	0.364689827	0.194763411	0.868047647	0.060839752	0.08437441	grey	0.24188184	0.02263162	GO:0055114,GO:0020037,GO:0046872,GO:0005506		AT3G07730.1	CYP71A13	cytochrome P450 family protein	cytochrome P450 family protein
Sapur.001G061000.2	0.602658127	-0.664517564	0.354394842	-1.8743	0.060888764	0.08509683	grey	-0.16494821	0.03897543	GO:0005085,GO:0016020,GO:0008810,GO:0051171,GO:0003333		AT4G13620.1		Amino acid permease family protein	amino acid transporter, putative
Sapur.T032400.1	0.258809009	-0.321583874	0.184988356	-1.87428	0.060893466	0.08513451	grey	-0.23733468	0.02738769			AT1G44640.1		2-oxoglutarate (KG)-dependent dioxygenase family protein	2-oxoglutarate
Sapur.010G022000.1	322.0858873	0.212380695	0.113357441	1.873549	0.060892646	0.08516133	grey	0.14878381	0.06293479	GO:0055114,GO:0020037,GO:0016705,GO:0005506		AT4G26320.1	CYP736B	cytochrome P450, family 71, subfamily B, polypeptide 36	cytochrome P450 family protein
Sapur.017G081600.1	45.28642091	0.210432526	0.112362331	1.873803	0.06109558	0.08175686	grey	0.17267941	0.03057156	GO:0043531		AT4G14640.1		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.011G012000.1	1.468063621	-0.51108861	0.272023053	-1.87365	0.061137395	0.08180495	grey	-0.17763869	0.03038558			AT5G53520.1	IBR1,SDR4	indole-3-butyric acid response 1	short-chain dehydrogenase/reductase family protein
Sapur.016G112900.1	83.78313987	0.168003956	0.090081414	-1.87168	0.061250316	0.08376079	grey	-0.13501586	0.03127419			AT5G15680.1		NAD(P)-binding Rossmann-fold superfamily protein	Tasselseed-like short-chain dehydrogenase/reductase, putative
Sapur.T015400.1	-0.604873674	0.4115372B6	0.220188238	-1.87068	0.061292	0.08216101	grey	-0.22395016	0.0362015			AT3G45610.1	CLE25	CLAVATA3/ESR-related 25	NA
Sapur.T025800.1	688.4546136	0.148537416	0.079416311	1.870411	0.061426739	0.08202223	grey	0.15035353	0.01249789	GO:0006468,GO:0004672		AT3G10070.1		Protein kinase superfamily protein	casein kinase II alpha subunit
Sapur.005G131800.1	217.5791177	0.516880323	0.2852244	-1.87014	0.061428363	0.08224136	grey	-0.14762252	0.06312583	GO:0055114,GO:0020037,GO:0008379,GO:0004601		AT3G17650.1		Peroxidase superfamily protein	peroxidase
Sapur.005G094500.1	16.97673145	-0.233705402	0.124968635	-1.87011	0.061468202	0.08244399	grey	-0.15847128	0.04979256						hypothetical protein
Sapur.016G280300.1	2.031473835	-0.305042225	0.163386824	-1.87009	0.061508326	0.08250093	grey	-0.19744762	0.01437809			AT5G6485.1		Domain of unknown function (DUF3421)	NA
Sapur.019G058200.1	0.923772581	0.456423338	0.246233444	1.869695	0.061526193	0.08211202	grey	0.22391245	0.0050976			AT1G70120.1	ATCBM1,ATRPO1,HET,XPO	exportin 1A	NA
Sapur.017G099800.2	3.079475518	0.385385486	0.185022488	1.869497	0.061553646	0.08245386	grey	0.13174239	0.10239609	GO:0005515		AT1G27420.1	transducin family protein / WD-40 repeat family protein	transducin family protein	
Sapur.003G142500.1	0.707975851	0.401654669	0.215779408	1.869392	0.061572248	0.08267086	grey	-0.16457257	0.03954724	GO:0016491		AT3G53130.1	AT5G53,5G53	RS domain-containing protein / RS zinc finger domain-containing protein-related	NA
Sapur.013G071500.1	0.670768344	0.59245937	0.317145331	1.868101	0.061748056	0.08298795	grey	0.1718655	0.01339658			AT5G17910.2			transmembrane protein, putative
Sapur.005G193200.1	2.902161553	0.354187504	0.189284933	1.867	0.06175185	0.08300476	grey	-0.13348888	0.09157089	GO:0008173,GO:0003196,GO:0003723		AT4G18480.1		tRNA/rRNA methyltransferase (Spou1) family protein	Trm9 family RNA methyltransferase
Sapur.019G140500.1	0.708582926	0.613775684	0.328605659	1.867818	0.061787452	0.08266741	grey	0.15181363	0.05381109						transmembrane protein, putative
Sapur.018G050500.1	3.360656669	0.422318883	0.2260829	1.867	0.061795	0.08271	grey	0.18312218	0.03291787	GO:0005515		AT4G07890.1	AtRLP7,RLP7	receptor-like protein 7	NA
Sapur.016G142900.1	386.8713449	0.060191769	0.032236127	-1.8672	0.061872236	0.08251888	grey	-0.14688613	0.06676519			AT5G07565.1		Protein of unknown function (DUF2755)	DIV and RAD interacting factor 2, putative
Sapur.016G232200.1	2.810086267	0.751588304	0.403164	1.86719	0.061875016	0.08280475	grey	0.16187916	0.06362371			AT5G56640.1			hypothetical protein
Sapur.010G095000.1	21.13166149	0.153679708	0.082307969	1.867133	0.061888005	0.08275023	grey	0.11401563	0.15125005	GO:0022900,GO:0016021		AT1G60260.1		calmodulin-binding family protein	NA
Sapur.006G144400.4	1.968513262	0.346234349	0.191522664	1.866855	0.061966895	0.08306643	grey	0.34441293	9.36E-06	GO:0048015,GO:0016301		AT4M4K ALPHA	Phosphatidylinositol 3- and 4-kinase family protein	phosphatidylinositol 4-kinase	phosphatidylinositol 4-kinase
Sapur.006G118800.1	26.72058858	0.340857333	0.182712689	1.865537	0.062106131	0.08304754	grey	0.14034086	0.07957744	GO:0055114,GO:0020037,GO:0016705,GO:0005506		AT4G14620.1	CYP72A8	cytochrome P450, family 72, subfamily A, polypeptide 8	cytochrome P450 family protein
Sapur.012G081200.1	1.017076705	0.452319869	0.242473318	1.865442	0.062119542	0.08362128	grey	0.14255871	0.07993651			AT1G14770.1		Nodulin MtN3 family protein	bidirectional sugar transporter SWEET2
Sapur.008G111200.1	580.2684047	0.153197438	0.082171254	1.864185	0.062441366	0.08480974	grey	-0.17476709	0.03918413	GO:0005385,GO:0046873,GO:0003017,GO:0016020		AT1G80100.1	IAR1	IAR1 protein	metal cation transporter, ZIP family protein
Sapur.002G060900.1	6.805724585	0.284769388	0.15294158	1.861949	0.062630311	0.08704816	grey	0.14079924	0.07859687	GO:0004648,GO:0004672		AT4

Sapur.006G007100.2	0.26601633	0.80969874	0.645452193	1.817921	0.060076236	0.09182757	grey	0.17450524	0.02882754				hypothetical protein
Sapur.016G135100.2	2.42605846	0.32513734	0.178878491	1.817645	0.06591841	0.09191542	grey	0.17491876	0.02844176	GO:0016192,GO:0006886	ATG2G5170.1	ATVPS11,VPS11	vacuolar protein sorting-associated-like protein
Sapur.013G227400.1	7.49879993	0.27670751	0.152325165	1.81607	0.06021239	0.09264477	grey	0.14510455	0.02809759				NA
Sapur.016G010100.1	1.86087258	0.41516891	0.228519889	1.816546	0.06026658	0.09237803	grey	0.11329197	0.16124299		ATG6457G.1		Protein of unknown function (DUF594)
Sapur.015G010500.1	0.27461784	1.291885491	0.711532837	1.81047	0.06001722	0.09264734	grey	0.31928231	0.03204821	GO:0055114,GO:0030037,GO:0006879,GO:0004601	ATG2G3180.1		Peroxidase superfamily protein
Sapur.005G190600.1	4.07421537	0.24577469	0.135358439	-1.81572	0.06941397	0.09289579	grey	-0.29450102	0.00018129	GO:0006468,GO:0005234,GO:0004672	ATG2G3452.1		Protein kinase superfamily protein
Sapur.016G270300.1	56.04062472	0.49039365	0.240631847	1.815625	0.06947781	0.09204447	grey	0.19637912	0.01708896		ATG2G2380.1		Copia-like polyprotein/retrotransposon
Sapur.T041800.1	4.35205362	0.24962015	0.137515145	-1.8152	0.06949341	0.09278875	grey	-0.11947486	0.13677356		ATG3845G.1	CLE25	CLAVATA/ESR-RELATED 25
Sapur.001G173700.1	1762.70509	0.08115045	0.044725348	1.814431	0.06961148	0.09254047	grey	0.12325093	0.13043443		ATG3G0160.1		Thioesterase superfamily protein
Sapur.003G078000.2	30.38615595	0.36397554	0.072735311	1.81365	0.06968627	0.09243439	grey	0.12902655	0.13022469		ATG2G0250.1		receptor serine/threonine kinase, putative
Sapur.15WG035800.1	0.18819544	1.75368029	0.647815194	1.813938	0.06962716	0.09264339	grey	0.32368551	0.3 E-05	GO:0016757	ATG3B170.1		Glycosyltransferase family 61 protein
Sapur.J003G147400.1	2.86503463	0.26230604	0.15374528	1.813881	0.06965163	0.09268721	grey	0.02727222	0.78712835		ATG2G3463.1		Protein of unknown function (DUF239)
Sapur.018G117800.3	4.96108377	0.29807404	0.164880397	1.81265	0.06985866	0.09286984	grey	0.13861354	0.08336131	GO:0006468,GO:0006472	ATG2G7180.1		Protein kinase superfamily protein
Sapur.013G230800.1	207.1618231	0.07810655	0.043119	1.812	0.06869817	0.09288064	grey	0.10410485	0.09219344	GO:0005515	ATE3F3A-1,ATTF3A1,EIF3A,I		eukaryotic translation initiation factor 3A
Sapur.004G137300.1	0.27033723	1.22416263	0.691043782	1.81263	0.06889275	0.09289758	grey	0.19328675	0.01598994		ATA3G1703.1		Arabidopsis protein of unknown function (DUF241)
Sapur.006G300400.2	14.51353927	0.42348924	0.233869524	1.812609	0.06903455	0.09318393	grey	-0.04855992	0.53123918	GO:0009073,GO:0004107	EMB6144		chorismate synthase, putative / 5-enolpiruvylshikimate-3-phosphate phospholyase, putative
Sapur.001G004400.1	144.9688894	0.48279627	0.266543898	1.81107	0.07013029	0.09385512	grey	0.18685276	0.03915209	GO:0055114,GO:0051537,GO:0016491,GO:0010277	ATE4G5650.1	ACD1-LIKE,PTC52,TIC55-IV	ACD1-like
Sapur.017G048400.1	0.34496675E	-0.60387518	0.367978841	-1.80954	0.07016448	0.09349562	grey	-0.23208358	0.03446721				NA
Sapur.015G260800.1	809.2295409	0.11482897	0.063439056	1.80912	0.07043216	0.09357965	grey	0.05618135	0.23889562		ATG7370.2		keratinocytes-associated protein
Sapur.001G248100.2	0.2431161E	-1.05977618	0.585807618	-1.80909	0.07047602	0.09382921	grey	-0.31897504	4.67E-05		ATG3I4090.1		hypothetical protein
Sapur.T107000.1	0.83072293	0.17383809	0.095077375	-1.80885	0.07064849	0.09360695	grey	-0.12602661	0.17203706				NA
Sapur.003G098500.1	29.26934485	0.80151163	0.443126122	1.808766	0.07087336	0.09361435	grey	0.16184361	0.04279157		ATG6I4160.1		Disease resistance-responsive (dirigent-like protein) family protein
Sapur.002G250600.1	136.9359968	0.08715568	0.048206382	1.807844	0.07092857	0.09383271	grey	0.11861015	0.13882039		ATG2G5120.1		Calcium-binding mitochondrial carrier protein
Sapur.007G035500.1	48.71122711	0.37800485	0.209260271	1.80638	0.07185066	0.09412971	grey	0.14768843	0.06493782		ATG2G6320.1	ATMES1,MES1	methyl esterase 1
Sapur.004G231300.1	405.4418619	0.07830254	0.043382746	1.805578	0.07189416	0.09286424	grey	0.04128746	0.23526366		ATG4G0280.1		postsynaptic protein-related
Sapur.012G037100.1	16.46709804	0.27409703	0.152948888	1.80556	0.07198543	0.09287083	grey	-0.14064642	0.07892033		ATG3I8260.1		Reticulon family protein
Sapur.009G268800.3	1.87307719	0.36138502	0.200156016	-1.80552	0.07199496	0.09291177	grey	-0.06304265	0.43281129		ATG4G6880.1	MEE13	myosin heavy chain-like protein
Sapur.T187700.1	116.1251896	0.45051127	0.2497897	1.806047	0.07209913	0.09405117	grey	0.30016634	0.00519755				hypothetical protein
Sapur.015G129400.1	4.90620142	0.25320697	0.141292602	-1.80523	0.07210222	0.09432288	grey	-0.15384169	0.06017612	GO:0055114,GO:0016614,GO:0050660	ATG4I4185.1		Glucose-methanol-choline (GMC) oxidoreductase family protein
Sapur.015WG008400.1	61.06352904	0.11488397	0.063594455	1.805225	0.07215705	0.09430954	grey	0.14227604	0.07548349	GO:0016757,GO:0008276,GO:0005635,GO:0006352	ATG3I3230.1		Cyclin-like F-box protein
Sapur.010G023600.1	298.2269904	0.07268274	0.04030388	1.804545	0.07314855	0.09478358	grey	0.12328863	0.10223301	GO:0016020,GO:0006487,GO:0003830	ATG1I2980.1		beta-1,6-N-acetylglucosaminyltransferase family protein
Sapur.017G300600.1	55.57605717	0.46028832	0.275276651	1.804115	0.07319105	0.09450882	grey	0.16778248	0.04036267	GO:0005515,GO:0045531	ATG4I4600.1		LRR and NB-ARC domains-containing disease resistance protein
Sapur.018G033300.1	69.1206505	0.18545477	0.10507633	1.804105	0.07324926	0.09452488	grey	-0.14429308	0.07138888				NA
Sapur.007G080200.1	36.28708884	0.21529481	0.1195425	1.804008	0.07329245	0.09478757	grey	-0.14767829	0.06489447				hypothetical protein
Sapur.010G039700.1	0.54882484	0.60010742	0.332663409	-1.80393	0.07334697	0.09450461	grey	-0.21065657	0.08080908		ATG3I2200.1		Uncharacterized protein family (UPF0497)
Sapur.006G231500.1	2.80709669	0.48408907	0.269338	1.803266	0.07368397	0.09480997	grey	0.12372595	0.10968866		ATG4G0180.1		hypothetical protein
Sapur.004G226400.1	34.75450641	-0.46510452	0.257939539	-1.80321	0.07373553	0.09473976	grey	-0.16444435	0.03958475	GO:0016829,GO:0010333,GO:0008152,GO:0003287	ATG6G1120.1	GES,TPS04,TPS4	(E)-nerolidol/(3E)-(E)-geranyl linalool synthase
Sapur.010G279400.2	24.4282795	0.65138859	0.090490451	-1.80282	0.07416536	0.09481093	grey	-0.13246634	0.09848624	GO:0043169,GO:0005975,GO:0003824,GO:0005509,GO:0004556	ATG6B832.1	ABH5,ATABH5	alpha-amylase-like 3
Sapur.007G078000.1	1.61964819	0.29845153	0.207287224	1.802584	0.07435648	0.09485555	grey	0.15099843	0.09061405		ATG8B520.1		Duplicated homologous-like superfamily protein
Sapur.006G139400.5	1.40299372	0.28656065	0.158975491	-1.80258	0.07454195	0.09485545	grey	-0.08109336	0.3062468	GO:0055114,GO:0016568,GO:0006351,GO:0005634	ATG4I5380.1	HIRA	homolog of histone chaperone HIRA
Sapur.005G072200.1	238.2828218	0.07268274	0.040341	1.802561	0.07455623	0.09487571	grey	0.12275704	0.15068688	GO:0006270,GO:0005515	ATG4I5290.1		RING/U-box superfamily protein
Sapur.T316600.1	0.16451588	1.06258789	0.57848149	1.80171	0.07510178	0.09502811	grey	0.38647825	5.75E-07				NA
Sapur.016G276000.1	0.22988504	0.97819236	0.543156	1.801611	0.07516007	0.09560551	grey	0.10614887	0.7356E-05	GO:0055114,GO:0016491	ATG2G2100.1	ATGA2OX8,GA2OX8	gibberellin 2-oxidase 8
Sapur.005G204800.1	492.3895123	0.16962705	0.094163387	-1.80147	0.07518257	0.09560574	grey	-0.15182849	0.0576945	GO:0008234,GO:0006508	ATG3B569.1	XCP2	xylem cysteine peptidase 2
Sapur.006G071200.2	2.70361459	0.42082826	0.233547171	-1.80106	0.07548208	0.09518624	grey	-0.19882812	0.08075665		ATG2G2230.1		Helicase2 dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.015G259800.1	0.2409189	1.26051934	0.699007306	-1.80098	0.07570601	0.09561153	grey	-0.35930765	3.81E-06				NA
Sapur.018G070200.1	13.06855728	0.15474762	0.085607014	1.800659	0.07639271	0.09581985	grey	0.13863295	0.09513183				hypothetical protein
Sapur.015G180800.1	34.3014538	0.35102607	0.19835769	1.800569	0.07739515	0.09580859	grey	0.12688014	0.11233375	GO:0005525	ATG5E680.1	ARA-6,ARAG,ATRABGC,ATRA	Ras-related small GTP-binding family protein
Sapur.15WG031400.1	0.41631682	-0.70001307	0.422003334	-1.80058	0.07769667	0.09320281	grey	-0.12988079	0.08058952				NA
Sapur.006G181000.1	0.94470047	0.45188218	0.261658052	1.800058	0.07816188	0.09381892	grey	0.07864836	0.32814987	GO:0046983	ATG3B660.2	bHLH121	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.016G301900.1	1341.95821	0.05637827	0.030929399	1.800223	0.07835374	0.09329655	grey	0.12389819	0.12517582	GO:0030324,GO:0007017,GO:0005874	ATG5G2600.1	TUB2	tubulin beta chain 2
Sapur.004G264100.1	-1.05187984	0.56466149	0.28208874	-1.79984	0.07875433	0.09525269	grey	-0.19358675	0.03541282	GO:0055114,GO:0005506,GO:0016705,GO:0005506	ATG4G2250.1	CYP71A1	cytochrome P450 family protein
Sapur.004G230400.1	13.20227287	0.34707041	0.192975102	-1.79956	0.07910029	0.09547748	grey	-0.15326028	0.05242661	GO:0016021,GO:0016531	ATG1G2510.1	SC3	secretory carrier 3
Sapur.005G233300.2	1.71627026	0.26811553	0.150367	1.799547	0.07924675	0.09517316	grey	-0.07984836	0.37194618	GO:0016829,GO:0006530	ATG3I9170.1		Tyrosine transaminase family protein
Sapur.009G060800.1	125.7562663	0.42815135	0.238249106	1.798601	0.07928178	0.09521406	grey	0.12889511	0.10193902		ATG2B320.1		Plectotrin homology (PH) and lipid-binding START domains-containing protein
Sapur.006G060900.1	3.59675068	0.52182468	0.29005181	1.798571	0.07938654	0.09521881	grey	0.14732875	0.06557248		ATG3I7420.1	ABNT4,NT4	nitrilase 4
Sapur.008G064000.1	229.3283062	-0.08566166	0.047733895	-1.79843	0.07972389	0.09546927	grey	-0.17368891	0.02961657	GO:0016592,GO:0006357,GO:0001104	ATG7F550.1	MED22B	Surfeit locus protein 5-subunit 22 of Mediator complex
Sapur.15WG010900.5	0.55824397	-0.69587394	0.386905311	-1.79803	0.07127232	0.09729991	grey	-0.17698077	0.03659017		ATG1I4420.2	RGLG2	RING domain ligase2
Sapur.003G048100.1	0.87202844	0.17186625	0.095612189	-1.79785	0.07220578	0.09763601	grey	-0.16852526	0.04859862				NA
Sapur.15WG042500.1	0.18403967	1.24050573	0.690589865	1.796377	0.07249588	0.09606307	grey	0.32371304	1.54E-05	GO:0006468,GO:0005524,GO:0004672	ATG5G2540.1		Protein kinase superfamily protein
Sapur.008G150500.1	0.67697577	0.41164224	0.230000	1.796026	0.07349763	0.09606314	grey	0.10377174	0.22661546	GO:0005085,GO:0016020,GO:0015197,GO:0015318,GO:0006855	ATG3I6190.1		MATE efflux family protein
Sapur.018G288000.1	139.7271461	0.32876263	0.183026073	1.796269	0.07402969	0.09608298	grey	0.15688145	0.06984989		ATG8B840.2	GME	GDP-D-mannose-3',5'-epimerase
Sapur.015G180800.1	1.53551583	0.34851214	0.194232272	1.794301	0.07502594	0.09648916	grey	0.12296451	0.13496104				NA
Sapur.T175600.1	1.53551581	0.34851214	0.194232272	1.794301	0.07502594	0.09648916	grey	0.12296451	0.13496104				NA
Sapur.015G260400.5	2.2584231	0.36821526	0.2	1.793585	0.07509	0.09667886	grey	0.18308825	0.03918256				hypothetical protein
Sapur.001G133500.1	0.27215676	-0.46240594	0.832080694	-1.79358	0.07839981	0.09633759	grey	-0.12691086	4.17E-05				prolamin-like protein
Sapur.003G342900.1	0.30075077	0.96346757	0.54622999	1.793296	0.07895804	0.09675836	grey	-0.20508582	0.01796345	GO:0055114,GO:0016491	ATG3J5820.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.016G222900.1	3529.772266	0.64815868	0.361606822	1.792445	0.07861662	0.09686306	grey	0.29319744	0.00024181		ATG2G7030.3	ACAM-2,CAM5	calmodulin 5
Sapur.T028500.2	28.48752863	0.36401285	0.203145321	1.791915	0.07914625	0.09697176	grey	0.17278721	0.03842804		ATG4G2680.1		SNF2 domain-containing protein / helicase domain-containing protein / RNH endonuclease domain-containing protein
Sapur.001G041100.2	1.02478234	0.56194887	0.313519722	1.791486	0.07915732	0.09697996	grey	0.02216632	0.77287385	GO:0006351,GO:0006468,GO:0005515	ATG3I3170.1		Leucine-rich repeat family protein-protein binding protein
Sapur.014G039300	14.06549399	0.17406528	0.098401655	1.791624	0.07919258	0.09705804	grey	0.13994246	0.08043852	GO:0006508,GO:0004197	ATG5D170.1	AMC1,ATMC1,ATMCPB1,LO	metacaspase 1
Sapur.013G012200.1	4.68465223	0.27088153	0.151165435	-1.7916	0.07937706	0.09727626	grey	-0.13709374	0.08873804		ATG4G7840.1		VHA8-like protein family
Sapur.010G092500.2	10.01743318	0.21152032	0.11888502	1.791269	0.07950145	0.09709431	grey	0.15875313	0.04975791		ATG2I5380.1	ATNDT2,NDT2	NAD+ transporter 2
Sapur.008G239600.1	208.6887542	0.08779331	0.049010857	-1.791	0.07951222	0.09724793	grey	0.15122023	0.06809684	GO:0006468,GO:0005524,GO:0004672	ATG5E5220.1		Protein kinase superfamily protein
Sapur.018G069600.1	0.3014855	0.95404766	0.532792766	1.790641	0.07953864	0.09719143	grey	0.20854513	0.00784421	GO:0055114,GO:0006468,GO:0005524,GO:0004672	ATG5I9300.1		Protein kinase family protein with leucine-rich repeat domain
Sapur.016G143800.2	2.35224656	0.32422556	0.181109486	-1.79849	0.07963491	0.09736211	grey	-0.12462064	0.11995208		ATG4B370.2		Thioesterase/thiol ester dehydrase-isomerase superfamily protein
Sapur.005G084500.1	11.0654823	0.69751629	0.394815884	-1.78693	0.07344545	0.09736211	grey	0.12821734	0.12203763	GO:0005515	ATG3J180.1	IQD30	IQ-domain 20
Sapur.014G036800.1	0.36146983	0.35200884	0.197860394	1.789485	0.07535781	0.09745861	grey	0.24982899	0.00102142		ATG4G8700.1	ATFIM4,FIM4	fimbrin 1
Sapur.014G013000.1	1.07468864	0.50157872	0.29938623	1.789384	0.07535358	0.09746459	grey	0.15452625	0.05353112				NA
Sapur.T161700.1	20.56976042	0.20100163	0.112330329	-1.78938	0.07535361	0.09746469	grey	-0.12629933	0.11518152	GO:0008270,GO:0008022,GO:0006625,GO:0005779	ATG4H4440.1	APM4,ATPX12,PDX12	pernorin-12
Sapur.014G028300.4	0.24208382	0.18174582	0.101574293	1.789371	0.07535639	0.09746475	grey	0.02239165	0.69733102	GO:0005515	ATG4G5120.1		SHOC domain / Transcription elongation factor S-II protein
Sapur.014G137300.4	0.28105437	0.68611859	0.38346567	1.789238	0.07576459	0.09760797	grey	0.30675073	9.32E-05		ATG2G7700.2		Protein kinase superfamily protein
Sapur.010G023900.1	0.21745824	0.27678835	0.154866	-1.78769	0.07597779	0.09776297	grey	-0.36896206	1.98E-06	GO:0006355,GO:0003700	ATG4G5160.1	DRN-LIKE,DRNL,ESR2,SOB2	DORMINOUSS-LIKE 2
Sapur.016G118000.2	242.0627555	0.13780191	0.077116103	1.787687	0.07824691	0.09808341	grey	0.31460982	6.42E-05	GO:0043562,GO:0009744	ATG1I170.1	AKINBETA1	5'/-AMP-activated protein kinase beta-2 subunit protein
Sapur.009G023000.1	0.33729126	0.75370233	0.422212	1.787677	0.07830118	0.09797933	grey	-0.15420348	0.01835493		ATG4E282.1	FLS2	Leucine-rich repeat family protein
Sapur.001G079800.1	3229.829404	0.06351829	0.038239566	1.787016	0.07839497	0.09797933	grey	0.08877744	0.28974403		ATG4G690.1	RTN4B3	Reticulon like protein B3
Sapur.015G161300.1	344.8337853	0.07267409	0.043842018	1.786269	0.07865903	0.09819763	grey	0.12268808	0.1341345		ATG4H3600.1		Nucleotide-diphosphate sugar transferases superfamily protein
Sapur.15WG136300.1	12.52049917	0.24024705	0.134432423	1.786955	0.07844745	0.09794372	grey	0.14512119	0.08741828	GO:0008270,GO:0005515	ATG8I180.1		RING/U-box superfamily protein
Sapur.014G036800.3	6.25677909	0.23888443	0.133738548	1.786231	0.07866788	0.09809573	grey	0.12472386	0.13962197		ATG4G8700.2	ATFIM4,FIM4	fimbrin 1
Sapur.017G050200.1	8.64945150	-0.24313786	0.134281616	-1.78619	0.07868905	0.09810071	grey	-0.14254245	0.09302775		ATG4G4030.1	RALR1,S2	ralf-like 32
Sapur.001G104200.1	1.98273227	-0.3543499	0.198392297	-1.78611	0.07880191	0.09811387	grey	-0.29302047	0.00019873	GO:0003723,GO:0003676,GO:0045131,GO:0000398	ATG5I1000.2		splicing factor-related
Sapur.015G118300.1	581.8013884	0.05880609	0.0329855	1.785588	0.07895153	0.09813672	grey	0.16889316	0.02765024	GO:0006629	ATG3K091.1		DHHC-type zinc finger family protein
Sapur.006G135200.2	16.58742216	0.18729224	0.104863718	1.785453	0.07914798	0.09824948	grey	0.13013052	0.10797841	GO:0009116,GO:0003824	ATG2B940.1		Phosphorylase superfamily protein
Sapur.005G087000.1	799.5723161	0.05287429	0.029617836	1.785224	0.07920809	0.09826266	grey	0.11481104	0.16226217		ATG6G0210.1		RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.008G018800.2	97.37063383	0.12739774	0.068749926	1.785308	0.07921415	0.09826206	grey	0.16162707	0.04104346		ATG4M0727,VAMP727	VAMP727	vesicle-associated membrane protein 727
Sapur.006G117200.1	5.07343316	0.24049487	0.135658677	1.785202	0.07924136	0.09828648	grey	0.1414247	0.07088406		ATG4I6800.1		ATP-dependent Clp protease/protease/chaperone family protein
Sapur.001G161100.1	37.08661642	0.13376125	0.076029722	1.78516	0.07925406	0.09826148	grey	0.15495858	0.05264141	GO:0003677,GO:0008289	ATG7B840.1	GL2	HD-ZIP IV family of homeobox-leucine zipper protein with lipid-binding START domain
Sapur.006G164400.2	1.08885047	0.42868483	0.243125789	1.785135	0.07926145	0.09828148	grey	0.13943852	0.08534003		ATG2T950.1		RING/U-box superfamily protein
Sapur.009G015400.5	7.15866827	0.20057452	0.112422754	-1.78441	0.07960526	0.09857784	grey	0.28498438	0.00297326	GO:0055085,GO:0022857,GO:0016021	ATG4G790.1	ZIFL2	zinc induced facilitator-like 2
Sapur.015G190900.1	0.79282617	0.55065413	0.308769349	1.783388	0.07962328	0.09858351	grey	0.11259999	0.16348768		ATG2S545.1		plant/fungal-12 protein
Sapur.005G091400.1	0.36313555	-0.76722542	0.430329455	-1.78289	0.07969693	0.09870696	grey	-0.20869002	0.03000917		ATG4D7120.1	SFT16	global transcription factor group protein
Sapur.016G183100.5	0.70100399	-0.53980129	0.296678885	-1.78174	0.07976476	0.09900532	grey	-0.17752519	0.03611784	GO:0007264,GO:0005525	ATG5B650.1		Small GTP-binding protein
Sapur.016G304200.1	11.10927744	0.16581386	0.09306144	1.78167	0.07980231	0.09915613	grey	-0.15038164	0.08481851				NA
Sapur.015G161300.1	583.5231677	0.06931674	0.03898582	1.781457	0.07987814	0.09954589	grey	0.17494718	0.02841542	GO:0004842	ATG1T205.1	UPL6	ubiquitin protein ligase 6
Sapur.016G084800.1	40.45263117	0.16347323	0.091765021	-1.78072	0.07989898	0.09921496	grey	0.12317646	0.04155155		ATG2I3120.1		protease inhibitor/seed storage/lipid transfer protein, DUF184
Sapur.013G162300.3	0.27661657	0.83737364	0.470629173	1.779362	0.07936806	0.09952175	grey	0.13307517	0.09624684	GO:0008168	ATG6D750.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.015G027700.1	0.72556519	0.24249487	0.136356629	1.779772	0.07546194	0.09880229	grey	-0.14927706	0.02406593		ATG5T180.1		Transducin/WD40 repeat-like superfamily protein
Sapur.015G251300.1	4.8622341	0.23788795	0.133824341	1.777627	0.07546595	0.09857273	grey	0.16619731	0.03750253	GO:0005515	ATG7B370.1		F-box and associated interaction domains-containing protein
Sapur.T031600.2	1.50350932	0.36325456	0.207772237	1.777184	0.07537913	0.09994629	grey	0.14975261	0.06121651	GO:0046961,GO:0031176,GO:0019991,GO:0016747	ATG4H5420.1	VHA-E3	vacuolar H+-ATPase subunit E isoform 3
Sapur.J003G100.1	0.88469194	0.48151217	0.245206033	-1.77688	0.07539791	0.10001857	grey	-0.15451459	0.05888739	GO:0006457,GO:0003677,GO:0005871	ATG1B370.1	ATMACA1,HK,MACK1	ATP binding-microtubule motor family protein
Sapur.001G098800.1	554.6926592	0.11879426	0.06851175	-1.77685	0.07559533	0.10001522	grey	-0.15398315	0.05418126	GO:0055114,GO:0016491,GO:0005507	ATG1I4210.1	SKU5	Cupredoxin superfamily protein
Sapur.005G280500.1	0.67827624	0.38536179	0.222	1.776667	0.07562206	0.10068944	grey	0.27617666	0.00402211		ATG4D7,SDG25	ATXR7,SDG25	SET domain protein 25
Sapur.006G122300.3	0.40296908	0.69446192	0.390974227	1.776439	0.07565546	0.10095876	grey	-0.10843684	0.21172422	GO:0005515	CKI1,CKI1	CKI1	casein kinase I-like protein
Sapur.015G251300.1	131.6015167	-0.06252646	0.035196097	-1.7427	0.07597651	0.10031857	grey	0.13184104	0.05628008	GO:0005515	ATG5T560.1		Protein of unknown function (DUF3755)
Sapur.006G141800.1	0.27000974	0.88039768	0.495780145	-1.77578	0.07568806	0.10024096	grey	-0.27017782	0.00062002		ATG6I080.1		Barwin-related endoglucanase
Sapur.018G056500.2	5.86086829	0.27409184	0.156000	-1.77568	0.07569	0.10024086	grey	0.12268204	0.12725717	GO:0055114,GO:0016491,GO:0008152	ATG8H524.1	ALDH3A1,ALDH3C,ALDH3	aldehyde dehydrogenase family 3 member A1
Sapur.005G005200.1	1.07695872	0.52721359	0.297001019	1.774765	0.07593647	0.10043025	grey	0.11857648	0.14791876	GO:0004857	ATG9I680.1		Plant invertase/pectin methylesterase inhibitor superfamily protein
Sapur.016G240500.1	251.3680166	0.10075539	0.057000	1.774	0.07597583	0.10094415	grey	0.05678043	0.61666402	GO:0005515	ATG4I580.2	NMA2,OR2,PPS	Calcium-dependent lipid-binding (CaLB domain) family protein
Sapur.016G033300.1	0.60807047	0.63329732	0.356884567	-1.77437	0.07600155	0.10050631	grey	-0.21256218	0.00751918				NA
Sapur.018G261200.1	0.36562504	0.79008303	0.445275068	1.774372	0.07602556	0.10050815	grey	0.16134321	0.03851996	GO:0055115,GO:0006468,GO:0005524,GO:0004672	ATG2I930.1		Protein kinase family protein with leucine-rich repeat domain
Sapur.003G284800.1	873.1687473	0.05422604	0.03064871	1.770	0.07605485	0.10052362	grey	0.09916195	0.21474793	GO:0016020,GO:0008233,GO:0006465	ATG2G6200.1		Peptidase S8/S53 family protein
Sapur.013G089900.1	13.62169552	0.38136055	0.21959888	-1.774	0.07626929	0.10058256	grey	-0.12751264	0.11158931				NA
Sapur.009G268300.1	2.51113387	0.42364627	0.239	1.769	0.07627139	0.10070047	grey	-0.14739756	0.06720605	GO:0046983	ATG3T850.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.014G122500.1	6.60114624	0.21014462	0.118513364	1.773246	0.07637885	0.10077311	grey	0.14753834	0.06518772				NA
Sapur.T035200.1	1.12505217	0.46237662	0.260886519	1.771564	0.07653193	0.10095456	grey	0.14739756	0.06720605				NA
Sapur.009G012200.1	210.6667799	0.05588462	0.031381784	-1.77136	0.07660719	0.10134575	grey	-0.16547665	0.03834730	GO:0048319,GO:0005783	ATG0B400.1		RIN7-1 / TIP-1 family
Sapur.008G181100.1	6.64505178	0.29968183	0.169	1.771	0.07662	0.10136	grey	0.13307464	0.08808963		ATG4G4160.1		DNA-binding protein-related
Sapur.15WG134300.1	0.92734124	0.63843305	0.360493763	1.771115	0.07664626	0.10180565	grey	-0.14500183	0.06998735	GO:0055115,GO:0006468,GO:0005524,GO:0004672	ATG6B850.1		Leucine-rich repeat receptor-like protein kinase family protein
Sapur.012G088800.2	0.57887495	0.87945587	0.383623395	1.771047	0.07691291	0.10191437	grey	0.07528319	0.34874789	GO:0005525	ATG4S160.1		Root hair defective 3 GTP-binding protein (RHD3)
Sapur.015G084100.1	1006.695613	0.31026498	0.174554456	1.770	0.07694756	0.10191434	grey	0.10734491	0.18143149	GO:0005515,GO:0003824,GO:0000287	ATG5I320.1		Thiamine pyrophosphate dependent pyruvate decarboxylase family protein
Sapur.017G022800.1	1.97127399	0.36155395	0.204191291	-1.77041	0.07695606	0.10234373	grey	-0.15400351	0.05413656	GO:0008234,GO:0006508	ATG6I730.2		Cysteine proteinases superfamily protein
Sapur.018G094400.1	151.6947911	0.22466586	0.126925	1.769	0.07697	0.10251884	grey	0.13184104	0.05628008	GO:0005515	ATG2I5520.1		ubiquitin-associated (UBA)/TS-N domain-containing protein
Sapur.007G075500.1	172.8907663	0.12235248	0.069123023	1.770068	0.07701756	0.10190539	grey	0.15040487	0.06097209	GO:0005488,GO:0003677	ATG3I2140.1	ATEME1B,EME1B	essential meiotic endonuclease 1B
Sapur.004G206100.1	725.2172823	0.07130179	0.04029	1.768	0.07762	0.10345552	grey	0.16132102	0.03654481	GO:0055114,GO:0016491,GO:0005507	ATG2D210.1	alx4	SKU5 similar 3
Sapur.015G040100.1	1.86576134

Sapur.01G0297800.1	85.69801262	0.11649407	0.06737616	1.729801	0.08380928	0.10201426	grey	0.12604009	0.11243074	GO:0006355;GO:0003677	AtSU11180.1	ANACO83,NAC083,VN2	NAC transcription factor
Sapur.01G0277900.1	172.2852157	0.09347876	0.05406766	1.72882	0.08384124	0.10219707	grey	0.13805505	0.08465905		AtSG07910.2	ATRNL,RNL	RNAgase
Sapur.01T0287700.2	200.7290004	0.07969829	0.04576268	1.72837	0.08383858	0.10188841	grey	0.13817043	0.10246382		AtSU11480.1		eukaryotic translation initiation factor-related
Sapur.01G0301900.2	0.45476973	-0.62769308	0.36615425	-1.72815	0.08364082	0.10389644	grey	-0.16956155	0.03334363	GO:0071704;GO:0016868;GO:0005975	AtSU51820.1	ATPGMP,PGM,PGM1,STF1	phosphoglucomutase
Sapur.01T0281900.1	13.18106562	0.32408143	0.19297036	1.67936	0.08400836	0.10490158	grey	-0.1452331	0.08908099		AtSU26461.1	RTN13.1	Reticulon like protein B13
Sapur.01G0233800.2	18.80455864	0.12414875	0.07189568	1.72659	0.08423876	0.10727209	grey	0.11389046	0.1553161		AtSG05100.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.01G0241100.2	24.53812568	0.15265174	0.08860179	-1.72622	0.08403167	0.10305725	grey	-0.14720948	0.06389576	GO:007034	AtSU17730.1	CHMP1B,VPS46.1	vacuolar protein sorting-46.1
Sapur.7S12280.2	2.36383819	-0.20294641	0.16973381	-1.72612	0.08419319	0.10866548	grey	-0.13625074	0.08955229	GO:0016787	AtSU52160.1	PPX-2,PPX2	protein phosphatase X 2
Sapur.0I8G0937000.1	16.754808	0.17542758	0.10163878	-1.72589	0.08434785	0.11087162	grey	-0.20461556	0.01015249		AtSG21150.1	BBX32	B-box 32
Sapur.0I6G0942200.1	50.47453328	0.15364774	0.09598705	1.72564	0.08441926	0.1105511	grey	-0.15971469	0.05855011		AtSG27960.1		
Sapur.0G6J1601000.5	4.91418838	-0.24688709	0.14315541	-1.72427	0.08464125	0.11243016	grey	-0.13123195	0.10138311		AtSG85330.1		RNI-like superfamily protein
Sapur.0G6J0517900.1	1.05822347	0.09112411	0.07904709	1.72429	0.08466188	0.11271664	grey	-0.11876866	0.04703849		AtJH081.1,PRD1		putative recombination initiation defect 1
Sapur.0I3G1671000.1	2623.179273	-0.05929771	0.03465126	-1.72351	0.08479554	0.11435039	grey	-0.17091301	0.03228789		AtSG19760.1		Mitochondrial substrate carrier family protein
Sapur.0I6G0920600.1	87.27506423	-0.45730449	0.26518511	-1.7379	0.08479567	0.11435039	grey	-0.21353622	0.03746291	GO:0055115;GO:0055114;GO:0046872;GO:0016702	AtSU50320.1	ATLOX1,LOX1	lipoxygenase 1
Sapur.01G0237700.5	4.41504169	0.24026501	0.13964592	1.72363	0.08491259	0.11182547	grey	-0.08827628	0.27929855		AtSG23600.2	DRB4	double-stranded RNA-binding protein 4
Sapur.01G0231300.2	0.75291134	-0.53027931	0.3078356	-1.72361	0.08508655	0.11320874	grey	-0.14785968	0.06432896		AtSU31880.1		
Sapur.0I7G0895100.1	0.82914227	-0.49177697	0.28549572	-1.72251	0.08477457	0.11158035	grey	-0.14594803	0.06818771				
Sapur.01G0282700.2	69.10654914	0.10837921	0.06295548	1.72235	0.08508923	0.11369944	grey	0.15973811	0.04568544	GO:0004648;GO:0006472	AtSU70740.1		Protein kinase superfamily protein
Sapur.0I6G0881600.1	77.62696868	0.09628937	0.05589561	1.72173	0.08509135	0.11372904	grey	0.11637968	0.14727059				
Sapur.01G0601000.1	3.88131847	0.22486635	0.13060673	1.72106	0.08512286	0.11385743	grey	0.11490823	0.15185135				
Sapur.0I5G1491600.1	0.91763563	0.41968466	0.2437122	1.72101	0.08524165	0.11398744	grey	0.14663926	0.09602501		AtSG68765.1	IDA	Putative membrane lipoprotein
Sapur.0I4G0244400.1	17.85419968	-0.09033921	0.10267935	-1.71976	0.08547525	0.11220885	grey	-0.13008909	0.10439671	GO:0004648;GO:0006472	AtSG29750.2	RKI1	receptor-like kinase in flowers 1
Sapur.0I5G0900100.1	5.94757426	-0.3678842	0.21396441	-1.71915	0.08554982	0.11282261	grey	-0.10618154	0.18207791	GO:0004544;GO:0006468;GO:0005524;GO:0004672	AtSU24580.1		Protein kinase superfamily protein
Sapur.0I0G0210400.1	0.19936018	-0.12496174	0.07458822	-1.71887	0.08562059	0.11247175	grey	-0.36008469	3.62E-06		AtSG26860.1	ATFPR1,FPR1	flowering promoting factor 1
Sapur.0I4G0238300.1	476.0793167	0.07208847	0.04194746	1.71879	0.08562535	0.11250931	grey	0.15609053	0.05126067	GO:0016887;GO:0005524;GO:0055085;GO:0042626;GO:0055021;GO:0006810	AtSG28270.1	ATATPA,ATMULSTA1	ABC transporter of the mitochondrion 3
Sapur.01T0260600.2	1.65330806	-0.48489368	0.28208007	-1.71877	0.08567164	0.11251023	grey	0.16770382	0.03752249	GO:0016811;GO:0016021;GO:0006672	AtCG22330.1	ATCS1	alkaline ceramidase
Sapur.01G0202800.2	6.06460549	-0.20128872	0.11715846	-1.71752	0.08585023	0.11285758	grey	-0.12266165	0.12595516	GO:0005515	AtSU38630.1	ATSWI3B,CHR2,SWI3B	switch subunit 3
Sapur.0I5G0610500.1	5.02366165	-0.30260037	0.16008019	-1.71701	0.08592291	0.11281018	grey	-0.14084273	0.07906537	GO:0016740	AtSU48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Sapur.01G0951300.1	0.30008807	0.70483809	0.42703852	1.71702	0.08597563	0.11291605	grey	0.12452382	0.12016634		AtSG07350.1		
Sapur.0I6G0500500.1	83.52795174	0.16620151	0.09080762	1.71693	0.08599135	0.11266068	grey	0.10275266	0.20604066	GO:0005515	AtSG22050.1		Embryo-specific protein 3, (ATS3)
Sapur.0I1G1883900.1	12.28873372	0.28519495	0.16613744	1.71668	0.08604556	0.11296025	grey	0.11540269	0.15081998	GO:0007165;GO:0005515	AtSG36930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.01G2254500.1	3.38382070	-0.2263784	0.13918855	-1.71488	0.08657728	0.11329887	grey	0.09420503	0.24168228		AtSG27540.1	PRA1.H	prenylated Rab acceptor 1.H
Sapur.0I5G0176800.1	2.01642925	0.32790644	0.19113877	1.71605	0.08615243	0.11330679	grey	0.13804694	0.09478589		AtSG33220.2		
Sapur.0I0G0370800.1	1174.132064	-0.07246573	0.04221557	-1.71581	0.08619744	0.11184746	grey	0.15224511	0.04531544	GO:0016701;GO:0016117	AtSU02630.1	LYC	lycopene cyclase
Sapur.0I8G1344000.1	306.0819635	0.00565356	0.05861743	1.71522	0.08623201	0.11321966	grey	0.12604063	0.13228205	GO:0009055	AtSG44330.1	ETFBETA	electron transfer flavoprotein beta
Sapur.0I6G0267000.2	4.05084731	0.10624355	0.06911038	1.71508	0.08626138	0.11401133	grey	0.13354545	0.11893251	GO:0005215;GO:0005886;GO:0000145	AtSU05450.1	ATEXO70A1,EXO70A1	exocyst subunit Exo70 family protein A1
Sapur.01W0819001.1	1.52141731	-0.31775438	0.19345348	-1.71464	0.08643075	0.11342133	grey	0.15762074	0.04897796	GO:0005515	AtSG27790.1		F-box family protein
Sapur.0I5G1883800.1	54.52558817	-0.09865799	0.05756076	-1.71457	0.08642748	0.11345753	grey	-0.12278863	0.12863974				
Sapur.0I0G0950500.2	13.31865575	-0.26353731	0.17124203	-1.71429	0.08656605	0.11355685	grey	-0.16013618	0.06164861	GO:0003677	AtSG35510.1	ATWOX13,HB-4,WOX13	WUSCHEL related homeobox 13
Sapur.0I6G1500900.1	96.15424203	0.11187797	0.06572245	-1.71401	0.08627122	0.11381444	grey	-0.12843614	0.10834249				
Sapur.0I6G0270300.1	0.17973779	0.58944482	0.42762662	1.71382	0.08657661	0.11361701	grey	0.14945818	1.88E-05	GO:0080270;GO:0003676			
Sapur.01G0107600.1	114.5384115	0.16970163	0.09907763	-1.71321	0.08667336	0.11760202	grey	-0.12010788	0.13181271		AtSU70040.1		Mannose-binding lectin superfamily protein
Sapur.0I6G0600100.1	1.69566267	0.31209882	0.22068873	1.71312	0.08671628	0.11760202	grey	0.16681929	0.03767568	GO:0005515	AtSU19120.1	ARLP50,RLP50	receptor like protein 50
Sapur.0I7G0381000.1	0.44706915	0.67817886	0.39626786	1.71275	0.08675376	0.11861019	grey	0.15875341	0.16158803	GO:0016021	AtSG15730.1		small molecule transporter, putative
Sapur.0I8G0881200.1	0.36464674	0.81828181	0.73944127	1.71219	0.08704208	0.11870179	grey	0.25471276	0.09182034		AtSG40660.1		vacuolar iron transporter (VIT) family protein
Sapur.01T0119100.1	1.41187507	0.39278546	0.2293681	1.71262	0.08691338	0.11888023	grey	0.11548861	0.05182823	GO:0031204;GO:0008565	AtSU79940.1	ATERD2A	Drs1 / Sec63 Brl domains-containing protein
Sapur.01G0122900.1	29.23048841	0.10695398	0.08172566	1.71251	0.08679249	0.11899136	grey	0.11392562	0.15492276		AtSG26630.1		C2H2-like zinc finger protein
Sapur.0I1G0227000.1	5.51600809	0.15788266	0.12112768	1.71129	0.08687267	0.11984507	grey	-0.24052258	0.05647358		AtSU12480.1	NF-YC11	nuclear factor Y, subunit C11
Sapur.01G0107200.1	28.7836313	0.18035676	0.10535789	1.71186	0.08692249	0.11455162	grey	0.12909649	0.10592447	GO:0016021;GO:0004252;GO:0006508	AtSG07250.1	ATRBL3,RBL3	RHOMBOID-like protein 3
Sapur.01G0272000.2	0.82151282	0.42709258	0.2871637	1.71173	0.08706633	0.11523162	grey	0.16879816	0.01236564		AtSG45361.1		Protein of unknown function, DUF538
Sapur.0I8G0680600.3	0.36645866	-0.76478369	-0.44525189	-1.71076	0.08712528	0.11408331	grey	-0.23580506	0.09284866	GO:0004412;GO:0005840;GO:0005622;GO:0003735	AtSG14205.1		Ribosomal protein L18p/L5e family protein
Sapur.0I8G0151700.1	1.09024855	-0.43636356	0.24451067	-1.71047	0.08719578	0.11437431	grey	-0.18201349	0.02510478	GO:0016021;GO:0005622;GO:0005840	AtSG06270.1		Protein kinase family protein
Sapur.01G0197600.1	95.06136902	-0.15873247	0.09289766	-1.70921	0.08741283	0.11669225	grey	-0.18765876	0.01859291		AtSG06150.1	EMB1444	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.0I6G0800100.1	962.8938373	0.05284007	0.03154837	1.70818	0.08754307	0.11481939	grey	0.11918278	0.19917799	GO:0005509	AtSU10190.1		Calcium-binding EF-hand family protein
Sapur.01G1241800.3	0.88791425	-0.45237134	0.26475045	1.70837	0.08775944	0.11488041	grey	0.16275043	0.03681853		AtSG26455.1	WIP5	WPP domain interacting protein 1
Sapur.01T0156300.1	0.70577803	-0.51623804	0.3078814	1.70639	0.08750703	0.11488041	grey	0.08752428	0.27566759		AtSG35753.1	ATCBL3,CBL3	calcineurin B-like protein
Sapur.01G0270600.2	1.24568034	0.44778429	0.26218522	1.70788	0.08765194	0.11497066	grey	0.12431882	0.13081866		AtSG72175.1		RING/U-box protein with domain of unknown function (DUF 1232)
Sapur.0I7G0571300.1	1.96828762	0.39215323	0.22972147	1.70693	0.08783164	0.11520075	grey	0.10884124	0.17479332				
Sapur.01T0581800.1	5.45511351	-0.25391675	0.15833214	-1.70604	0.08794711	0.11541556	grey	-0.12021504	0.13703164	GO:0004648;GO:0005524;GO:0004672	AtSTR830.1	ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1
Sapur.01G0458800.1	1329.301814	0.04150944	0.02638728	1.70605	0.08790451	0.11535697	grey	0.17882721	0.03469548		AtSG56660.1	SMP1	Pre-mRNA splicing Prp18-interacting factor
Sapur.0I4G0882000.4	2.52087924	0.24308033	0.1594269	-1.70553	0.08806502	0.11592267	grey	0.10664118	0.19303315		AtSG16860.1		
Sapur.0I8G0860100.1	72.79623517	0.09678179	0.05750792	1.70538	0.08812348	0.11592122	grey	0.17527258	0.02881809	GO:0005515	AtSU02480.1	FRS11	FAR1-related sequence 11
Sapur.01G0227500.1	102.0715104	0.15192782	0.08931657	1.70507	0.08818205	0.11634439	grey	-0.14917225	0.05260222	GO:0004412;GO:0005840;GO:0003735	AtSU47320.1	RPS19	ribosomal protein S19
Sapur.01G0811000.1	0.46464746	-0.82770684	0.48549557	-1.705	0.08819355	0.11545124	grey	0.27902246	0.00338482		AtSG61970.1		signal recognition particle subunit SRP68
Sapur.0I6G0882300.1	1230.567219	0.04230833	0.02484919	1.7044	0.08826139	0.11576867	grey	0.09317745	0.24398452		AtSU31351.1	ATFLA11,FLA11	fucose-like AGP protein
Sapur.0I9G0910600.3	1.14324618	0.40169307	0.23727014	1.70406	0.08839804	0.11583495	grey	0.21372864	0.06718214		AtSU19400.2		2-hydroxyacid dehydrogenase, putative
Sapur.0I8G0915700.3	1.01060047	0.45498433	0.3011878	1.70557	0.08819235	0.11524439	grey	0.18642135	0.03936214	GO:0003723	AtSG53130.1	PUM11,PUM10	pumilio 11
Sapur.1W0G0445500.1	33.67476866	-0.12675129	0.07436563	-1.70395	0.08839685	0.11585183	grey	-0.17588249	0.02747181		AtSG21881.1	AtCBE20,CIE20	carboxypeptidase 20
Sapur.1W0G0153300.3	0.89325788	-0.27876926	0.16362939	-1.70379	0.08842622	0.11591758	grey	-0.10915347	0.17098459		AtSG26681.1	ATNBS1,NBS1	nijmegen breakage syndrome 1
Sapur.0I6G2310200.1	15.69162179	0.09271567	0.11370344	-1.70366	0.08844124	0.11597546	grey	-0.12756772	0.12874823		AtSG22461.1		Transducin/WD40 repeat-like superfamily protein
Sapur.01G0133900.2	0.68552877	-0.53549505	0.31433529	-1.70355	0.08846262	0.11596776	grey	-0.12178925	0.12870538	GO:0004648;GO:0005524;GO:0004672	AtSG69220.1	SIK1	Protein kinase superfamily protein
Sapur.01G0281100.1	961.6311888	0.07744944	0.02779868	1.70343	0.08849575	0.11599274	grey	0.11880014	0.16819173		AtSG05010.1		Calcium-binding EF-hand family protein, transmembrane-40
Sapur.01G1188700.1	425.866781	-0.27264293	0.04269246	-1.70296	0.08857699	0.11609137	grey	-0.12781728	0.11664284		AtSMC7,SPD,MCT		Nucleotide-diphosphо-sugar transferases superfamily protein
Sapur.01G0581200.1	26.11288892	0.43556614	0.27318343	1.70291	0.08867742	0.11622884	grey	0.20343016	0.01612021		AtSU16910.1		
Sapur.0I5G0240800.2	0.18665803	0.92023342	0.54567954	1.701979	0.08879319	0.11632602	grey	0.06236604	0.43771164	GO:0071365;GO:0005515;GO:0043531	AtSG12010.1		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.0I6G0260800.1	780.3648945	0.06928761	0.04108744	1.70318	0.08884549	0.11640229	grey	0.14428291	0.07405748	GO:0004376	AtSG66680.1		Single-domain cysteine and histidine-rich domain protein
Sapur.0I4G0253700.2	7.40182425	0.18270981	0.10746423	1.70047	0.08905259	0.11689604	grey	0.14341781	0.07114231		AtSG38580.1		Protein of unknown function (DUF616)
Sapur.7S12280.1	0.32182277	-0.68106144	0.40015648	-1.70041	0.08908242	0.11699584	grey	-0.23482471	0.03179519	GO:0016787	AtSU52160.1	PPX-2,PPX2	protein phosphatase X 2
Sapur.0I7G0121200.1	1.75607477	0.17139655	0.10183876	1.70037	0.08909569	0.11705267	grey	0.15257243	0.05703156		AtSG64680.1		
Sapur.1W0G0365000.1	1.09019569	0.52402168	0.30822046	1.70014	0.08910892	0.11752743	grey	0.14659958	0.03444889	GO:0016757	AtSU18180.1		Glycosyltransferase family 61 protein
Sapur.0I8G0930700.1	711.3593628	-0.05498791	0.03232323	1.69825	0.08919331	0.11802495	grey	0.12831915	0.18327515		AtSG26190.1		PLACE family protein
Sapur.1W0G0974000.1	92.01288879	0.12007814	0.07068841	1.69954	0.08921671	0.11885957	grey	-0.27621257	0.00451991	GO:0005515	AtSG06130.1	SKIP16	SKP1/ASK-interacting protein 16
Sapur.0I0G0854000.2	0.72447864	-0.52136706	0.30682746	-1.6983	0.08933535	0.11964706	grey	-0.15201144	0.05729465		AtSG27461.1		Protein of unknown function (DUF620 and DUF622)
Sapur.0I6G0908800.3	0.24706615	0.75466223	0.44425787	1.69672	0.08937381	0.11789927	grey	0.21473962	0.06919647	GO:0005515	AtSG59690.1	IQD13	IQ-domain 13
Sapur.0I8G0931300.1	18.18285571	0.16878698	0.09938152	1.69847	0.08941594	0.11746451	grey	0.14210604	0.07353648	GO:0016021	AtSG03570.1		Endomembrane protein 70 protein family
Sapur.01B0114600.1	1.17887709	0.45605241	0.26853535	1.69838	0.08944653	0.11780569	grey	0.14862549	0.06328611		AtSG37113.1		
Sapur.0I3G0103300.3	20.14326241	0.10503303	0.06188164	1.69741	0.08964359	0.11871884	grey	0.06784824	0.38581764		AtSG46680.1		Mo25 family protein
Sapur.0I3G0438000.6	1.89184068	0.34782705	0.20076625	1.69747	0.08963712	0.11871884	grey	0.09204899	0.30590942		AtSU10095.1		Protein prenylhexaprenase superfamily protein
Sapur.0I7G0111000.2	13.36791973	0.38152729	0.22480747	1.69729	0.08967225	0.11745365	grey	0.23423499	0.00705485	GO:0016192	AtSG01430.1	Got1/VPS2-like vesicle transport protein family	vesicle transporter GOT1B, putative
Sapur.0I5G0875200.1	0.38127822	-0.24189794	0.18049897	-1.69686	0.08973375	0.11748982	grey	-0.22452376	0.06497194		AtSG84731.1	Terpene synthase-type family protein	TPS protein
Sapur.7S01200.1	2.71362119	0.26201945	0.15483787	1.69667	0.08976958	0.11757054	grey	0.15072891	0.05912287		AtSU86860.1	NYAD1,NYD5	NYAD-related Kinase 5
Sapur.0I8G0000300.1	2.50955528	0.29459514	0.17372367	1.69568	0.08984645	0.11798764	grey	0.28236135	0.00349967	GO:0016491	AtSU41361.1		Aldose-type UDP-glucose dehydrogenase family
Sapur.01G0277000.4	0.3875165	-0.66983541	0.38332824	-1.69563	0.08995516	0.11780684	grey	-0.23195874	0.03346104		AtSG17801.1	emb1703	embryo defective 1703
Sapur.0I5G0920100.1	31.11152752	-0.14544629	0.08162373	-1.69399	0.08999773	0.11856221	grey	0.12774674	0.06680667		AtSU22001.1	AKT2,KAT2,SLAT1,KT2/3	potassium transport 2
Sapur.0I3G0363000.1	2.52059835	-0.27137291	0.16008514	-1.69519	0.09009107	0.11790683	grey	-0.12392592	0.12243278		AtSU10040.1	AtTRS120,TRS120	TRS120
Sapur.0I6G0541600.1	26.53874156	0.30347434	0.17889647	1.69547	0.09001073	0.11856821	grey	0.12746243	0.08384976	GO:0005085;GO:0016020;GO:0051297;GO:0051328;GO:0000855	AtSU31351.1		MATE efflux family protein
Sapur.0I4G0164000.1	12.83278423	0.16119129	0.09509981	-1.69453	0.09016589	0.11857013	grey	-0.15384249	0.05439166		AtSG22875.1		transmembrane protein, putative
Sapur.0I7G0187700.1	0.79032425	0.57455784	0.33906889	1.69429	0.09018734	0.11870725	grey	0.15268136	0.03609764				
Sapur.0I7G0116400.1	9.83627936	-0.15870063	0.09435318	-1.69438	0.09019236	0.11884544	grey	-0.11387609	0.16487654				
Sapur.01G0362800.1	29.15239964	0.30420045	0.12052941	-1.69429	0.09021929	0.11930307	grey	-0.15493013	0.05267622		AtSG43150.1		hypothetical protein
Sapur.01G0980100.1	145.9834231	0.21840594	0.12893761	1.69411	0.09024125	0.11841791	grey	0.12898462	0.10479858		AtSU29160.1	ATPP2-A1,ATPP2A-1,PP2-A1	phloem protein 2-A1
Sapur.0I9G0967000.1	95.79629412	0.21905581	0.13013528	-1.69341	0.09037769	0.11830604	grey	-0.13362608	0.09112769		AtSG03670.1		ankyrin repeat family protein
Sapur.0I6G0651500.1	-1.06037319	0.66004182	0.37576624	-1.69371	0.09038699	0.11831204	grey	0.12516879	0.11392019				hypothetical protein
Sapur.01G0276400.1	234.0233004	-0.17872661	0.10553323	-1.69328	0.09040898	0.11892662	grey	-0.12730971	0.12832469		AtSG78850.1		D-mannose binding lectin protein with Apple-like carbohydrate-binding domain
Sapur.01G0581800.6	2.80017748	0.27237996	0.16401171	1.69118	0.09089195	0.11830647	grey	0.09588885	0.12347319	GO:0016021;GO:0004190	AtSPM4,SPP4	SIGNAL PEPTIDE PEPTIDASE-LIKE 4	signal peptide peptidase-like protein
Sapur.7G0870001.1	7.72664258	0.43908029	0.25932316	1.69292	0.09047241	0.11841304	grey	0.12515727	0.11728858		AtSU77110.1	ATCRMI1,ATKPCI1,HET2,KPCI	exportin 1A
Sapur.0I8G0747600.1	4.57863214	0.32980117	0.19495154	1.69292	0.09048317	0.11870373	grey	0.15241676	0.05139207	GO:0005524	AtSG61461.1	EDA16	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related
Sapur.0I2G1180600.1	24.95024892	0.14789017	0.08746206	1.69084	0.09058885	0.11880942	grey	0.05488886	0.23419137	GO:0009733	AtSG60690.1		SAUR-like auxin-responsive protein family
Sapur.0I6G1868500.1	0.58755501	0.19679563	0.70783767	1.69080	0.09087699	0.11892925	grey	0.33421507	1.90E-05		AtSG07730.2		Disease resistance-responsive (dirigent-like protein) family protein
Sapur.0I6G0000100.1	2.04602814	0.15816425	0.10270795	-1.69077	0.09089138	0.11899121	grey	-0.10233851	0.21220928	GO:0016779;GO:0009058	AtSU30210.1	APL3	Glucose-1-phosphate adenylyltransferase family protein
Sapur.7D02100.1	6.98895239	-0.60258372	0.04969011	-1.69069	0.09089527	0.11894271	grey	-0.11213251	0.16204192				
Sapur.01B0283000.1	0.31661884	0.80977924	0.48111227	-1.68897	0.09102969	0.12027424	grey	0.27232047	0.00334999	GO:0055114;GO:0050661;GO:0050660;GO:0004499	AtSG35620.2	YUCG	Flavin-binding monooxygenase family protein
Sapur.01B0007700.1	179.7007214	0.14332785	0.08482781	-1.68863	0.09108951	0.11934245	grey	-0.16615246	0.07594009		AtSG37560.1	NAGK	N-acetyl-L-glutamate kinase
Sapur.0I6G0142400.1	17.38955147	0.16444211	0.10294882	-1.68879	0.09106208	0.11940162	grey	0.12298158	0.11883451	GO:0055114;GO:0016491;GO:0016633;GO:0005506	AtSU36190.1	CER1,CLP1,WAX2,YRE	Fatty acid hydroxylase superfamily
Sapur.0I7G0249900.1	4.85828905	0.21782151	0.13624453	-1.6885	0.09131564	0.11948893	grey	-0.10900573	0.17415476		AtSG36660.1		Protein of unknown function (DUF1195)
Sapur.0I6G0000200.1	2.00827275	0.58060624	0.34387164	1.68811	0.09134429	0.11961105	grey	0.12988462	0.10439553		AtSU29160.1	Tpp/Bsh-CAR protein family protein	BaBsh/TBC domain protein
Sapur.01G0105500.2	10.44639216	0.18609852	0.11028399	-1.68736	0.09154834	0.11976163	grey	-0.12615348	0.14360471	GO:0008152;GO:0003824	AtSG15320.1	AAE18	acyl-CoA synthetase 18
Sapur.0I5G0917500.1	0.58353578	0.38178153	0.22614691	1.68685	0.09160236	0.11983564	grey	0.11429899	0.16408385	GO:0004298;GO:0006508;CIAO	AtSG06200.1		Peptidase S24/S26A/S26B/S26C family protein
Sapur.0I7G0140400.1	851.6722246	0.08306089	0.04976149	1.68669	0.09163673	0.11985462	grey	0.08026356	0.31887184	GO:0004412;GO:0005840;GO:0003735	AtSU31617.1	NFD3	Ribosomal L18p/L5e family protein
Sapur.1W0G1448800.3	0.79644405	-0.48433477	0.28700858	-1.68648	0.09194227	0.11948941	grey	-0.22377815	0.76713315	GO:0004518;GO:0006281	AtSG48900.1		single-stranded DNA endonuclease family protein
Sapur.01T0121000.1	295.7754379	0.06484798	0.03202118	1.68956	0.09206292	0.10209496	grey	0.12290037	0.12488667		AtSU77300.1		zinc ion binding
Sapur.01B0249900.1	2.41529662	0.25765755	0.15282934	-1.68584	0.09216921	0.12009794	grey	-0.11541011	0.1505376				
Sapur.0I0G0810300.1	46.03567368	0.20219504	0.09976622	-1.68547	0.09220905	0.12037424	grey	-0.14002669	0.06894645	GO:0138120;GO:0019237;GO:0000776	AtSU16680.1	CENP-C	centromere protein C
Sapur.01B0107400.1	11.0568895	0.37891549	0.22482896	1.68535	0.09193106	0.12021347	grey	0.17529361	0.03071531	GO:0000160	AtSZ51180.1	ARR12,RR12	response regulator 12
Sapur.0I4G0188200.1	41.79870604	0.12156427	0.07214026	1.68447	0.09231473	0.12053074	grey	-0.10162413	0.08426787		AtSU02610.1		hypothetical protein
Sapur.0I3G0222300.3	66.91542001	0.10897304	0.06478144	-1.68382	0.09235865	0.12058416	grey	-0.12497065	0.11001195		AtSU13800.1		Metallo-hydrolase/oxidoreductase superfamily protein
Sapur.0I6G0280300.3	4.70204502	0.20128197	0.12000229	1.68377	0.09237288	0.12076173	grey	0.13422684	0.09375885	GO:0016787	AtSU48830.1	atnudt8,NUDT8	nudix hydrolase homologue 8
Sapur.0I6G2362200.1	593.9209556	0.09120277	0.05420165	1.68298	0.09237853	0.12079259	grey	0.12403229	0.12076848	GO:0016021	AtSG52870.2		Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein
Sapur.0I8G0278400.1	28.79719897	0.16046165	0.09539303	-1.6821	0.09254839	0.12100163	grey	-0.13789715	0.14278071				
Sapur.01W0283700.1	1.27968854	-0.36661621	0.2269557	-1.68169	0.09257515	0.12107989	grey	-0.16287473	0.04503911				
Sapur.0I1G1494000.1	1.62194933	0.42792949	0.25404157	1.68195	0.09257834	0.12109733	grey	-0.10982188	0.17268446		AtSG13845.1		transmembrane protein, putative
Sapur.0I6G1541200.1	0.33564218	0.68168629	0.51602261	-1.68107	0.09274939	0.12125763	grey	0.25788863	0.05113339	GO:0005524;GO:0003676	AtSDC1,LDC1.4	dicer-like 4	endoribonuclease dicer-like protein
Sapur.01G0807000.5	4.34074223	0.27775188	0.16234041	1.68069	0.09278382	0.12130416	grey	0.29309187	0.00018894	GO:0006355;GO:0005667;GO:0003700;GO:0007049	AtSG03415.1	ATDPB,DPB	Transcription factor DP
Sapur.01B0060600.1	0.32305788	0.94231227	0.55462693	1.68027	0.09282127	0.12132886	grey	0.40276522	1.54E-11		AtSU27210.1	SPT16	global transcription factor C
Sapur.0I7G0751500.1	199.7855073	0.10669328	0.06348255	-1.68068	0.09281575	0.12

Sapur.T046300.4	36.17043866	0.15609663	0.09719495	1.64216	0.100556843	0.138055249	grey	0.007438663	0.92633245	AT4G13730.1	Pectin lyase-like superfamily protein	pectate lyase, putative
Sapur.01G0261300.1	0.32339601	0.683458598	0.416267628	1.640089	0.100557492	0.130609164	grey	0.126408633	0.115788495			NA
Sapur.0906230.2	0.27701176	0.806401863	0.497252524	-1.6413	0.100755105	0.131100453	grey	0.273877622	0.00957084			NA
Sapur.01G0201700.1	302.6897361	-0.459895155	0.2864195	-1.64036	0.100930171	0.131322658	grey	-0.183001181	0.023293498	GO:0055114,GO:0050660,GO:0016491	FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.01G0137300.1	14.40136429	0.147757879	0.090075572	1.640353	0.100931009	0.131322658	grey	0.143245805	0.073451337	GO:0016020,GO:0008283,GO:0005215	NIP6;NIP6;1,NLM7	NOD26-like intrinsic protein 6;1	aquaporin, MIP family,NIP, NIP subfamily protein
Sapur.01G0294000.1	34.9513339	0.147387623	0.089896146	1.639569	0.101094888	0.131529535	grey	0.117386742	0.143836321			hypothetical protein
Sapur.01G0275000.1	3.551589983	-0.423028388	0.258076236	-1.63916	0.101179812	0.131634847	grey	-0.149532222	0.061603703		protein kinases;ubiquitin-protein ligases	NA
Sapur.0180245000.1	1.88162268	0.425452331	0.259589344	1.638881	0.101238127	0.131705534	grey	0.088462521	0.264104552			NA
Sapur.0080260000.2	0.64813476	0.515888941	0.314848059	-1.63885	0.101244372	0.131708439	grey	-0.152791185	0.056081491		DNAse I-like superfamily protein	type I inositol-1\4\5-trisphosphate 5-phosphatase
Sapur.0060217500.1	374.7893048	0.738275157	0.450160191	1.638459	0.101338793	0.131887993	grey	0.131776214	0.138187993	GO:0007165;GO:0006468,GO:0005524,GO:0004672	CBL-interacting protein kinase 25	CIPK25,SnRK3.25	calcineurin B-like protein interacting kinase
Sapur.0040245000.1	2152.562238	0.115382842	0.070402416	1.638067	0.101409715	0.131905536	grey	0.123388823	0.129911942	0.0016788	GDSL-like Lipase/Acylhydrolase family protein	GDSL-lipase, putative
Sapur.0080260000.1	775.2029938	0.266394301	0.173553164	1.636403	0.101420703	0.131913852	grey	0.109615752	0.175562126	GO:0016021,GO:0008233,GO:0006508,GO:0004197	Signal peptidase subunit	signal peptidase subunit
Sapur.0140111600.1	91.81326743	0.123385771	0.075266138	1.637968	0.101422147	0.131913802	grey	0.122140038	0.127521928			hypothetical protein
Sapur.0170280400.1	1.834554834	0.690563142	0.421486184	1.636178	0.101426138	0.131985827	grey	0.273877622	0.00957084	GO:0016021,GO:0008152,GO:0016020	AGILIS,FUL	AGAMOUS-like B	MADS box protein
Sapur.0092680200.1	8.90406191	-0.186401964	0.113855173	-1.63718	0.101581853	0.132124138	grey	-0.131395213	0.096450354		Major facilitator superfamily protein	UNC93-like protein
Sapur.0140281200.1	1.389769437	0.374341544	0.247785516	1.636293	0.101582915	0.132140427	grey	-0.174128947	0.032427139			NA
Sapur.0032G0340.8	1.24672273	0.46995559	0.274681067	1.636315	0.10173372	0.132350254	grey	0.143661416	0.073052287		Erythronate-4-phosphate dehydrogenase family protein	erythronate-4-phosphate dehydrogenase family protein
Sapur.0050121800.1	2.04097051	0.411511932	0.251550209	1.635622	0.101936637	0.132530897	grey	0.088879531	0.268315418	GO:0008080	Acyl-CoA N-acyltransferases (NAT) superfamily protein	NA
Sapur.0140210700.1	0.630957835	0.451843595	0.29538856	1.635515	0.101941611	0.132557513	grey	0.101944611	0.132557513			NA
Sapur.0032G0990800.1	159.5542723	0.092591056	0.11775892	-1.63547	0.10195078	0.132568873	grey	-0.124545848	0.12015055	GO:0016597,GO:0008152,GO:0055114,GO:0051287,GO:0016616		NA
Sapur.0100204900.1	51.2973004	0.150207758	0.092531267	1.635428	0.101956315	0.132568873	grey	0.123195315	0.050389546	GO:0016020,GO:0008236,GO:0006508	D-3-phosphoglycerate dehydrogenase	NA
Sapur.0086101700.1	33.33246672	-0.450767561	0.275630371	-1.63541	0.101962966	0.132571595	grey	-0.191948116	0.016020045	GO:0055085,GO:0016020,GO:0051297,GO:0015238,GO:0006855	armadillo repeat only 4 protein	armadillo repeat only 4 protein
Sapur.0180245000.1	258.0460976	0.185224481	0.088041156	1.635124	0.102022969	0.132643094	grey	0.122372225	0.155756663	GO:0016758,GO:0005886	UDP-Glycosyltransferase superfamily protein	NA
Sapur.7006100.1	58.54314522	-0.115455978	0.07050215	-1.63507	0.102033871	0.132652954	grey	-0.175995132	0.027466032	GO:0005515	SDG20,SUVR3	SET domain protein 20	NA
Sapur.0101218800.1	0.387450868	0.690563142	0.422649955	1.635408	0.102080056	0.132709482	grey	-0.220150292	0.027509832	GO:0016020		CAAX protease self-immunity protein
Sapur.0180261500.1	6.32061671	0.210496469	0.128766108	1.63472	0.102107859	0.132737868	grey	0.118466687	0.14773258			transmembrane protein, putative
Sapur.0086201000.1	6.02947585	0.187921879	0.114990604	1.634237	0.102209138	0.132864341	grey	0.145104599	0.089795525			hypothetical protein
Sapur.0042680100.1	17.73934657	0.124988542	0.076488543	-1.63385	0.102205548	0.132864847	grey	-0.150117247	0.060175539		TBL39	TRICHOME BIREFRINGENCE-LIKE 39	NA
Sapur.0050161600.1	1.896991996	0.338254205	0.207052753	1.633662	0.102329851	0.133017039	grey	0.109268987	0.171880795			hypothetical protein
Sapur.7150200.1	2.28805556	0.361858735	0.1108597	1.633355	0.102554	0.133303887	grey	-0.130205546	0.086784006	GO:0006468,GO:0005524,GO:0004672	Protein kinase superfamily protein	NA
Sapur.0180284600.1	26.08525919	0.418387163	0.256127632	1.63351	0.102361685	0.133061631	grey	0.11256188	0.1606995			NA
Sapur.0052G0190.1	0.30887020	0.182137317	0.147678838	-1.63338	0.102388073	0.133070694	grey	-0.21831475	0.050389546	GO:0016020,GO:0008236,GO:0006508	Peptidase S26/S26A/S26B/S26C family protein	serine-type peptidase
Sapur.0120494300.1	107.1864343	0.271074528	0.165968337	1.633293	0.102407439	0.133090637	grey	0.153065542	0.058891385	GO:0043531	NB-ARC domain-containing disease resistance protein	NA
Sapur.0180262800.1	1228.122251	0.121227884	0.074868487	1.63258	0.102497247	0.133203142	grey	0.060602449	0.230340877			hypothetical protein
Sapur.0070124300.1	13.22926174	0.176318349	0.108918257	-1.63186	0.102708882	0.133471909	grey	-0.137911301	0.089787093	0.0055515	Leucine-rich repeat (LRR) family protein	Serine/Threonine kinase, plant-type protein%2C putative	
Sapur.0140297800.4	2.34664386	0.495188227	0.305864104	-1.63177	0.102720662	0.133491669	grey	-0.143878962	0.072216516		dioxolignan1-acylthioesterase family	dioxolignan1-acylthioesterase family protein	
Sapur.0301309001.1	1.937616182	0.352054314	0.215853308	-1.63112	0.102839398	0.13365773	grey	-0.156229398	0.055725582	0.0009733	SAUR-like auxin-responsive protein family	auxin-responsive family protein	
Sapur.0162202300.1	0.832828054	0.451472205	0.27678939	-1.6311	0.102884435	0.133858244	grey	-0.16804586	0.029767963			NA
Sapur.0050288800.1	459.6050461	0.075766668	0.046434224	-1.63075	0.102928323	0.133752679	grey	0.107936856	0.194307724	GO:0005515,GO:0051568,GO:0016575,GO:0005634		CAMK protease self-immunity protein
Sapur.0020471000.1	18.75127914	0.127857868	0.078543386	1.627436	0.102964598	0.134650372	grey	0.119427195	0.132774431			NA
Sapur.0170294400.2	8.383113729	0.347102278	0.214822719	1.627007	0.103356661	0.134747987	grey	-0.001608664	0.99509942	0.0045735	RmlC-like cupins superfamily protein	nutrient reservoir protein, putative
Sapur.0020695800.1	750.3673839	0.102344044	0.062951809	-1.62575	0.104002373	0.135079518	grey	-0.135743882	0.09007567		alpha/beta-Hydrolases superfamily protein	sigma factor sigb regulation protein rsbq protein
Sapur.0151131300.1	10.30419893	0.150180554	0.093175295	-1.62562	0.104063408	0.135106684	grey	-0.144994008	0.030119968	GO:0006355;GO:0003677	NAC domain containing protein 2	NAC transcription factor
Sapur.0120364000.1	23.23187257	1.408130286	0.866338101	1.625344	0.104089196	0.135180668	grey	0.127989163	0.000423264			NA
Sapur.0062G0180.1	690.081832	0.356477015	0.240004287	1.625344	0.104097654	0.135180669	grey	0.127989163	0.000423264	GO:0016887;GO:0005524	RPT3	regulatory particle triple-A ATPase 3	26S proteose regulatory subunit 6B
Sapur.0096060000.1	4.240362157	0.209559687	0.12895069	1.625122	0.104136347	0.135214482	grey	-0.108047576	0.17791228			hypothetical protein
Sapur.0180269000.1	1081.915701	0.288883821	0.178000513	1.624597	0.104184763	0.135288833	grey	-0.143878962	0.072216516		ITN1	Ankyrin repeat family protein	ankyrin repeat plant protein
Sapur.0051121600.1	73.53558216	0.217129289	0.074025152	1.624869	0.104196652	0.135293532	grey	0.089361164	0.261720091	GO:0016021,GO:0008150,GO:004679	ATDA01	Defender against death (DAD family) protein	defender against apoptotic death protein
Sapur.1590G151200.2	0.40908754	-0.660143241	0.40628188	-1.62484	0.104196555	0.135293532	grey	-0.213738747	0.007190897	GO0006355;GO0006508;GO0070700;GO0048583;GO:0003677	AGL19;GLE19	AGAMOUS-like 19	MADS box transcription factor
Sapur.0050275400.1	921.6753484	0.152382582	0.094719732	1.624579	0.104208526	0.135302651	grey	-0.126408296	0.114490192	GO:0005515;GO:0006468,GO:0004672	Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain	Serine/Threonine kinase-like protein	Serine/Threonine kinase-like protein
Sapur.0170249900.1	2.37292817	0.191931997	0.20888224	-1.62423	0.104230354	0.135451494	grey	-0.143843556	0.073091227		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.7130600.1	0.65109427	0.194313319	0.120532363	-1.62406	0.104233187	0.135453262	grey	0.16621654	1.674-05			NA
Sapur.0130G0870000.1	12.88827141	0.161051263	0.099188494	-1.62334	0.104257576	0.135480653	grey	-0.109827729	0.17090971		ARM repeat superfamily protein	hypothetical protein
Sapur.0130G0861000.1	2503.132764	0.107220019	0.066377906	-1.62309	0.104267390	0.135512984	grey	-0.129570337	0.105767729	GO:0055114,GO:0008113,GO:0030091,GO:0016671,GO:0006979	peptide methionine sulfoxide reductase 4	peptide methionine sulfoxide reductase	
Sapur.0105294900.1	84.20643934	0.240258495	0.148038798	1.622943	0.104601649	0.135797532	grey	0.152460009	0.056622719			NA
Sapur.0180263000.1	938.6384669	0.117316445	0.072613183	1.622383	0.104731282	0.135921169	grey	0.142716132	0.074157578	GO:0009086;GO:0008270;GO:0003871;GO:0008652	ATCMS1;ATMETL;ATMS1	Cobalamin-independent methionine synthase family protein	
Sapur.0020385000.1	639.4338706	0.048351141	0.029803025	-1.62236	0.104736972	0.135934221	grey	-0.172569334	0.08648126		ATHMT-2;HMT-2;HMT2	homocysteine methyltransferase 2	homocysteine S-methyltransferase
Sapur.0162B87000.1	0.19171307	1.401238303	0.863831735	1.62212	0.104777764	0.135980474	grey	0.320695643	4.27E-05			NA
Sapur.0180261000.1	0.543976546	0.574061287	0.355188858	-1.62104	0.104850563	0.136040087	grey	0.199249047	0.012374065		ATOEP16-4	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	outer envelope pore protein 16-4
Sapur.0170202600.1	0.20425796	1.302007093	0.796630164	1.621446	0.104921955	0.136105587	grey	0.237532727	0.002740169	GO0006468;GO0005524,GO:0004672		Protein kinase superfamily protein	NA
Sapur.0180262400.1	0.194682491	1.288883821	0.794229453	-1.6249	0.104938763	0.136288833	grey	-0.143878962	0.072216516		IQD31	IQ-domain 31	IQ calmodulin-binding motif protein
Sapur.0120221700.1	74.4231391	0.206086231	0.127165562	1.621011	0.105051136	0.136371083	grey	0.089361164	0.261720091	GO:0016021,GO:0008150,GO:004679	ATDA01	Protein of unknown function (DUF761)	cotton fiber, putative
Sapur.1590G151200.2	527.8123884	0.168357075	0.103573344	-1.62027	0.105076987	0.136567328	grey	-0.148506453	0.012839443	GO0006487;GO:0000145	ATEXO70F;EXO70F1	exocyst subunit exo70 family protein f1	exocyst complex component, putative
Sapur.0051191100.1	5.944952118	0.309687729	0.191081024	1.62062	0.105090161	0.136569171	grey	0.062264741	0.438653962	GO:0016491,GO:0008152		NADP(H)-binding Rossmann-fold superfamily protein	short chain dehydrogenase/reductase, putative
Sapur.0180263800.1	6.033428377	0.186314946	0.115758693	-1.62055	0.105097427	0.136576583	grey	0.191274427	0.167189197	GO:0006629;GO:0006869	Polyketide cyclase/dehydrase and lipid transport superfamily protein	polyketide cyclase/dehydrase Bet V family protein	polyketide cyclase/dehydrase Bet V family protein
Sapur.0161190400.1	1.416097069	0.381112391	0.235365451	1.619298	0.105381122	0.136728571	grey	0.15147221	0.058240682		Ankyrin repeat family protein	transmembrane protein, putative	
Sapur.0180263900.1	26.72763093	0.161911191	0.100151734	-1.61911	0.105405197	0.136745596	grey	-0.143800016	0.073341617		ENTH/VHS family protein	RNA polymerase II binding protein	RNA polymerase II binding protein
Sapur.0051B81000.1	1.802895135	0.327475213	0.202275584	1.618972	0.105453347	0.136807249	grey	0.162630301	0.041847205		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein, putative	PPR containing plant protein, putative
Sapur.0161470800.1	175.1349972	0.408351999	0.252247236	-1.61886	0.105478521	0.136814337	grey	-0.213426251	0.007277998		Protein of unknown function (DUF247)	DUF247 family protein	DUF247 family protein
Sapur.0130140400.1	27.03779376	0.174131781	0.108779243	-1.61875	0.105505139	0.136857217	grey	0.140576219	0.079076201	GO:0016021	GCN51-like protein 1	GCN51-like protein 1 (GCN5L1) protein	GCN51-like protein 1 (GCN5L1) protein
Sapur.0162B98800.5	4.116408633	0.215726768	0.133278869	-1.61866	0.105530327	0.136878036	grey	-0.133645948	0.091578514		D-glucose binding protein with Leucine-rich repeat domain	D-glucose-binding protein with LRR protein	D-glucose-binding protein with LRR protein
Sapur.0120G0240.1	98.5929744	0.150207261	0.093817926	-1.61779	0.105736093	0.137347164	grey	-0.128003514	0.141245124	GO:0008270;GO:0005622	Zinc finger (B-box type) family protein	B-box zinc finger protein	B-box zinc finger protein
Sapur.0120230600.1	0.247252582	1.462862272	0.906375581	1.617526	0.105764792	0.137790095	grey	0.242840357	0.021895645	GO:0016491	ATSDT16;ATSTS4;CDR-7-SC	sulfotransferase 16	flavonol 3-sulfotransferase, putative
Sapur.7180600.1	51.6567863	0.171681486	0.106155848	1.617297	0.105816266	0.137822415	grey	0.101682679	0.285925171	GO:0016020		NA	ABC 2 type transporter family protein
Sapur.7020600.1	13.06102092	0.109744762	0.067859501	1.617235	0.105827557	0.13726427	grey	0.186492155	0.019355006			NA	
Sapur.0180278500.1	175.8187934	-0.153272372	0.095060364	-1.61721	0.105832327	0.137245457	grey	-0.12867026	0.182368184	GO:0071805;GO:0016020;GO:0015079	KUP6	K+ uptake permease 6	high-affinity potassium transporter protein, putative
Sapur.0130107200.1	0.426120959	0.543876693	0.336760337	1.615003	0.106309095	0.137850958	grey	0.395510783	2.95E-07	GO:0016021;GO:0005789		OPR0D1 family protein	OPR0D1 family protein
Sapur.0162B72000.2	8.578631666	0.171318963	0.108475475	-1.61455	0.106489416	0.137861336	grey	-0.302805193	0.000115883			NA	palade
Sapur.0120G0270000.1	0.275421562	0.765447156	0.4606129	-1.61429	0.106473809	0.138060695	grey	0.144876035	0.06632507			hypothetical protein	hypothetical protein
Sapur.0180261800.1	1.085763353	0.452601086	0.280400370	-1.61412	0.106501119	0.138090976	grey	-0.144970978	0.070318192	GO:0055114,GO:0020037,GO:0006979,GO:0004601	Peroxidase superfamily protein	NA	NA
Sapur.0160B60600.1	0.986609276	0.168141881	0.104158284	1.614066	0.106506627	0.138092561	grey	0.133842293	0.09403933			hypothetical protein	hypothetical protein
Sapur.0105135300.1	1128.298693	0.05208101	0.034128146	1.613947	0.106539982	0.138129881	grey	0.113615781	0.15653283	PSC52	delta 1-pyrroline-5-carboxylate synthase 2	delta-pyrroline-5-carboxylate synthetase	delta-pyrroline-5-carboxylate synthetase
Sapur.0070265700.9	0.40543483	0.168565191	0.108316855	1.613166	0.106671643	0.138295322	grey	0.151151408	0.05816518			retrograde transport Golgi-like protein	retrograde transport Golgi-like protein
Sapur.0170076500.3	9.514266235	0.158085764	0.098104079	1.612948	0.106759593	0.13839927	grey	0.123077003	0.126618863		PHD finger family protein	sister chromatid cohesion protein	
Sapur.0180263200.1	1.786405421	0.377079553	0.234315507	1.612223	0.106913151	0.138598264	grey	0.15135624	0.102405604	GO:0006468,GO:0005524,GO:0004672	5-lox-out-like protein kinase family protein	NA	NA
Sapur.0301327300.1	0.501261644	0.670267902	0.416581288	1.611789	0.107007785	0.138715039	grey	0.081188711	0.312146958			NA	NA
Sapur.0180268800.1	0.357416932	0.627172344	0.389297731	1.610935	0.107192343	0.138856769	grey	-0.128870426	0.172364628	GO0043531	Disease resistance protein (TIR-NBS-LRR class) family	NA	NA
Sapur.0162B79100.4	7.700357622	0.163491047	0.101503046	-1.607	0.107344931	0.139011554	grey	0.081608864	0.309509042	GO:0015770;GO:0008515,GO:0005887	ATSUC1;ATSUT2;SUC1;SUT1	sucrose transporter 2	sucrose transporter 2
Sapur.0105135200.1	1.998611168	0.313028161	0.194379462	1.610947	0.107380311	0.139077989	grey	0.143399552	0.076897669			NA	NA
Sapur.0092680800.1	55.10236754	-0.125566376	0.07618854	-1.61043	0.107569124	0.139077989	grey	-0.147768092	0.064790946		Protein of unknown function (DUF3645)	cinnabulin-binding protein, putative	
Sapur.0070127300.1	185.173005	0.203932665	0.126392222	-1.61034	0.107232859	0.139096212	grey	-0.153009406	0.055741773	GO:0016758,GO:0008152	UGP-glucosyltransferase 7#2	UGP-glucosyltransferase 7#2	NA
Sapur.0180261800.1	2.189978814	0.345895854	0.214057522	1.609828	0.107433149	0.139310193	grey	-0.138151596	0.08331563		Calcium-binding EF-hand family protein	calcium-binding protein CML11, putative	calcium-binding protein CML11, putative
Sapur.0140205900.1	3.624052282	0.222319164	0.1380488	-1.60971	0.107460186	0.139257821	grey	-0.10879832	0.175035659	GO0022916;GO:0008168	Leucine carboxyl methyltransferase	Leucine carboxyl methyltransferase	leucine carboxyl methyltransferase
Sapur.0051371200.1	17.10445727	0.102856688	0.067404183	1.607967	0.107824246	0.139742245	grey	0.118574486	0.139116628	GO:0016567;GO:0006608	IBR domain-containing protein	E3 ubiquitin-protein ligase BAH1	ubiquitin-1 protein, putative
Sapur.0151155800.1	1429.572625	0.054399513	0.033885643	1.605386	0.108408905	0.140470759	grey	0.140660378	0.078883306		tetratricopeptide repeat (TPR)-containing protein	TPR containing protein	NMDA receptor-regulated protein
Sapur.0180261900.1	0.353637774	0.702068846	0.437485517	-1.6051	0.108470767	0.140545641	grey	-0.218609806	0.055300022	GO:0005886	RHO guanyl-nucleotide exchange factor 2	RhoGuanine nucleotide exchange factor, putative	RhoGuanine nucleotide exchange factor, putative
Sapur.0092G170400.1	3.227160209	0.304163294	0.189548894	1.604737	0.108551685	0.140664746	grey	0.096658853	0.23891611			NA	transmembrane protein, putative
Sapur.0180263600.1	159.6560848	0.124884323	0.077836762	-1.60464	0.108573003	0.140666037	grey	-0.119337004	0.13723841			hypothetical protein	hypothetical protein
Sapur.0130064200.1	408.891119	0.099367021	0.061934107	1.604399	0.108636123	0.140730165	grey	0.108915804	0.174368466	GO:0006468,GO:0004672	shaggy-related kinase 11	shaggy-related kinase 11	glycogen synthase kinase-3 protein
Sapur.0301441200.1	0.200882897	-1.016721434	0.63400454	-1.60357	0.108809744	0.140954675	grey	-0.359876696	3.67E-06		sulfotransferase 2A	SULTA,ST2A	NA
Sapur.0051541200.1	747.4041964	0.057305127	0.035802508	-1.60303	0.108957152	0.141098851	grey	-0.112168312	0.141498712	GO:0016020	Homeobox-leucine zipper superfamily protein	LD	Homeobox-leucine zipper protein
Sapur.0170134800.1	0.71037026	0.550088536	0.343387335	1.601948	0.109167185	0.141403441	grey	0.108249568	0.174873598		Plant self-incompatibility protein S1 family	plant self-incompatibility protein S1 family	plant self-incompatibility protein S1 family
Sapur.0050275400.1	2.364776132	-0.3640496	0.2274661	-1.60168	0.109247499	0.141601393	grey	-0.122068418	0.12033174		Tudor/PWWP/MBT superfamily protein	enhancer of ag-4 protein, putative	enhancer of ag-4 protein, putative
Sapur.0201691500.2	9.85408804	0.339429002	0.211955611	1.601389	0.109270772	0.141552486	grey	0.228321686	0.004026335	GO:0071805;GO:0016020;GO:0015079	K+ uptake transporter 3	K+ uptake transporter 3	potassium transporter
Sapur.0201561200.1	39.04967384	0.370029161	0.231019347	1.601185	0.109319347	0.141605288	grey	0.118371604	0.147452268		SPX (SYG1/PHO81/XPR1) domain-containing protein	SHA1,NLA	1-diquinzin-protein ligase BAH1
Sapur.0130130500.1	0.33027996	0.654499591	0.408931366	1.60071	0.109441264	0.141730701	grey	0.142201883	0.075363443	0.0055515	receptor like protein 12	ARLR12,RLP12	receptor like protein 50
Sapur.0180262500.1	2.616273138	0.258463886	0.161498585	1.600585	0.109648823	0.141760834	grey	0.135142811	0.105552661	0.0055515	receptor like protein 50	ARLR50,RLP50	receptor like protein 50
Sapur.0162G120300.3	19.41173406	0.114218723	0.071363798	1.600514	0.109487411	0.141775864	grey	0.147684473	0.066917089	GO:0019773;GO:0006511;GO:0004175;GO:0051603;GO:0005839;GO:0004298	PAC1	20S proteasome alpha subunit C1	proteasome subunit alpha type-4 protein
Sapur.0596G0300.2	8.323937295	-0.146390128	0.091496059	-1.6	0.109599317	0.141918715	grey	-0.12537152	0.117691875		MA3 domain-containing protein	topoisomerase-like protein	topoisomerase-like protein
Sapur.0061G120300.1	42.52246865	-0.146879657	0.09250727	-1.59897	0.110648555	0.142176569	grey	-0.147585652	0.050308299		Glycosylase/Protease/Protease inhibitor/Oleuropeane superfamily protein	Glycosylase/Protease/Protease inhibitor/Oleuropeane superfamily protein	lactoylglutathione lyase
Sapur.0081G120300.3	0.352219394	-0.736391145	0.462509474	-1.59908	0.110802994	0.142371321	grey	-0.091884818	0.253420993		ARM repeat superfamily protein	NA	NA
Sapur.0180261500.1	2.309667788	0.162218129	0.1027889	-1.59849	0.110904328	0.142320224	grey	0.123008574	0.181810013	0.0055515	F-box family protein	F-box family protein	NA
Sapur.0160A07700.1	16.46811908	0.146736401	0.091804092	-1.5936	0.109661811	0.142630326	grey	-0.14838876	0.06363553			hypothetical protein	hypothetical protein
Sapur.0180261400.1	1.071330608	0.441213338	0.279088673	-1.59095	0.110217347	0.142432239	grey	0.078634734	0.324667207	GO0003677		NA	B3 DNA-binding domain protein
Sapur.0092680800.1	134.5553434	-0.077685886	0.04861965	-1.59783	0.110801042	0.14250344	grey	-0.123160702	0.124360943	GO0008270;GO0003676	GRF-zinc finger / Zinc knuckle protein	GRF-zinc finger protein	GRF-zinc finger protein
Sapur.0060221700.1	0.538628677	0.425466594	0.267154968	-1.59756	0.316434666	1.59736	grey	-0.244896456	0.032325926			hypothetical protein	hypothetical protein
Sapur.0201002000.1	62.52855889	-0.085699506	0.053928383	-1.59712	0.110238843	0.142696548	grey	-0.128885206	0.113291678		ATP binding/nucleic acid binding/helicases	NA	NA
Sapur.0180262700.1	0.52369717	-0.545595674	0.343427885	-1.59676	0.110318409	0.142793562	grey	-0.156549002	0.051022223		with no tyrosine kinase motif	ATWNK6,WNK6,ZWK	NA
Sapur.0140251500.1	11.60246223	-0.346513951	0.21716359	-1.59602	0.110484765	0.143003683	grey	-0.118347552	0.139881017	GO:0055114,GO:0020037,GO:0016705,GO:0005506	cytochrome P450, family 704, subfamily A, polypeptide 2	CYP704A2	cytochrome P450, family 704, subfamily A, polypeptide 2
Sapur.0092G340400.1	38.00854438	0.118381351	0.071232531	1.595988	0.110604148	0.143306724	grey	0.123762992	0.125191919	0.0005160	Signal transduction histidine kinase, hybrid-type, ethylene sensor	ERH4	Signal transduction histidine kinase, hybrid-type, ethylene sensor
Sapur.0130137800.1	1662.810504	-0.070854651	0.04623809	-1.59502	0.110750611	0.143809564	grey	-0.115217071	0.084390564	GO:0055114,GO:0016616,GO:0009699,GO:0003854	cinnamoyl-coa reductase 1	ATCCR1,CCR1,IRX4	cinnamoyl-CoA reductase
Sapur.7092700.1	5.890806439	0.155916122	0.09828251	-1.5947	0.110779312	0.143860893	grey	-0.114607555	0.152927502			NA	NA
Sapur.0120G0280000.1	0.98663963	0.187124907	0.118046187	1.594669	0.110824158	0.143446261	grey	0.123008208	0.269161341	GO:0006468,GO:0005524,GO:0004672	Protein kinase superfamily protein	NA	NA
Sapur.0120G0850000.1	0.72853881	-0.658813463	0.286602227	-1.59487	0.110919317	0.14353805	grey	-0.103019902	0.199075444			NA	NA
Sapur.0180263300.1	1.532593879	0.209692834	0.13862595	-1.59383	0.111066373	0.143744194	grey	0.079460004	0.12232201			NA	NA
Sapur.0070202900.1	0.735593485	0.671082846	0.431249285	1.593078	0.111142777	0.14381597	grey	0.163085589	0.043864227	GO:0055114,GO:0020037,GO:0016705,GO:0005506	CYP721A1	cytochrome P450, family 721, subfamily A, polypeptide 1	NA
Sapur.0151171200.1	45.54507511	0.164388832	0.108409785	-1.59325	0.111261019	0.143858848	grey	-0.138718267	0.094804842	GO:0005886	CORI,CORI6,ERB143,FUS7	CORI signaloosome, subunit CNB	NA
Sapur.0120389800.1	0.23149764	-0.796329201	0.500554486	-1.59248	0.111275801	0.143971202	grey	-0.285157005	0.00294767			NA	NA
Sapur.7040700.1	27.68852664	0.116586203	0.073476494	1.592202	0.111339434	0.144067984	grey	0.089026191	0.247469354	0.0055515	Dor/lin alpha motif (SAM) domain-containing protein	Dor/lin alpha motif (SAM) domain-containing protein	SAM domain protein
Sapur.0180262700.1	1.279039904	-0.415200883	0.2634786	-1.59198	0.111388819	0.144307467	grey	-0.011888819	0.816887781	GO:0055087;GO:0005524,GO:0004140	dephospho-CoA kinase family	dephospho-CoA kinase	dephospho-CoA kinase
Sapur.0162Q80800.1	2.297216935	0.289298242	0.1818559	1.591248	0.111535813	0.144313065	grey	0.104172118	0.194161401			NA	NA
Sapur.7107300.1	0.604437344	0.151379962	0.10646311	1.590595	0.111708803	0.144692314	grey	0.143008833	0.076315178			NA	NA
Sapur.0161A07900.1	3.320767049	0.299077615	0.188030991	1.590576	0.111709888	0.144692231	grey	0.118518847	0.139092996	GO0006468;GO0005524,GO:0004672,GO:0030246	Concanavalin A-like lectin protein kinase family protein	NA	NA
Sapur.0301461000.1	0.208802873	-0.610008264	0.3847786	-1.59037	0.111718322	0.144506825

Sapur.01G0102000.1	1.27882904	0.37906514	0.24568994	1.542865	0.12863511	0.15840869	grey	0.11789566	0.14141123	EG:0006351,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AT4G45650.1	AGL6	AGAMOUS-like 6	NA
Sapur.15W0007300.1	650.9834746	-0.05501737	0.03602907	-1.54241	0.12397071	0.15875727	grey	-0.10716376	0.18169705	GO:0004386	AT5G12490.1	EMB2733,ESP3	RNA helicase family protein	NA
Sapur.01G0300200.1	148.8947758	-0.12861751	-0.08149456	-1.54149	0.12308879	0.15841687	grey	-0.14873007	0.18330492		AT1G67360.1			hypothetical protein
Sapur.09G0260900.1	29.23120037	-0.04296991	0.06764932	-1.54188	0.12310698	0.15843152	grey	-0.12025913	0.13154868	GO:0005515	AT3G19260.1		RING/FYVE/PHD zinc finger superfamily protein	PHD-Finger protein
Sapur.03G0210900.1	4.08031012	-0.23235304	0.10072875	-1.54157	0.12317538	0.15852072	grey	-0.13243634	0.18846206	GO:0003674	AT5G17640.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1)-like protein
Sapur.01G0241100.1	0.31869851	0.88634125	0.57503585	1.541368	0.12327341	0.15879308	grey	-0.14527323	0.08947628	GO:0016829,GO:0010333,GO:0008152,GO:0000287	AT5G23960.1	ATTPS21,TPS21	terpene synthase 21	terpene synthase
Sapur.01G0207000.1	1.72206293	0.35070167	0.22750549	-1.54123	0.12320143	0.15880177	grey	-0.11870035	0.15569829		AT5G56900.1		Transducin/WD40 repeat-like superfamily protein	aladin
Sapur.09G0135000.2	0.19141234	1.08756151	0.67148139	1.540975	0.12322016	0.15876499	grey	0.26742518	0.00262213	GO:0006468,GO:0006472	AT2G38670.1		ACT-like protein tyrosine kinase family protein	tyrosine kinase domain protein
Sapur.09G0202000.8	0.34816386	0.60817269	0.39475159	1.540633	0.12360105	0.15877765	grey	0.16595782	0.02777984	GO:0006468,GO:0006472	AT4G32660.1	AME3	Protein kinase superfamily protein	Serine/Threonine kinase AFC3
Sapur.04F0150700.1	170.9032245	0.85268452	0.55656167	1.539348	0.12361487	0.15879057	grey	0.09947929	0.21128227	GO:0006355,GO:0003700	AT1G12120.1	ATSIB-E,ATERF4,ERF4,RAP2.4	ethylene responsive element binding factor 4	AP2/ERF domain transcription factor
Sapur.05G0300600.1	201.5077827	-0.05881191	0.08286656	1.540516	0.12340719	0.15880106	grey	0.09478534	0.12765934		AT5G05170.1		Phosphoglycerate mutase family protein	NA
Sapur.09G0298400.1	1.04549249	-0.35806702	0.23260429	-1.53879	0.12383604	0.15931267	grey	-0.01317617	0.03833571	GO:0043169,GO:0005975,GO:0003824,GO:0004553	AT5G03650.1	SBE2.2	starch branching enzyme 2.2	starch branching enzyme II
Sapur.01T0061200.1	0.70021045	-0.42266799	0.28120719	-1.53862	0.12388048	0.15937411	grey	-0.11706207	0.14426611		AT3G28455.1	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.01G0251400.1	1.70041543	0.38778574	0.24906518	-1.53813	0.12407261	0.15938125	grey	0.15243512	0.03456348	GO:0006468	AT2G26040.1		HXXXD-type acyltransferase family protein	2-hydroxybenzoyl-2-deoxyxoxol N-benzoyltransferase, putative
Sapur.09G0298900.5	5.90463942	0.25000382	0.16257636	1.537961	0.12405856	0.15956623	grey	0.25995904	0.00109107		AT2G03420.1		Protein of unknown function (DUF789)	plant/F21B7-13 protein
Sapur.09G0298000.1	200.7134676	0.08078325	0.05058604	1.537863	0.12408248	0.15959183	grey	0.12738131	0.11268551		AT2G27730.1		Polynucleotide/nucleotide, ribonuclease H-like superfamily protein	NA
Sapur.02G0339900.1	122.0093466	0.11316185	0.07362174	1.536843	0.12433182	0.15990259	grey	0.05208419	0.23559104		AT2G32180.1	ATOPI5L,OPI5L	ovate family protein 16	NA
Sapur.07G0418000.5	30.9365669	0.35268325	0.08550926	1.536562	0.12460541	0.15985424	grey	0.17040851	0.03286884	GO:0003676	AT5G42240.2		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif protein
Sapur.09G0410500.2	28.18623176	0.35203957	0.07108475	1.536552	0.12463031	0.15985524	grey	0.14561223	0.07938364		AT5G47420.1		Tryptophan RNA-binding attenuator-like protein	tryptophan RNA-binding attenuator-like protein
Sapur.09G0130200.1	214.5874349	0.09750904	0.06246694	1.536374	0.12464586	0.16005239	grey	0.13518254	0.09140231	GO:0005515	AT5G67530.2	ASHH1,SDG26	SET domain group 26	histone lysine-N-methyltransferase
Sapur.05G0286400.2	0.59131456	0.05168317	0.29016667	-1.53292	0.12464356	0.16006227	grey	-0.21898458	0.08682829		AT5G61461.1	ATSER,SR	serine/arginine dehydratase enzyme racemase	serine/threonine dehydratase enzyme
Sapur.04G0102600.3	0.47613807	0.52055295	0.34548741	-1.53153	0.12465453	0.16028343	grey	-0.14133821	0.07745856		AT4G18290.1	KAT2	potassium channel in Arabidopsis thaliana 2	inward rectifying potassium channel protein
Sapur.09G0260200.1	961.6800268	0.05806746	0.03302585	-1.53071	0.12468485	0.16029168	grey	0.10825093	0.17217358	GO:0005525	AT2G28410.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	large subunit GTPase-like protein
Sapur.04G0271200.2	0.28723034	-0.66656891	0.43416794	-1.53473	0.12485164	0.16054569	grey	-0.16081304	0.04423051	GO:0006412,GO:0005840,GO:0003735	AT5G61170.1		Ribosomal protein S19e family protein	40S ribosomal protein S19
Sapur.01G0600300.1	1.78008458	0.38775574	0.24906518	-1.53413	0.12527428	0.15481	grey	0.15243512	0.03456348	GO:0006468,GO:0004672	AT5G60240.1		HXXXD-type acyltransferase family protein	Serine/Threonine kinase
Sapur.01G0100000.2	3.47255753	0.26036477	0.16987979	1.53265	0.12528121	0.16116267	grey	0.11453443	0.15303366	GO:0009116	AT4G12440.2	APT4	adenine phosphoribosyltransferase 4	adenine phosphoribosyltransferase
Sapur.01G0121300.1	284.0057518	0.06525894	0.04255571	1.532013	0.12532085	0.16135041	grey	0.10318079	0.20553118	GO:0006468,GO:0006472	AT5G22050.2		Protein kinase superfamily protein	kinase family protein
Sapur.03G0169600.1	0.20097611	-0.34164605	0.42628826	-1.53184	0.12550176	0.16160166	grey	0.10316156	0.00115505		AT5G65135.1	AT-EXPLATEXP5,ATEXPA5.4	expansin A5	alpha-expansin
Sapur.08G0118400.1	1.07598233	-0.47661152	0.31337259	-1.53083	0.12581073	0.16174485	grey	-0.51972613	0.3 -06-12		AT1G60910.1			DUF4238 domain protein
Sapur.01T0080600.1	0.20791493	-0.27964183	0.17462842	-1.53056	0.12589254	0.16180574	grey	0.22301601	0.00488945	GO:0007165,GO:0005515,GO:0043531	AT2G15160.1		disease resistance protein (TIR-NBS-LRR class), putative	TIR-NBS-LRR TIR type disease resistance protein
Sapur.01G0090900.1	1026.956925	0.04706474	0.03118520	1.529779	0.12607194	0.16202608	grey	0.10377214	0.19588445	GO:0005681,GO:0006606,GO:0005737,GO:0005634,GO:0005515	AT5G09270.1	IMPA-4	inositol monophosphatase family protein	inositol monophosphatase
Sapur.01G0281100.1	334.6705167	-0.07158024	-0.04918479	-1.5192	0.12619762	0.16208786	grey	-0.12268898	0.08682829		AT3G19220.1		SWI/SNF complex subunit SWI3B (ATRIP12) protein family protein	zinc ion-binding protein
Sapur.01G0118500.3	2.03604887	-0.32171943	0.21063277	-1.51961	0.12631868	0.16209786	grey	0.02671256	0.17983232		AT3G17330.2		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	DNA methyltransferase, putative
Sapur.01G0202500.4	2.52456214	0.21145079	0.13809462	-1.51782	0.12663945	0.16268691	grey	0.11138805	0.16492022	GO:0005085,GO:0016020,GO:0008811,GO:0005216	AT1G22020.1	AKT2,AKT2/3,AKT3,KT2/3	potassium channel in Arabidopsis thaila 2	pulvinus inward rectifying channel for potassium SPICK1 protein
Sapur.04G0241100.2	0.78766704	-0.46388553	0.30363891	-1.51776	0.12673179	0.16269494	grey	-0.20648395	0.08947601		AT5G05830.1		RING/FYVE/PHD zinc finger superfamily protein	RING-variant domain protein
Sapur.01G0281800.1	44.21435357	-0.20426888	0.13424869	-1.51688	0.12704732	0.16303595	grey	0.13764218	0.11362915		AT3G54340.1		RNA polymerase family protein	PHD domain protein
Sapur.05G0193300.2	1.12589823	-0.36904074	0.24183163	-1.52605	0.12689758	0.16315184	grey	-0.18228719	0.03490591	GO:0051082,GO:0009570,GO:0009507	AT5G42190.1	AtHsp90-7,AtHsp90.7,HSP90	Chaperone protein HSP90 family protein	heat shock protein
Sapur.09G0809900.1	0.35260704	-0.97174286	0.63817795	-1.52594	0.12725277	0.16318709	grey	-0.27617091	0.00462365		AT4G08960.1	ATCLC-C,CLC-C	chloride channel C	NA
Sapur.01G0341200.1	586.3202804	-0.06539268	0.04281685	-1.52465	0.12737085	0.16349488	grey	-0.11233186	0.16182915	GO:0043565,GO:0008270,GO:0006355,GO:0003700	AT4G17490.1	GATA4	GATA transcription factor 1	GATA transcription factor, putative
Sapur.T012400.5	0.32777602	0.05965969	0.38738392	1.524679	0.12739374	0.16357073	grey	0.34988276	7.01E-06	GO:0033179,GO:0015991,GO:0015078	AT5G52360.2		ATPase, V0 complex, subunit E	ATP synthase subunit H
Sapur.09G0188000.1	209.9282761	0.26108898	0.17171196	1.52467	0.12747251	0.16374624	grey	0.11318266	0.17139182	GO:0016021,GO:0008080,GO:0005783	AT3G17190.1			NA
Sapur.09G0241900.1	231.8675715	-0.15892911	0.10408788	-1.52458	0.12756603	0.16390558	grey	-0.14884004	0.06274642		AT5G42420.1	TBL36	TRICHOME BIREFRINGENCE-LIKE 36	Pmr5/CaZy GDSL/SGNH-like acyl-esterase family protein
Sapur.T158400.1	1.62526166	0.48907153	0.31875217	-1.52175	0.12817147	0.16397024	grey	-0.07604023	0.19188034		AT4G27062.2	AHTHO2,THO2	THO2	NA
Sapur.01G0222800.2	0.95443488	-0.40388516	0.26505841	-1.52226	0.12794001	0.16410783	grey	0.04301029	0.19274178		AT4G00190.1		RNA ligase/cyclic nucleotide phosphodiesterase family protein	2'-5' RNA ligase family protein
Sapur.09G0260400.1	410.498313	0.06410848	0.04044743	1.521988	0.12808214	0.16420751	grey	0.10864216	0.17407227	GO:0016480	AT3G22461.1		transcription factor	NA
Sapur.T156100.1	0.21352871	0.78922134	0.51878754	1.52128	0.12818964	0.16424659	grey	0.18990056	0.01720645		AT5G24280.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.01G0194600.1	130.1716509	0.24268888	0.15953693	1.521468	0.12829549	0.16435084	grey	0.05685071	0.47842885	GO:0016747	AT3G18660.1		HXXXD-type acyl-transferase family protein	5-trehalose family protein
Sapur.01G0261300.1	187.3777734	0.06482946	0.03978386	-1.52029	0.12843672	0.16491226	grey	0.15489913	0.04741743	GO:0006468,GO:0005524,GO:0046872,GO:0005515	AT4G19330.1		Concanavalin A-like lectin protein kinase family protein	L-type lectin-domain receptor kinase
Sapur.09G0211500.1	0.72481476	-0.46320193	0.30478999	-1.5201	0.12848701	0.16496815	grey	-0.12362317	0.18636467	GO:0045261,GO:0015986,GO:0015078	AT4G22240.1		ATPase, F0 complex, subunit B/B', bacterial/chloroplast	ATP synthase subunit B' protein
Sapur.T053500.1	0.16452631	-1.10324153	0.73068465	-1.51868	0.12854148	0.16508382	grey	0.34275256	8.63E-06					NA
Sapur.01G0241000.2	0.81243036	-0.3970386	0.26160707	-1.51769	0.12900338	0.16570892	grey	-0.09127291	0.25121574		AT4G04032.2		Protein of unknown function (DUF639)	DUF1639 family protein
Sapur.09G0511100.1	0.4039979	0.50856025	0.33568514	-1.51682	0.12919174	0.16585109	grey	0.11147564	0.16456128					NA
Sapur.08G0289900.1	2991.03992	0.08009421	0.05281677	1.516449	0.12940569	0.16610074	grey	0.07238769	0.16101693	GO:0005515	AT5G42300.1	UBL5	ubiquitin-like protein 5	ubiquitin-like protein
Sapur.09G0140700.1	7.99681009	0.22136104	0.14610205	1.516264	0.12960824	0.16624128	grey	0.17614896	0.07372608	GO:0006950,GO:0008468,GO:0004672	AT5G57630.2		CLK/STY kinase family protein	NA
Sapur.01G0609500.1	512.8010776	0.06266709	0.04094509	1.515862	0.12954258	0.16286772	grey	0.07836542	0.34491202		AT5G52610.1			NA
Sapur.09G0580500.1	239.2418513	0.05605855	0.03699333	1.515605	0.12963326	0.16283043	grey	0.10452423	0.15368073	GO:0015031,GO:0008565,GO:0016020	AT5G08660.1		Clathrin adaptor complex small chain protein	AP-1 complex subunit sigma protein
Sapur.08G0283800.1	29.84485910	0.04969147	0.12873261	1.514895	0.12979089	0.16858089	grey	0.13570037	0.09094103	GO:0004572,GO:0003755,GO:0006413	AT5G66554.2		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	cyclophilin-type peptidyl/prolyl cis-trans isomerase family protein
Sapur.15W0362300.1	10.22296863	-0.36170989	0.23876199	-1.51482	0.12981904	0.16860489	grey	-0.16070728	0.03609586		AT2G27740.1	EMB3161,EMB2751,EMB2775	ATPase family associated with various cellular activities (AAA)	NA
Sapur.01G0279900.2	36.18554661	0.07008346	0.04667286	0.07060149	-1.51364	0.16660428	grey	-0.11839328	0.15185977	GO:0005515,GO:0003723	AT5G07670.1	eIF4e4E1	MRNA dormancy protein (PAM2 eIF4E-binding protein)	eukaryotic translation initiation factor iso4G
Sapur.01G0243400.2	69.15438636	0.08190688	0.05354872	1.514354	0.12993612	0.16705583	grey	0.14315451	0.0726558		AT5G06500.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RRM containing protein, putative
Sapur.09G0197000.1	130.1716509	0.24268888	0.15953693	1.514349	0.12992739	0.16705584	grey	0.11534424	0.15297779		AT5G23140.1		RNA-like superfamily protein	LRR protein
Sapur.01G0117500.1	0.25352286	0.68379266	0.45179175	1.513582	0.13013823	0.16697564	grey	0.20653809	0.08945152	GO:0005515	AT5G61730.1	AtRLP13,RLP13	receptor like protein 13	NA
Sapur.09G0251100.1	26.47997834	0.09000622	0.05948932	1.51318	0.13012614	0.16697664	grey	-0.10882637	0.17116602		AT5G58320.2		Protein of unknown function (DUF565)	transmembrane protein, putative
Sapur.T143700.1	27.16510283	0.21027268	0.13897324	1.513305	0.13026007	0.16743228	grey	0.14910207	0.06234651		AT5G17020.1	ATCRM1,ATXPO1,HET2,XPO1	exportin 1A	NA
Sapur.15W0258800.1	85.30468869	0.07183862	0.05182829	-1.51125	0.13064304	0.16763113	grey	0.10409247	0.19188034		AT5G42420.1	EMB2733,ESP3	RNA helicase family protein	NA
Sapur.04G0281000.1	2.63774225	0.38089234	0.25189732	1.512091	0.13053806	0.16764305	grey	0.08529161	0.21898143	GO:0006468,GO:0006355,GO:0005634,GO:0003700	AT2G32330.1	ATHSFA3D,HSFA3D	heat shock transcription factor A3D	HSF-type DNA-binding protein family
Sapur.09G0270300.1	1464.709718	0.04356837	0.03027514	1.511967	0.13054536	0.16765153	grey	0.13824046	0.08346384	GO:0055114,GO:0016491,GO:0008152,GO:0010930,GO:0006807,GO:0016638,GO:0006563	AT5G18260.1	FD,GOGAT,GLS1,GLU1,GLU1	glutamate synthase 1	ferredoxin-dependent glutamate synthase
Sapur.08G0202500.2	25.14497604	-0.12821335	0.08523158	-1.51161	0.13063258	0.16758267	grey	0.06891658	0.19113953		AT3G28625.1			hypothetical protein
Sapur.01G0195900.1	0.38198322	-0.61700135	0.40840182	-1.51077	0.13084555	0.16787767	grey	-0.15452922	0.05257968		AT5G23380.1		Protein of Unknown Function (DUF239)	Protein of unknown function
Sapur.09G0251700.2	1.76448884	0.08240438	0.08882042	-1.51069	0.13088045	0.16784477	grey	0.11451803	0.13123869	GO:0016787	AT5G22200.1	PYD2	pyrimidine 2	dihydropyrimidinase
Sapur.01G0271200.1	147.5658328	-0.05026444	0.03248218	-1.51055	0.13090826	0.16790926	grey	-0.15660931	0.05005426		AT3G27110.2	FRS3	FARS-related sequence 3	COIN6M domain protein, putative
Sapur.T056200.1	1.00845259	-0.37134301	0.24509219	-1.5097	0.13111563	0.16830312	grey	-0.13201572	0.09327869		AT3G26615.1	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.01T0261000.1	0.45222514	0.50303687	0.33364575	1.509477	0.13117851	0.16835363	grey	0.10717859	0.16152827	GO:0006468,GO:0005524,GO:0004672	AT4G26980.1	SNC4	suppressor of npr1-1 constitutive 4	NA
Sapur.01G0560200.1	2.56189727	0.30720164	0.20360743	1.509408	0.13119456	0.16836154	grey	0.07059396	0.19188034					NA
Sapur.05G0197200.3	0.46561855	0.62747439	0.41573183	1.509325	0.13121546	0.16842069	grey	0.46085921	1.26E-09	GO:0008270	AT5G27280.1		Zim17-type zinc finger protein	DNL zinc finger protein
Sapur.01G0134100.1	10.64252117	0.28202746	0.18569674	1.508661	0.13156561	0.16892265	grey	0.15615691	0.1872242		AT3G60930.1			hypothetical protein
Sapur.03G0127400.1	60.09447777	-0.12743626	-0.08207055	-1.50777	0.13161054	0.16876562	grey	0.14432945	0.09331425		AT3G48660.1		Protein of unknown function (DUF3339)	transmembrane protein, putative
Sapur.01G0298800.2	7.55721874	0.36567885	0.10905625	1.507467	0.13188213	0.16885568	grey	0.19930143	0.08166858	GO:0006221,GO:0003883	AT4G02120.1		CTP synthase family protein	CTP synthase
Sapur.01G0258000.1	177.3872469	-0.46427032	0.30281626	-1.50727	0.13190521	0.16891591	grey	-0.20544749	0.08846628					NA
Sapur.01G0495500.1	103.7604847	0.12307448	0.08164926	1.507148	0.13172695	0.16896676	grey	0.12824113	0.10950817		AT3G18640.2	PSP	3-phosphoserine phosphatase	phosphoserine phosphatase
Sapur.05G0490100.1	0.20641932	0.78582703	0.49473876	1.5073	0.13177069	0.16896676	grey	-0.21020285	0.05684455	GO:0016567,GO:0006842	AT4G27440.1	UBC13	ARM repeat superfamily protein	E2 ubiquitin ligase PUB14, putative
Sapur.15W0256100.1	11.0873974	-0.12299088	0.08795751	-1.50701	0.13180928	0.16883771	grey	-0.07450134	0.15218232	GO:0008017,GO:0007018,GO:0055124,GO:0030377,GO:0005871	AT5G18430.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.05T0144600.7	21.98071334	-0.08845163	0.07193261	-1.50699	0.13181383	0.16883771	grey	-0.11521762	0.15074264		AT3G54340.2			hypothetical protein
Sapur.01B0202800.1	16.15946134	-0.11281138	0.07488436	-1.50647	0.13194757	0.16916326	grey	-0.12601452	0.13241884	GO:0009976	AT4G12770.1	ATSDX1,VTE1	tocopherol cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose-export defective 1 (SXD1)	tocopherol cyclase
Sapur.09G0807200.4	0.30163768	0.50148193	0.40002247	-1.50621	0.13198565	0.16918264	grey	-0.07924263	0.31928225	GO:0016887,GO:0005524	AT5G67520.1	ATNAP7,NAP7	non-intrinsic ABC protein 7	iron-sulfur cluster-interaction ABC transporter
Sapur.T076600.1	7.27914386	-0.16710652	0.10928993	-1.50624	0.13205797	0.16910128	grey	0.09363873	0.24346414		AT4G16450.2			NA
Sapur.01G0214000.1	99.11893815	0.07105159	0.04724555	1.505771	0.13212566	0.16937589	grey	0.10347478	0.19188034		AT2G20790.1		clathrin adaptor complexes medium subunit family protein	adaptor complexes medium subunit family protein
Sapur.07G0462000.1	0.97033816	-0.41509688	0.27633402	-1.50519	0.13227572	0.169543	grey	0.18080737	0.0234671					NA
Sapur.05G0203900.1	0.34418658	0.82232286	0.54636583	1.504885	0.13235689	0.16963847	grey	0.19955327	0.01233369		AT3G55000.3		peptidoglycan-binding LysM domain-containing protein	NA
Sapur.09G0217900.1	5.24454573	0.07107256	0.04728584	1.504808	0.13240552	0.16970194	grey	-0.20544749	0.08846628					NA
Sapur.09G0127100.1	0.49101863	0.12307448	0.08164926	1.504148	0.13172695	0.16896676	grey	0.12824113	0.10950817		AT3G07033	PDV1	plastid division1	NA
Sapur.01G0361000.2	0.20641932	0.78582703	0.49473876	1.50313	0.13277069	0.16896676	grey	-0.21020285	0.05684455	GO:0016567,GO:0006842	AT4G27440.1	UBC13	LOB domain-containing protein 13	E2 ubiquitin ligase PUB14, putative
Sapur.03G0181000.1	414.3621164	0.04257179	0.06934035	1.503557	0.13265432	0.17004795	grey	0.10059327	0.21000806	GO:0003824	AT4G10750.1		Phosphoenolpyruvate carboxylase family protein	2K2C4-dihydroxyhept-2-ene-1%2C7-dioic acid aldolase
Sapur.01G0491200.2	0.67660664	-0.34681396	0.12291922	1.503501	0.13279918	0.17050997	grey	0.11273687	0.16673218		AT5G49120.1	ATSNAP33,ATSNAP33B,SNA	soluble n-ethylmaleimide-sensitive factor adaptor protein 33	synaptosome-associated protein
Sapur.05G0607000.1	0.30118811	-0.82766606	0.57581912	-1.53346	0.12271647	0.17006841	grey	-0.21497166	0.03387805		AT5G10130.1		Pollen Ole e 1 allergen and extensin family protein	pollen protein Ole E 1-like protein
Sapur.01G0243600.1	126.6214969	0.17330291	0.11435128	1.502564	0.13272422	0.17007527	grey	-0.11439255	0.15498568		AT4G34250.1		Uncharacterized protein	4F5 family protein
Sapur.09G0294300.1	264.4576431	0.13177365	0.08765423	1.503332	0.13275106	0.17009054	grey	-0.11769198	0.14210584	GO:0016887,GO:0005524,GO:0016020	AT2G69510.1	ATPDR11,PDR11	pleiotropic drug resistance 11	pleiotropic drug resistance ABC transporter family protein
Sapur.09G0297000.2	2.56890274	0.32568391	0.22168581	-1.5313	0.13277334	0.17054003	grey	-0.06577968	0.41343682	GO:0005524,GO:0004812	AT5G67060.1		Protein kinase superfamily protein	CDK-related kinase
Sapur.03G0158300.2	4.23183503	-0.26697783	0.17784022	-1.5085	0.13339349	0.17080114	grey	-0.20927414	0.71775647	GO:0005840,GO:0005622,GO:0003735	AT2G37850.1		Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L18
Sapur.15W0023100.1	0.26795518	-0.71076543	0.47357597	-1.50085	0.13395468	0.17080114	grey	-0.21605507	0.00643407					NA
Sapur.01G0217900.2	4.53073994	-0.21384121	0.14245148	-1.50029	0.13404203	0.17107067	grey	-0.10424348	0.19385112		AT5G53150.1		DNA/ heat shock N-terminal domain-containing protein	Dnaj family & protein
Sapur.01T0126900.1	2.88002391	0.68975122	0.45988737	1.499827	0.13365178	0.17216687	grey	0.11970873	0.13149001					NA
Sapur.01G0181500.1	24.67021884	0.17816185	0.11882834	1.49956	0.13395138	0.17365512	grey	-0.1361625	0.08939045	GO:0005515	AT4G34150.1		Calcium-dependent lipid-binding (CaLB domain) family protein	C2 domain protein
Sapur.04G0138800.1	4.38018553	-0.36260593	0.24196892	-1.49872	0.13347297	0.17157204	grey	-0.10385741	0.19558791					NA
Sapur.01G0264700.1	0.36861977	0.76097842	0.51588408	1.497679	0.13423178	0.17301005	grey	0.20898205	0.08622212		AT3G10160.1		Plant protein of unknown function (DUF247)	NA
Sapur.01G0230300.1	0.79123863	-0.42000114	0.28776627	-1.4975	0.13426321	0.17364334	grey	-0.12715003	0.11234955	GO:0003682,GO:0005515	AT5G50620.1		RING/FYVE/PHD zinc finger superfamily protein	PHD Finger protein
Sapur.09G0187300.1	1.30958716	0.15968583	0.10848103	-1.49718	0.13439359	0.17396058	grey	-0.13031926	0.10369883	GO:0006468,GO:0005524,GO:0004672	AT5G60660.1		Protein kinase family protein	NA
Sapur.05G0247700.1	60.89642363	0.17932218	0.11984162	1.49641	0.13456881	0.17231786	grey	0.12734368	0.12245077	GO:0048544,GO:0006468,GO:0055124,GO:0004672	AT5G34300.1		lectin protein kinase family protein	NA
Sapur.01G0257500.1	0.30568756	-0.80580674	0.53834346	-1.49637	0.13457422	0.17220614	grey	-0.29324052	0.00017417					NA
Sapur.01T0072300.1	1.38271519	-0.90539303	0.60458692	-1.49576	0.13473115	0.17251614	grey	-0.16231115	0.41175514	GO:0006355,GO:0003700	AT1G19790.1	RAP2.11	related to AP2 11	AP2/ERF domain transcription factor
Sapur.01G0247000.1	179.4357114	-0.45682765	0.30558816	-1.49504	0.13492797	0.17274564	grey	-0.19055473	0.01824818					NA
Sapur.01G0560600.1	443.1010234	0.07588508	0.05078264	1.494664	0.13491819	0.17276784	grey	0.09923872	0.21231993		AT5G15980.1		ARM repeat superfamily protein	NA
Sapur.01G0211900.1	0.26238247	0.87820258	0.58808934	1.493429	0.13532691	0.17327623	grey	0.17625879	0.07231527		AT5G10040.1		RWP-RK domain-containing protein	NA
Sapur.09G0260500.1	0.88648437	0.50180557	0.33613269	1.492924	0.13545699	0.17340065	grey	0.25858685	0.00017417	GO:0006355,GO:0003700	AT4G13J3,GLR3.3		glutamate receptor 3.3	glutamate receptor
Sapur.09G0087000.1	21.75367066	-0.61266232	0.18820999	-1.49273	0.13550746	0.17394388	grey	-0.23671003	0.00281561	GO:0016020,GO:0008378,GO:0004886,GO:0030246	AT4G21060.2		Galactosyltransferase family protein	galactosyltransferase family protein
Sapur.01G0284000.1	0.53459845	-0.21384121	0.14245148	-1.49259	0.13554203	0.17409387	grey	-0.10424348	0.19385112		AT4G27600.1	VAP27-2	vamp/synaptobrevin-associated protein 27-2	NA
Sapur.04G0220800.1	17.30283447	0.44873271	0.30036305	1.492439	0.13558426	0.17581806	grey	0.18974444	0.01275309		AT5G54330.1	AGD5,NEV	ARF-GAP domain 5	NA
Sapur.01G0113000.1	0.61871984	0.54680336	0.36453077	1.492363	0.13563506	0.17341454	grey	0.13883388	0.18194107					NA
Sapur.04G0230900.2	0.31667751	0.68284734	0.45752524	1.49171	0.13575303	0.17376427	grey	0.10482427	0.19145368	GO:0006468,GO:0004672	AT4G03390.1	SRF3	STRUBBELIG-receptor family 3	strubbelig family receptor kinase, putative
Sapur.15W0227300.1	2.28080434	0.29273152	0.19650278	-1.4917	0.13579568	0.17376427	grey	-0.13168795	0.10016751		AT4G45470.1		Protein of unknown function (DUF594)	transmembrane protein, putative
Sapur.09G0137000.1	186.0070924	0.06273956	0.04207234	-1.49147	0.13588813	0.17867373	grey	0.10482427	0.19145368	GO:0006468	AT2G20920.1		Protein kinase superfamily protein	transmembrane protein, putative
Sapur.01G0219900.2	0.62752885	0.51186497	0.34323501	1.49061	0.13585159	0.17409763	grey	0.10258579	0.18940792	GO:0006260,GO:0005634	AT4G12530.1	PSF2	DNA replication complex GINS protein PSF2	DNA replication complex GINS protein psf2
Sapur.06G0097700.4	0.27331898	0.64204564	0.48682455	-1.49058	0.13607297	0.17446884	grey	-0.17562167	0.07598463

Sapur.T154700.1	2.31264828	0.22002353	0.159535542	-1.44734	0.14780403	0.18817078	grey	-0.115694284	0.14904569	GO0006468;GO0005524;GO0004672	KTSG02680.1	Protein kinase superfamily protein	NA
Sapur.G06G194500.1	2.00569873	0.29315754	0.202970037	-1.44719	0.14784445	0.18821404	grey	-0.18677813	0.03916593	GO0016021;GO0125111	KTSG25890.1	Oleosin family protein	NA
Sapur.G03G188600.4	4.63773779	0.52389076	0.361715163	-1.44674	0.14795949	0.18824723	grey	-0.05394865	0.52195407		KTSG26100.1	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.G02G209000.3	0.25257982	0.27481897	0.664150526	1.44669	0.14798394	0.18836422	grey	-0.0397784	0.621930095	GO0008270;GO0004089	KTSG14740.1	BETA CA2,CA1;CA2	carbonic anhydrase
Sapur.G13G136001.1	0.71672224	0.45049663	0.313152631	-1.44581	0.14821553	0.18857175	grey	-0.12447042	0.12037604		KTSG0551.1	HIT-type Zinc finger family protein	zinc finger protein
Sapur.G02G050500.1	0.30549126	-0.69408256	0.481000018	-1.44572	0.14825687	0.18871557	grey	-0.48927827	7.91E-11	GO003477	KTSG35532.1	ATWOX1,3;AB-4;WOX13	WUSCHEL related homeobox 13
Sapur.T167100.1	5.56267493	0.27639392	0.191186282	1.44567	0.14828298	0.18872489	grey	0.11347305	0.15719344				NA
Sapur.T095700.1	0.30619984	0.50225015	0.347612	1.44458	0.14899746	0.18900327	grey	0.10070881	0.28201208				NA
Sapur.G04G124100.1	26.76169964	0.09322268	0.133826215	1.44457	0.14857646	0.18908822	grey	0.10172751	0.20495401	GO0009733	KTSG18840.1	SAUR-like auxin-responsive protein family	NA
Sapur.G05G188400.1	441.26261139	0.55025508	0.564635959	1.44447	0.14866698	0.18919182	grey	-0.11531876	0.102969318	GO005515	KTSG16310.1	LDL1	lysine-specific histone demethylase, putative
Sapur.G17G09800.4	1.86823621	-0.30444494	0.21077311	-1.44443	0.14867343	0.18925433	grey	0.16891878	0.03666577	GO005515	KTSG34260.1	transducin family protein / WD-40 repeat family protein	transducin family protein
Sapur.G04G207400.4	2.45147204	0.74482464	0.52576254	-1.44384	0.14875438	0.18950274	grey	-0.11482421	0.13264869	GO0031588	KTSG18410.1		elongator subunit 5b1
Sapur.G13G023900.1	0.42101694	-0.57403679	0.397602279	-1.44372	0.14881599	0.1893657	grey	-0.19749343	0.03617954	GO005515;GO003676	KTSG48410.1	AGO1	Stabilizer of iron transporter SufD / Polynucleotidyl transferase
Sapur.G02G406600.1	1.18378999	0.07583021	0.2335	1.44368	0.14883486	0.18937002	grey	0.11531262	0.15102703		KTSG36100.1		NA
Sapur.I59G119200.1	88.2056551	0.11631709	0.080593185	1.44362	0.14894692	0.18951583	grey	-0.09346993	0.26425504	GO0010120;GO0080278;GO0006538;GO0004222	KTSG24148.1	Matrilin family protein	matrix metalloproteinase
Sapur.G14G123000.1	138.3883819	0.10374285	0.110439855	1.44358	0.14896068	0.18956623	grey	0.11318861	0.16419755	GO0016192	KTSG35782.1	Gnt1/SPO-like nucleotide transport protein family	vesicle transporter G371A
Sapur.G03G109100.4	3.02035807	-0.23757684	0.164675143	-1.44262	0.14952878	0.18975286	grey	-0.10568891	0.18863027		KTSG16580.1	Protein phosphatase 2C family protein	protein phosphatase 2C, putative
Sapur.G12G094400.2	31.90352581	0.09080499	0.07614209	1.44219	0.14926046	0.1898925	grey	0.13261329	0.095190149		KTSG32780.1	Protein of unknown function (DUF179)	electron transporter, putative
Sapur.S07G004600.1	257.2924157	0.09455126	0.078774709	1.44189	0.14933273	0.18996751	grey	0.12265687	0.18966751	EMB2001	KTSG22870.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	ribosome biogenesis GTP-binding protein YsxC/EngB
Sapur.D10G005700.2	21.83640037	0.13423832	0.093129936	1.441881	0.14933589	0.18996751	grey	0.13050884	0.10313478	GO0008152;GO0003824	KTSG15940.1	Fumarylacetoacetate (FAA) hydrolase family	fumarylacetoacetate hydrolase domain protein
Sapur.T041100.1	0.23768910	0.50225015	0.312581315	1.44116	0.14949107	0.19015152	grey	0.13270906	0.07205449		KTSG7020.1	ATCBM1,ATKPDI1,HT2,XPO	Carbohydrate-binding protein
Sapur.D02G092900.1	50.7258333	-0.03793039	0.134488936	-1.44096	0.14956273	0.19026895	grey	-0.12341971	0.12383548	GO0004689;GO0005524;GO0004672	KTSG27750.1	Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.J12G000100.1	2.25519893	0.36848086	0.33161648	-1.44076	0.14963176	0.19036002	grey	0.09449753	0.29105484		KTSG29600.1	basic helix-loop-helix (bHLH) DNA-binding family protein	NA
Sapur.D10G031100.2	0.52861222	-0.55956641	0.38840121	-1.44054	0.14971546	0.19038321	grey	-0.08809763	0.27205268	GO016787	KTSG18280.2	APY2,ATAPY2	apyrase 2
Sapur.T181000.1	0.41921739	0.07980144	0.027638302	1.44009	0.14985256	0.19045246	grey	0.11531262	0.15102703				NA
Sapur.I10G117300.1	0.21036575	0.91429145	0.634731182	1.440348	0.14989838	0.19054185	grey	0.19705578	0.03371287		KTSG17210.1	ATHSL;HS1	heat stable protein 1
Sapur.D16G083900.1	0.2554369	0.71206959	0.495023081	1.440207	0.14988802	0.19054553	grey	0.12813671	0.10835684	GO005524;GO0003700	KTSG26600.1	RING/U-box superfamily protein	NA
Sapur.D10G097000.1	2546.330057	0.09080499	0.063896623	1.440027	0.14993024	0.19062964	grey	0.15787826	0.04836778	GO0055114;GO0030037;GO0016705;GO0005506	KTSG7834.1	CYP71B34	cytochrome P450 family protein
Sapur.D05G189600.1	0.93284567	-0.46796135	0.311286271	-1.43903	0.15014171	0.19093772	grey	-0.19206655	0.01548924		KTSG15320.1		transmembrane protein, putative
Sapur.D11G056300.1	1.75305562	0.09455126	0.062944795	1.43256842	0.15038888	0.19094524	grey	-0.14373881	0.07287505		KTSG30130.1		transmembrane protein, putative
Sapur.D03G093500.1	98.06417756	0.28906879	0.200917392	-1.43865	0.15021022	0.19100653	grey	-0.15404192	0.05407767		KTSG12530.1		NA
Sapur.D10G011400.1	10.00211444	0.13878938	0.096461348	1.438488	0.15029229	0.19166331	grey	-0.12970906	0.03102049				hypothetical protein
Sapur.D13G125500.1	4.40194693	0.28565584	0.198588254	1.438407	0.15033749	0.1909206	grey	0.12465593	0.12326329	GO0010151;GO0005886;GO0005783	KTSG10880.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
Sapur.D08G184500.2	1.46732976	0.21605371	0.148889849	1.438315	0.15034422	0.19117866	grey	0.12197956	0.11908668	GO0016829	KTSG14630.1	isopropyl malate/citrate/homocitrate synthase subunit 1	3-isopropylmalate dehydratase, large subunit
Sapur.D01G076000.1	0.23370663	0.96859492	0.67153571	-1.43807	0.15046466	0.19159202	grey	-0.27212884	0.00056495		KTSG19170.1	SLP3	subtilisin-like serine protease 3
Sapur.D12G063000.2	0.48346625	0.29565584	0.203867	1.43766	0.15063766	0.19181834	grey	0.13813702	0.09814624	GO0007264;GO005525	KTSG23120.2	ATARL8;ARL;ATGB1;GB1	GTP-binding protein
Sapur.D09G081400.1	452.5272111	0.04793787	0.033361303	1.43633	0.15088492	0.19240914	grey	-0.12460508	0.13997126		KTSG5280.1	DNA/ heat shock N-terminal domain-containing protein	NA
Sapur.D03G136300.1	2.35682156	0.24877406	0.173218569	1.43619	0.15089236	0.19188056	grey	0.09948692	0.21539328				NA
Sapur.D13G209600.1	0.17367589	0.91546788	0.63743672	1.436099	0.15098245	0.19205574	grey	-0.25283037	0.05412577	GO0048500;GO0008312;GO0006614	KTSG18160.1	signal recognition particle 19 kDa protein, putative / SRP19, putative	NA
Sapur.D05G201400.1	0.34167865	-0.62339282	0.434117211	-1.436	0.15100171	0.19185877	grey	-0.23155952	0.00512309	GO005634	KTSG7630.1	CYC2;-4	cyclin B2
Sapur.D01G101200.1	181.3070877	0.09455126	0.065462446	1.435647	0.15105248	0.19185877	grey	-0.07308202	0.13148759	GO004725	KTSG3120.1	ATEYA;PYA	eyes absent-like protein
Sapur.D05G069600.1	0.71423204	-0.46859343	0.31253627	-1.43535	0.15118784	0.19223119	grey	-0.16075216	0.04432165		KTSG1275.1		transmembrane protein, putative
Sapur.D05G160600.1	180.1119092	0.09455126	0.063044887	1.435169	0.15120108	0.19231045	grey	0.06813013	0.36632015		KTSG6090.1	alpha/beta-Hydrolases superfamily protein	GDSL esterase/lipase
Sapur.D05G129800.1	280.8802115	0.12349841	0.08604705	1.435215	0.15125751	0.19215646	grey	0.11539651	0.15023458		KTSG7810.1		hypothetical protein
Sapur.T037300.1	0.25949138	0.58226685	0.40813639	1.435	0.15124416	0.19217269	grey	0.12049958	0.13801417				NA
Sapur.D10G110100.1	0.22177568	-0.70790701	0.49338033	-1.43503	0.15127849	0.19220912	grey	0.29564058	0.00017489		KTSG26910.1		hypothetical protein
Sapur.D10G241000.1	34.00873534	0.07834907	0.12429311	-1.43491	0.15132793	0.19240527	grey	-0.12427831	0.12098602		KTSG8648.1	ATFS1;FLS;FLS1	flavanol synthase 1
Sapur.D10G004045.1	409.7844679	0.05118305	0.038412744	-1.4349	0.15136504	0.19240527	grey	0.08617836	0.21503171		KTSG7000.1	myb-like transcription factor family protein	myb-like transcription factor family protein
Sapur.D05G199900.1	1412.312613	0.06885188	0.048719539	1.434704	0.15137598	0.19240623	grey	0.06495898	0.42817638	GO0017947;GO005743	KTSG7620.1		NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, putative
Sapur.D13G089100.1	0.18804928	0.91546788	0.67474702	1.434609	0.15138405	0.19235576	grey	0.25307905	0.05384349		KTSG7802.1	AtMYB56;MYB56	myb domain protein 56
Sapur.D18G099100.1	8.39787667	0.45372088	0.10172388	-1.43447	0.15143913	0.19270688	grey	-0.11378182	0.15597718	GO0003677;GO0046983	KTSG4173.1	BED zinc finger /MAT family dimerization domain	hAT-like transposase
Sapur.D03G118800.1	60.08410361	0.09455126	0.06351781	1.433697	0.15160083	0.19328316	grey	-0.10225117	0.06038869				NA
Sapur.I59G136200.1	0.28972028	-1.17619754	0.82069859	-1.4331	0.15182083	0.19285116	grey	-0.20646504	0.00947657	GO0048527;GO0042545;GO0030599;GO0005618	KTSG45220.1	Plant invertase/pectin methylesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.D01G138300.1	14.17825264	0.09455126	0.065922149	1.432976	0.15207168	0.19287599	grey	-0.12469303	0.12193724	GO0045454;GO0016026;GO0006662	KTSG5010.2	ATOL;TOL	tuboulin
Sapur.D11G111200.1	34.77637783	0.26098716	0.182278625	1.431804	0.15219998	0.19331701	grey	0.15058247	0.05974608	GO0055114;GO0016491	KTSG10500.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	non-heme dioxygenase in morphine synthesis enzyme-terminal protein
Sapur.D03G185000.1	0.34469453	0.80827349	0.56468841	-1.431131	0.15233384	0.19347327	grey	0.16074694	0.03337259	GO0016829;GO0030170;GO0008017;GO0000287	KTSG25820.1	ATTPS-CN;TPS-CN	terpene synthase-like sequence-1,8-cineole
Sapur.D16G244000.1	41.62519669	0.13709798	0.095799599	1.431092	0.15240974	0.19355691	grey	0.07561923	0.32218137				transmembrane protein, putative
Sapur.D08G005800.4	53.35998074	0.12776199	0.089329164	1.430318	0.15282672	0.19330588	grey	0.10920377	0.17338342	GO0005885;GO0020037;GO0016021	KTSG11750.1	2IP1.1	zinc induced facilitator-like 1 family protein
Sapur.D16G217001.1	6.60881129	0.07434874	0.10035924	-1.430067	0.15277607	0.19400786	grey	0.09449018	0.63037382	GO0004648;GO0005524;GO0046872;GO0005515	KTSG13154.1	SPA1	SPA1-related 3 protein
Sapur.D16G222900.1	1363.990558	0.06480374	0.045347868	1.429403	0.15288463	0.19452403	grey	0.10864241	0.17557518	GO0020750;GO0015923;GO0006013;GO0005975;GO006559	KTSG14950.1	ATGMM;GMM1	golgi alpha-mannosidase II
Sapur.D03G000600.1	0.52175870	0.16849429	0.117922211	1.429108	0.15290188	0.19449814	grey	0.07947836	0.16389849	GO0016324;GO0004672;GO0005886	KTSG18610.1	Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.D05G089800.1	0.82863717	0.68278016	0.342232242	1.428264	0.15321953	0.19453322	grey	0.12027024	0.21238116	GO005515	KTSG7190.1	ARIP15;RLP15	receptor like protein 15
Sapur.D05G094900.1	0.65464294	0.46682377	0.32837939	1.427	0.15344643	0.19470867	grey	-0.12015008	0.11884863	GO0055114;GO0016491	KTSG9400.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2OG-Fe(II) oxygenase family protein
Sapur.D16G187000.1	9.41062496	0.18142589	0.12706503	1.427792	0.15351797	0.19470867	grey	-0.11210121	0.16217029	GO0008270;GO005515	KTSG4923.1	RING/U-box superfamily protein	RING-U2 finger protein AT1L1L, putative
Sapur.D14G111000.1	1601.620649	0.09455126	0.066218149	1.427	0.15364136	0.19487464	grey	-0.11349136	0.09188124	GO0016887;GO005524	KTSG6410.1	bZIP transcription factor family protein	AtC-type transport system protein
Sapur.D12G045500.1	11.70876887	0.24453068	0.171454029	-1.42622	0.15380535	0.19526074	grey	-0.10837857	0.17659838		KTSG3670.1	ankyrin repeat family protein	NA
Sapur.D06G261400.1	15.54391228	0.09455126	0.066253808	-1.42603	0.15381133	0.19528949	grey	-0.22660317	0.03832705		KTSG5170.1	Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.D02G165500.1	5.63815596	-0.27911329	0.195776545	-1.42567	0.15382939	0.19546773	grey	-0.13782506	0.08508853	GO0016746;GO0008152	KTSG0192.1	ATGPAT3;GPAT3	glycerol-3-phosphate acyltransferase 3
Sapur.D08G007000.2	15.22346018	-0.12117369	0.084907891	-1.42561	0.15385589	0.19562947	grey	-0.12613514	0.11430057		KTSG6910.1		NA
Sapur.T100500.1	0.15889723	-0.54227411	0.38047396	-1.42545	0.15402958	0.19555418	grey	0.28991813	0.00320045		KTSG4880.1	Helicase/SNF2-associated, DNA binding protein	NA
Sapur.D01G090000.1	2.71245036	-0.24371535	0.170948643	-1.42481	0.15421215	0.19570626	grey	-0.11397056	0.15123623	GO0046415;GO003747	KTSG2850.2	Class I peptide chain release factor	immature colon carcinoma transcript 1 protein
Sapur.D13G204800.1	0.27453617	-0.62379187	0.43664677	-1.42466	0.15423546	0.19578338	grey	-0.16205966	0.04724268	GO0005515;GO045131	KTSG2510.1	NB-ARC domain-containing disease resistance protein	NA
Sapur.D14G132400.1	44.46068752	0.12007129	0.084305275	-1.42452	0.15437434	0.19330271	grey	0.10439699	0.19331348		KTSG4530.1	Auxin-responsive family protein	auxin-induced in root cultures protein, putative
Sapur.D06G092700.1	88.27885257	0.09455126	0.06618849	-1.42447	0.15441047	0.19587516	grey	0.10297216	0.19913348		KTSG8640.1	Protein of unknown function (DUF567)	bubby C 2 protein
Sapur.D19G056800.1	379.7518626	-0.05306948	0.03736259	-1.42408	0.15462035	0.19597819	grey	-0.13315328	0.09591022	GO0008138;GO006470	KTSG10940.1	dual specificity protein phosphatase (DsPTP1) family protein	dual specificity protein phosphatase, putative
Sapur.D18G061500.1	82.45600969	-0.47077184	0.33060575	-1.42396	0.15464863	0.19601619	grey	-0.22754954	0.09610993		KTSG2060.1	Lactoylglutathione lyase / glyoxalase I family protein	lactoylglutathione lyase-like lyase
Sapur.D02G344000.1	10.96350849	-0.18058672	0.12692107	-1.42282	0.15479373	0.19624252	grey	-0.12421182	0.13668315	GO0006351;GO0005634;GO0003677	KTSG4240.1	Transcription elongation factor (TFIIS) family protein	TFIIS helical bundle-like domain protein
Sapur.D01G112500.3	2.45632817	0.25397653	0.178388837	-1.42163	0.15512588	0.19688464	grey	-0.10272104	0.20047301	GO0016746;GO0008152;GO0003837	KTSG2200.1	ACT1,ATS1	glycerol-3-phosphate acyltransferase
Sapur.D13G193000.1	0.60343907	-0.46423631	0.34063893	-1.421487	0.15517005	0.19690348	grey	-0.15157005	0.16006500	GO0005515;GO005886;GO005783	KTSG6880.1	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	NA
Sapur.D07G051000.1	0.65398652	0.48576879	0.34180369	1.421099	0.15528795	0.19700485	grey	0.10388496	0.00109217		KTSG1040.2	RTH	RTE1/GR-like protein
Sapur.D16G179200.1	1.36052626	0.36849783	0.259321884	-1.421005	0.15531416	0.19735794	grey	0.08959765	0.26455064		KTSG9520.1	basic helix-loop-helix (bHLH) DNA-binding family protein	transcription factor bHLH113, putative
Sapur.D11G070400.1	0.20091273	1.27119149	0.894637245	1.420821	0.15538881	0.19711847	grey	0.28178172	0.00349812				NA
Sapur.D14G051500.1	0.48618737	0.57488941	0.40414587	-1.41075	0.15539397	0.19717782	grey	-0.16688629	0.03105882	GO0055114;GO0016491	KTSG5183.1	AT2G31;ATGA20OX2;GA20D2	gibberellin 20 oxidase 2
Sapur.D20G072800.1	0.39765731	-0.56019981	0.394808013	-1.41882	0.15595294	0.1976387	grey	-0.10597006	0.1865281				NA
Sapur.D03G085400.2	0.56017891	0.57788023	0.38117429	-1.41859	0.15618309	0.19791809	grey	0.04508384	0.57515762		KTSG1760.1	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.D06G015500.5	1.4664974	0.30352909	0.21970022	-1.41852	0.15630796	0.19797603	grey	-0.16236204	0.04218192	GO0008270;GO006355	KTSG2170.2	RHY3	FAR-RED elongated hypocotyl protein
Sapur.D13G058800.1	2.30221480	0.30352909	0.219816373	1.415206	0.15645863	0.19816137	grey	-0.09096561	0.21783613	GO0008270;GO0046872;GO0005524;GO004672	KTSG4880.1	BIR1	BAK1-interacting receptor-like kinase 1
Sapur.D05G154100.2	1.00361056	0.45384839	0.32553385	1.415891	0.15680737	0.19889667	grey	-0.12416401	0.12128884				transmembrane protein, putative
Sapur.D06G041600.1	525.1303546	-0.06200017	0.04387359	-1.41565	0.15687838	0.19897183	grey	-0.10386485	0.20617558		KTSG7570.1	ARM repeat superfamily protein	zinc finger, C2H2-type protein, putative
Sapur.D06G151000.8	1.47078336	-0.46423631	0.33406893	-1.415487	0.15690575	0.19904348	grey	0.09096496	0.17938463		KTSG4270.1	HD domain-containing metallophosphorylhydrolase family protein	metal-dependent phosphohydrolase HD domain protein
Sapur.D02H060000.1	0.38155589	0.71819855	0.507433114	1.41525	0.15709569	0.19932221	grey	0.02109656	0.6897764	GO0005885;GO006020;GO0015297;GO0015238;GO006855	KTSG6320.1	MATE efflux family protein	multidrug resistance family protein
Sapur.D13G125300.1	5.50971668	0.18319353	0.12947884	-1.41484	0.15719184	0.19963368	grey	-0.06513256	0.61482109	GO0016021	KTSG7310.1	Endomembrane protein 70 protein family	NA
Sapur.D10G191000.1	2.23493535	2.43653589	0.30857646	1.414661	0.15767787	0.19980095	grey	0.08007809	0.31878451	GO016788	KTSG3610.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-like Lipase/Acylhydrolase family protein
Sapur.D06G136300.1	588.3713474	-0.05064527	0.035802743	-1.41456	0.15769397	0.19920696	grey	-0.13794727	0.08693755		KTSG2325.1	Splicing factor 3B subunit 5,RNG9 complex subunit 10	splicing factor 3B subunit
Sapur.D14G058500.1	0.44855979	0.49470515	0.34963944	1.414516	0.15710493	0.19939819	grey	0.07845073	0.12018887	GO0006355;GO003700	KTSG19790.1	RAP2.11	related to AP2 11
Sapur.D03H092000.1	0.22082615	0.82631614	0.58427027	1.41437	0.15724588	0.19987443	grey	0.18488648	0.02496657	GO0071805;GO0015079	KTSG7170.1	ATKT1;AKT4;TWK1	Potassium transporter family protein
Sapur.D14G012200.1	1.69185064	-0.40799559	0.28846808	-1.4142	0.15730191	0.1994329	grey	-0.15889912	0.04683623				hypothetical protein
Sapur.D05G185200.1	11.04163073	0.22334619	0.157867529	-1.41413	0.15734818	0.19954324	grey	-0.11457726	0.13454883		KTSG4721.1	Cystathionine beta-synthase (CBS) family protein	cystathionine beta-synthase (CBS) family protein
Sapur.D12G097900.1	0.21917856	0.70226051	0.49670001	1.41386	0.15743146	0.19954589	grey	0.18393353	0.02111208	GO0008270;GO003676	KTSG2180.1		NA
Sapur.D11G077900.1	1910.12098	0.07507224	0.053121135	1.413236	0.15758214	0.19970273	grey	0.08756991	0.27558512	GO0055114;GO003743;GO003091;GO0016671;GO0009379	KTSG3670.1	ATMSR81;MSR81	methionine sulfoxide reductase B 1
Sapur.D09G080100.1	24.76177318	0.14682402	0.10389508	-1.41315	0.15761511	0.19796484	grey	0.10506165	0.18208859		KTSG5680.1	Calcium-binding EF-hand family protein	polcalcin Jun proteins O, putative
Sapur.T086700.1	138.8370748	0.11693487	0.07604211	-1.413121	0.15763068	0.19979373	grey	0.13489567	0.09568823				NA
Sapur.D11G085200.1	0.85355734	0.39142884	0.31375655	1.41187	0.15784651	0.19988394	grey	0.11084604	0.16427283	GO005515	KTSG2730.1	F-box/RNI-like/FBD-like domains-containing protein	NA
Sapur.D06G107500.4	0.34795754	0.50314247	0.35620179	1.4125	0.15780283	0.20014337	grey	0.10437762	0.19348575	GO0043565;GO006355;GO003700;GO0006351	KTSG5040.1	bZIP19	bZIP transcription factor family protein
Sapur.D18G093700.1	461.3404768	0.09455126	0.06706325	-1.41247	0.15789248	0.20046438	grey	0.05789748	0.47408561		KTSG2520.1		hypothetical protein
Sapur.I59G107900.2	3.38793332	0.38007835	0.269106164	-1.41237	0.15804154	0.20066438	grey	-0.13931771	0.08902582	GO006396	KTSG4240.1	ELF5	proline-rich family protein
Sapur.D02G180000.1	1.90593553	0.44382883	0.31433882	-1.41052	0.15873434	0.20153132	grey	0.14347425	0.07317569	GO0048544;GO006488;GO004672	KTSG6160.1	ARKL;RK3	receptor kinase 3
Sapur.D07G108300.2	36.33174114	0.12044491	0.085085523	1.411872	0.15879736	0.20221288	grey	0.10659762	0.18365508		KTSG21865.1	PEX22	peroxin 22
Sapur.D18G252900.3	0.41774581	-0.54387979	0.38528658	-1.41186	0.15798954	0.20221288	grey	-0.19380416	0.01607150	GO0055114;GO004673;GO0080601	KTSG3110.1	CSD3	copper/zinc superoxide dismutase 3
Sapur.D08G165900.2	1.22606060	0.09455126	0.066926612	1.411797	0.15805149	0.20250564	grey	-0.08420234	0.29367407	GO0006468;GO005524;GO004672	KTSG8100.1	Protein kinase superfamily protein	Serine/Threonine kinase P851, putative
Sapur.D04G078600.1	5787.529808	0.09186922	0.13588565	-1.4109	0.15872679	0.20305584	grey	-0.11539128	0.15840684		KTSG2468.1	CPuORF9	conserved peptide upstream open reading frame 9
Sapur.D05G075200.6	4.67238502	0.20898499	0.139157591	-1.41004	0.15873739	0.20380605	grey	0.16147176	0.03196329	GO0016491	KTSG4670.1	ATMST1,ATRDHG,MST1,ST1	monosulfate(1)-monosaccharide(4) sulfotransferase
Sapur.T039200.1	18.20847688	0.34725162	0.24650007	1.409422	0.15870728	0.20380658	grey	0.16509457	0.02873147	GO0005524;GO0016787;GO0003677;GO0005622;GO0005634;GO0030528	KTSG16760.1		Introduction 1,3,4-thiadiazole-2(3H)-thione family protein
Sapur.D03G268000.3	3.75131384	-0.19794118	0.140409274	-1.4089	0.15885048	0.20136109	grey	-0.08420234	0.29367407	GO0046483;GO005524	KTSG2472.2	mycosin-heavy chain-related	WPP domain associated protein, putative
Sapur.D05G061100.1	30.15823023	0.13487624	0.09574571	-1.40871	0.15890335	0.20132647	grey	-0.11398581	0.16109731	GO0005975;GO0045015;GO005105;GO0070015			glucan 1%2C3-beta-glucosidase
Sapur.D11G042200.1	0.33917641	0.07583021	0.053848192	-1.40767	0.15914121	0.20180792	grey	-0.11531262	0.15102703	GO0016787;GO0003824;GO005515	KTSG4570.1	ARACI,ATRACI,ATBORT,RA	Ras-related C3 plant family protein
Sapur.D04G117200.1	61.82513971	-0.27760848	0.19701522	-1.4078	0.15919104	0.20163256	grey	-0.12569798	0.11672807		KTSG7520.2	ATRIL;RLE;RSM3	RAD-like 6
Sapur.D13G051500.1	5.82438881	-0.27223533	0.193195	-1.40765	0.15923632	0.20172313	grey	-0.12788614	0.11717087		KTSG6470.1	Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.D17G251100.1	0.94014679	0.46321825	0.33086005	1.406248	0.15965153	0.20239316	grey	-0.10232606	0.20356162	GO0046483;GO005524;GO004672	KTSG7010.1	receptor serine/threonine kinase, putative	NA
Sapur.D18G251800.2	-1.09073885	0.34072345	0.242336562	1.405993	0.15972369	0.20281614	grey	0.07231174	0.00341154		KTSG2060.1	Alpha/beta-Hydrolases superfamily protein	acyl-protein thioesterase
Sapur.D18G114300.1	2307.320826	-0.09455761	0.06617487	-1.40586	0.15975778	0.20323902	grey	-0.12845706	0.10877561	GO0016740;GO0003824	KTSG4850.1	ATMAL;ALS;CSR1;IMR1;TIPS	malate synthase; isocitrate lyase type 2 protein
Sapur.D04G087500.1	6.65362913	-0.15102486	0.10786341	-1.40549	0.15987501	0.20245101	grey	-0.05158819	0.48925943	GO003676	KTSG0150.1	ATPTB1;PTB;PTB1	polypyrimidine tract-binding protein 1
Sapur.D05G062600.1	707.8017544	0.09455126	0.067488768	-1.40514	0.15989538	0.20266649	grey	0.08941008	0.26545264				RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.D14G120100.3	0.52243649	-0.51849082	0.36896767	-1.40494	0.16003977	0.20267602	grey	0.17124134	0.03111554		KTSG6060.1	NADP(+)-linked oxidoreductase superfamily protein	aldo/keto reductase family protein
Sapur.D06G037100.1	25.43693002	0.11092268	0.07906181	-1.40476	0.16005166	0.20270071	grey	0.00501065	0.98334272	GO0008270;GO005515	KTSG3910.1	RING/U-box superfamily protein	hypothetical protein
Sapur.D13G015500.1	127.7268058	-0.45531466	0.32427851	-1.40471	0.16010779	0.20278194	grey	-0.14872043	0.06203532		KTSG2680.1	CAD1	MAC/Perforin domain-containing protein
Sapur.D05G150500.1	0.70464574	-0.17128184	0.12197	-1.40468	0.16012660	0.20277738	grey	-0.12649806	0.18002043	GO0043565;GO006355;GO003700	KTSG4040.1	WRKY DNA-binding protein 45	WRKY transcription factor
Sapur.D08G207000.6	0.24891351	0.78211669	0.55688664	1.40445	0.16019497	0.20280017	grey	0.20580599	0.00842224	GO0046540;GO0003700	KTSG2800.1	Pre-mRNA-splicing factor 3	U4/U6 small nuclear ribonucleoprotein PRP3, putative
Sapur.D13G185000.1	19.97585629

Sapur.15WG079600.1	188.7350675	-0.07706375	0.056385453	-1.36589	0.173974334	0.216369841	grey	-0.156266702	0.050505281		ATSG13481.1		NA
Sapur.005G110400.1	15.21268505	0.225656047	0.16546691	1.365546	0.172861435	0.316766506	grey	0.072803732	0.3648089				NA
Sapur.016G161300.1	0.171175419	0.912369857	0.168172864	1.365401	0.172139388	0.2168152	grey	0.261408089	0.00093077	GO:0006468;GO:0005634;GO:0004672	ATSG56120.1	Leucine-rich repeat transmembrane protein kinase	receptor-like kinase, putative
Sapur.008G118100.3	0.466972077	-0.482116309	0.153180325	-1.36506	0.172233085	0.2169403	grey	-0.304741536	0.000104198	GO:0003676	ATSG33435.1	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif protein
Sapur.005G163200.1	691.0878097	-0.050655769	0.043426644	-1.3669	0.172256466	0.2168238	grey	-0.097383234	0.225363008		ATSG66093.1	NAD(P)-linked oxidoreductase superfamily protein	aldo/keto reductase family protein
Sapur.015G069100.1	0.768075259	0.272159565	0.270824567	1.364809	0.173231982	0.2170251	grey	-0.104593995	0.192339272	GO:0048544;GO:0006468;GO:0004672	ATSG11340.1	S-locus lectin protein kinase family protein	NA
Sapur.002G189400.1	14.00862201	0.145511392	0.105196155	1.364607	0.173276657	0.2170798	grey	0.06219768	0.430387517		ATSG82662.1		transmembrane protein, putative
Sapur.016G278001.1	23.76215051	0.11604056	0.092866606	1.364583	0.173280416	0.2170616	grey	0.060709296	0.258562584		ATSG79180.1		NA
Sapur.005G066600.1	0.888146552	0.393114439	0.288127337	-1.36438	0.172448804	0.2171373	grey	-0.149232329	0.062088352		ATSG21940.4	ATSK1,SK1	shikimate kinase 1
Sapur.014G065300.1	74.31278671	-0.214344709	0.157188261	-1.36418	0.172509998	0.2169164	grey	-0.122652516	0.115436458	GO:0016592;GO:0006357;GO:0001104	CCT,CRP	RNA polymerase II transcription mediators	NA
Sapur.008G164200.1	0.566051437	-0.435173269	0.319017669	-1.3641	0.172534845	0.2173618	grey	-0.312170207	0.07966412		NF-YB5	nuclear factor Y, subunit B5	nuclear transcription factor Y subunit B18, putative
Sapur.006G194900.2	0.312464124	0.340450146	0.340016876	1.363991	0.173576318	0.2172138	grey	0.10218037	0.102868577	GO:0030246;GO:0005975;GO:0004553	BGAL1	beta galactosidase 1	beta galactosidase
Sapur.003G135300.4	0.336391276	-0.539838652	0.39588709	-1.36389	0.173800139	0.2173013	grey	-0.15953681	0.04595648		ATSG64530.1	Translation elongation factor EF1B/ribosomal protein S6 family protein	30S ribosomal protein S6 alpha, putative
Sapur.002G408300.3	2.758125219	0.298609307	0.176578934	1.363851	0.173860871	0.2173607	grey	0.124878213	0.031732021	GO:0005488;GO:0006281;GO:0006289;GO:0005634;GO:0004519;GO:0003697	ATSG56120.1	D1-D2 adenosine deaminase family protein	DNA repair protein UVR1, putative
Sapur.008G941700.2	1.472722731	0.304097379	0.223009507	1.363607	0.173892512	0.2174269	grey	0.109796419	0.170324959		ATSG51380.1	UBC14	ubiquitin-conjugating enzyme 14
Sapur.006G156100.2	0.483356217	0.183022383	0.177856125	-1.3619	0.173239446	0.2188003	grey	0.108502002	0.176162778		ATSG50810.1		hypothetical protein
Sapur.014G118500.1	408.1137558	0.114652075	0.08406998	1.361754	0.17328801	0.2185133	grey	-0.082859594	0.103793174	GO:0048046;GO:0016762;GO:0006370;GO:0005618;GO:0005975;GO:0004553	ATSG23730.1	XTH16	xyloglucan endotransglucosylase/hydrolase 16
Sapur.018G292700.1	0.488574655	0.493092023	0.362997442	1.361699	0.173292918	0.2185133	grey	0.118592232	0.139054784	GO:0005515	ATSG76190.1	AtRLP15,RLP15	receptor like protein 15
Sapur.002G278001.1	8.194431179	-0.025885622	0.11174942	-1.36057	0.173849169	0.2188104	grey	0.204492643	0.021881964	GO:0008270	ATSG23181.1		Zinc finger (CCCH-type) family protein
Sapur.012G103400.1	159.7638843	-0.064804181	0.047604499	-1.36028	0.173242914	0.2188023	grey	-0.102045706	0.203467652		ATSG62140.1		hypothetical protein
Sapur.012G082600.1	866.5154394	0.073287427	0.05016524	1.36021	0.173255326	0.2188422	grey	-0.120039318	0.162672241		ATSG39552.1	ATHZ,ATTRXZ,ATTRXHZ,TRX	thioredoxin Z
Sapur.016G051700.1	197.1885509	-0.147786268	0.10648878	1.359892	0.173866025	0.2188283	grey	-0.118853523	0.094656822	GO:0008270;GO:0003677;GO:0003705	ATSG38180.1	FRS5	FAR1-related sequence 5
Sapur.006G134800.1	94.39215676	0.129219688	0.092052223	1.359488	0.173984847	0.2188117	grey	-0.123049605	0.130956782	GO:0003723	ATSG17370.1	UBP1B	oligouridylate binding protein 1B
Sapur.007G043300.1	70.81165888	0.0790907	0.058179712	1.359421	0.174013341	0.2189984	grey	0.1172418	0.143646827		ATSG50370.1		NA
Sapur.016G267500.1	5.689113842	0.249609016	0.183729852	1.359391	0.174028792	0.2190587	grey	0.124907613	0.118316063	GO:0004674;GO:0048544;GO:0006468;GO:0004672	ATSG56120.1	ARK3,RK3	receptor kinase 3
Sapur.008G291300.1	4.161701874	0.179381443	0.132015781	-1.35879	0.174213816	0.2192553	grey	-0.08664	0.280969141	GO:0005515;GO:0005783	ATSG15580.2	LAG13	LAG1 longevity assurance like protein
Sapur.008G202200.1	178.4515573	0.078308221	0.057605586	1.357548	0.174607238	0.2197388	grey	0.102134265	0.202282485	GO:0005515	ATSG51530.1		Kelch repeat-containing F-box family protein
Sapur.016G284005.6	7.546549682	0.151408524	0.10718513	1.357284	0.174691101	0.2198154	grey	0.16476903	0.19164946	GO:0005515;GO:0004672	ATSMKK1,MMK3	mitogen-activated protein kinase kinase 3	dual specificity MAP kinase kinase
Sapur.T099300.1	0.145637731	0.971936651	0.736102626	1.357259	0.174689967	0.2198125	grey	0.312726209	6.675-05				NA
Sapur.005G120900.1	2.364441939	0.202892738	0.429763269	1.356692	0.174934394	0.2200792	grey	0.079093798	0.124775044	GO:0005662;GO:0003824	AT5G45400.1	BEN1	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.018G056900.1	3.47143573	0.250091574	0.184332155	1.356455	0.174960825	0.2201537	grey	0.102615649	0.200819904	GO:0005515	ATSG18190.2	AtRLP9,RLP9	receptor like protein 9
Sapur.004G089900.1	2.080573869	0.201159207	0.219181869	1.355604	0.175125532	0.2203717	grey	-0.120039318	0.162672241				NA
Sapur.004G015400.1	35.99424586	0.141431354	0.10430729	-1.35591	0.175117633	0.2201823	grey	-0.095707087	0.232853293	GO:0048046;GO:0006472	AT5G19180.1	CRK10,RLK4	cysteine-rich RLK (RECEPTOR-like protein kinase) 10
Sapur.008G127000.6	8.301609007	0.150661688	0.11777814	-1.35561	0.175212122	0.2204052	grey	-0.08268864	0.309369942		ATSG61120.1		Plant protein of unknown function (DUF247) with plant pleckstrin homology-like region
Sapur.006G097500.1	248.6294906	0.262300313	0.193152523	1.355328	0.175312297	0.2205242	grey	0.112210914	0.161717137	GO:0016758;GO:0008152	UGT71C4	UDP-glucosyl transferase 71C4	UDP-glucose flavonoid 3-O-glucosyltransferase, putative
Sapur.006G159300.1	26.40581002	0.192367612	0.139451165	1.355164	0.175317107	0.2205016	grey	0.207425061	0.018320746		CPuORF20	conserved peptide upstream open reading frame 20	NA
Sapur.003G109600.1	73.22097793	0.182788562	0.134886663	1.355127	0.175337681	0.2205061	grey	0.072839028	0.148708386				NA
Sapur.014G076100.1	14.11892867	0.284025494	0.20968059	-1.35482	0.175476562	0.2207456	grey	-0.143804026	0.079491307				NA
Sapur.004G087000.3	13.06117994	0.300764498	0.08104853	1.354306	0.175638729	0.2209587	grey	0.10057202	0.230383305		ATSG64290.1	Thioesterase superfamily protein	acyl-coenzyme A thioesterase
Sapur.010G061500.1	155.9642336	0.402090548	0.297227035	1.353815	0.175795268	0.2210263	grey	0.168858879	0.034507282	GO:0043565;GO:0006355;GO:0003700	ATSG55610.1		LAG1 longevity assurance-like protein
Sapur.005G084000.1	1.049862994	0.192303638	0.246264257	1.353439	0.175934441	0.2212573	grey	0.077259455	0.365302341		ATSG55615.1		F-box/kelch-repeat plant protein
Sapur.005G159800.1	5.894380601	-0.162531083	0.120063207	-1.35334	0.175947176	0.2215689	grey	-0.141661916	0.076763158		ATSG65530.1		hypothetical protein
Sapur.018G152200.1	6.918258115	0.217031884	0.15774318	1.353	0.176237007	0.2216127	grey	-0.039035037	0.019387865	GO:0005508;GO:0004252	AIR3	Subtilisin-like serine endopeptidase family protein	NA
Sapur.018G051300.1	117.2860152	-0.103713894	0.076713463	-1.35197	0.176386827	0.2219217	grey	0.138449753	0.087154102	GO:0016491;GO:0008152	ATSG42370.4	ALDH11A3	aldehyde dehydrogenase 11A3
Sapur.004G263700.1	0.559668833	0.216081689	0.160386111	-1.35187	0.176417546	0.2221802	grey	-0.062238264	0.446120775	GO:0046563;GO:0006355;GO:0003700	ATSG35130.1	BEE2	basic leucine zipper 42
Sapur.002G162900.2	0.83871548	-0.429604339	0.317876305	-1.35148	0.176540846	0.2226112	grey	-0.142623634	0.078974331	GO:0043169;GO:0005975;GO:0003824	ATSG25000.1	AMY1,ATAMY1	alpha-amylase
Sapur.008G158900.1	446.5882	0.352897984	0.260267884	1.353885	0.175615175	0.2220988	grey	0.207425061	0.018320746	GO:0005488;GO:0004674;GO:0006468;GO:0004672	ATSG27280.1		S-locus lectin protein kinase family protein
Sapur.006G245000.8	2.140489891	-0.256107984	0.189561389	-1.35106	0.176627761	0.2226128	grey	0.083139639	0.305572949		ATSG37140.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.011G050000.1	32.79949566	0.18149244	0.134337214	1.351021	0.176889602	0.2232163	grey	0.095764681	0.232925564		ATSG18820.1		AAA-type ATPase family protein
Sapur.013G054500.4	6.726752573	0.264977623	0.197736609	1.35076	0.176721	0.2231849	grey	-0.051932631	0.518302017		ATSG60290.2		HNH nuclease, putative
Sapur.002G240900.2	82.07078814	-0.087278391	0.064525072	-1.35053	0.178845588	0.2230859	grey	-0.086187755	0.318119667		ATSG55610.1		Protein of unknown function (DUF1195)
Sapur.001G135200.1	0.260105254	0.365899399	0.07757476	-1.34961	0.177140858	0.2236167	grey	-0.091134602	0.254332033		ATSG11050.1		plant/TIM17-60 protein
Sapur.016G309300.1	6.738315288	0.15773935	0.116903365	1.349349	0.177225006	0.2237563	grey	0.114463267	0.15353178		ATSG26455.1	WIP1	WIP domain interacting protein, putative
Sapur.T082000.1	1.124634217	0.220000127	0.152961922	1.34927	0.177203314	0.2237704	grey	0.08398673	0.355028189		ATMAT5,MDE5	RNA-related protein	NA
Sapur.012G369000.2	19.36504473	0.110518876	0.081607084	-1.34888	0.177363181	0.2229081	grey	-0.107576961	0.179908391			RING/U-box superfamily protein	RING-finger protein, putative
Sapur.006G188800.4	16.14152434	0.201204504	0.148866851	1.34883	0.177365691	0.2230753	grey	-0.073715164	0.368402324		ATSG39150.2	DNA heat shock activator-like protein	Dnaj heat shock activator terminal domain protein
Sapur.005G084000.2	62.70847039	0.094679629	0.070215361	1.348418	0.17752406	0.2230629	grey	-0.040881155	0.534992209	GO:0003676	ATSG57853.3		RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.007G030600.7	8.399349082	0.093367589	0.141272322	-1.34752	0.17781211	0.2234693	grey	-0.113123515	0.119220128	GO:0003688;GO:0008270;GO:0000534;GO:0005515	ATSG23740.2		nucleic acid binding;sequence-specific DNA binding transcription factors;zinc ion binding
Sapur.T014G057001.1	1176.179372	0.101688023	0.048709425	1.347186	0.177552029	0.2235675	grey	0.060846659	0.272283117	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP704A2	cytochrome P450 family 704, subfamily A, polypeptide 2	cytochrome P450 family monooxygenase
Sapur.007G107700.2	8.220875533	0.12865631	0.091370649	1.346395	0.178175207	0.2238796	grey	0.106329224	0.186991837				NA
Sapur.013G071300.1	22.48605087	0.214705832	0.158229665	-1.3458	0.178305054	0.2240106	grey	-0.100463051	0.215362387	GO:0006850;GO:0005743	ATSG30090.2	Uncharacterized protein family (UPF0041)	brain-like protein
Sapur.016G269900.3	3.12613066	0.228460919	0.169831646	1.345268	0.178538777	0.2243118	grey	0.048967568	0.542679989		ATSG61010.1		hypothetical protein
Sapur.004G151500.1	0.547526143	0.463819309	0.344360387	1.345223	0.178557208	0.2242709	grey	0.102682275	0.30562778		ATSG45410.2		hypothetical protein
Sapur.015W0018800.2	0.681612043	-0.405486583	0.30147799	-1.345	0.178636367	0.2244000	grey	-0.125208895	0.11817167		ATSG29680.1		NA
Sapur.013G160400.1	12.28339123	0.244000472	0.182322459	-1.34499	0.178629872	0.2244067	grey	-0.174884051	0.031797856	GO:0046983;GO:0003677	AGL87	AGAMOUS-like 87	MADS box protein, putative
Sapur.003G164800.2	0.276032063	0.512918554	0.381556492	1.344279	0.178580037	0.2246719	grey	0.103036427	0.199116975		ATSG30900.1	BPM0-3,1/SR3,1/SVR6	vacuolar sorting receptor 6
Sapur.018G085600.1	0.358641897	0.562367786	0.418568441	1.344061	0.178635457	0.2247816	grey	0.065487843	0.643003676		ATSG07232.1		Ankyrin repeat family protein
Sapur.007G031100.14	9.01059431	-0.13259903	0.088743351	-1.34287	0.179315562	0.2252638	grey	0.010557778	0.9005765	GO:0008234;GO:0006508	ATSG35620.1	Cysteine proteinases superfamily protein	Ulp1 protease family, carboxy-terminal domain protein
Sapur.001G025200.1	0.34019638	0.534343681	0.397918889	1.342866	0.179121734	0.2252638	grey	0.096809018	0.227299658				NA
Sapur.001G192700.1	631.1509012	0.055886443	0.02968769	1.342635	0.179217892	0.2254904	grey	-0.113178961	0.158145881		ATSG45010.1	PLACE family protein	cell number regulator 12
Sapur.002G109100.2	34.60955029	-0.097808096	0.072847817	-1.34264	0.179288892	0.2254904	grey	-0.087515482	0.275790084	GO:0018324	ATSG16580.1	Protein phosphatase 2C family protein	protein phosphatase 2C, putative
Sapur.U045022800.1	2.660361677	0.400083007	0.297904791	-1.34245	0.179494944	0.2253670	grey	-0.147518966	0.052217462	GO:0003677;GO:0046983	ATSG41170.1	BED zinc finger, hAT family dimerization domain	NA
Sapur.016G069200.2	0.142278223	0.920406208	0.68439455	1.340929	0.179845129	0.2298647	grey	0.32687876	2.94E-05	GO:0003677	ATSG36080.1	AP2/B3-like transcriptional factor family protein	B3 DNA binding domain protein
Sapur.018G139400.1	193.4137553	0.102427476	0.170288156	-1.34652	0.180077584	0.2261162	grey	-0.125828576	0.192561122	GO:0003676;GO:0006355;GO:0005634;GO:0003677	ATSG17070.1	GC-rich sequence DNA-binding factor-like protein with Tuftelin interacting domain	tuftelin-interacting protein
Sapur.014G060700.1	0.994944545	0.328579187	0.245286383	-1.33957	0.18183938	0.2268173	grey	-0.128833566	0.131690102				NA
Sapur.018G319300.1	5.555675534	0.231177798	0.173617899	-1.33925	0.180406562	0.2268517	grey	-0.128088528	0.182272513		ATSG20190.1	Tetratricopeptide repeat (TPR)-like superfamily protein	hypothetical protein
Sapur.T043700.1	0.170089509	0.118083605	0.834908862	1.339168	0.180515842	0.2263157	grey	0.327321547	2.86E-05		ATSMCL5EF	HIT-type Zinc finger family protein	NA
Sapur.018G135000.2	0.475839176	0.488359168	0.364568439	1.339108	0.180535632	0.2268775	grey	0.084930358	0.280247585		ATSG11397.1	PRA1.A3	prenylated RAB acceptor 1.A3
Sapur.U045027200.1	580.81186	0.052248561	0.039034445	-1.33868	0.180631794	0.2267329	grey	0.050705581	0.532502283	GO:0016021;GO:0004190	PS2	Presenilin-2	NA
Sapur.016G164100.1	6.362765945	-0.228577567	0.170767773	-1.33854	0.180725195	0.2268408	grey	-0.102391056	0.201934068	GO:0008180	ATSG42820.1	ATSAGT1,GT-SAGT1,SAGT1	UDP-glucosyltransferase family
Sapur.016G289600.2	0.244534511	0.751681846	0.561172674	-1.33842	0.180791798	0.2270257	grey	-0.228660304	0.002633039	GO:0005515;GO:0004331	ATSG17080.1	Nucleotidyl cyclase/adenylyl cyclase family protein	UDP-sugar transporter, putative
Sapur.15WG122300.4	27.13344956	0.080466708	0.060139493	1.337669	0.181005511	0.2270192	grey	0.01684881	0.252608806	GO:0008374;GO:0006629	ATSG19860.1	alpha/beta-Hydrolases superfamily protein	lecithine cholesterol acyltransferase-like protein
Sapur.005G197100.1	4.439376764	0.223727863	0.166536837	-1.33749	0.181026278	0.2266428	grey	-0.140421482	0.079420311		ATSG56010.1	Ribosomal protein L30/L7 family protein	NA
Sapur.018G091600.1	0.71476139	0.40081735	0.296698845	1.337396	0.181034636	0.2270628	grey	0.113900095	0.162589462	GO:0005515	ATSG76190.1	AtRLP15,RLP15	receptor like protein 15
Sapur.004G137700.1	56.03808034	-0.065761987	0.072567149	-1.3371	0.181035576	0.2270457	grey	-0.088460276	0.270535325		ATSG35460.1	GPP1	glycerol-3-phosphatase 1
Sapur.003G069600.1	0.378191297	0.496449119	0.375171297	1.33608	0.181532003	0.2278065	grey	0.046125962	0.566200004		ATSG64550.1		hypothetical protein
Sapur.016G268800.1	28.18102960	0.207322504	0.231177798	1.335625	0.181906562	0.2260857	grey	-0.116437245	0.146434769		ATSG20280.1		c-Jun-dependent kinase inhibitor siamese protein, putative
Sapur.006G123500.2	3.85041937	0.37778843	0.280010902	1.334987	0.181906883	0.2280629	grey	0.157312064	0.049110422	GO:0004145;GO:0004177	ATSG29490.1	Metallopeptidase M24 family protein	Xaa-pro dipeptidase
Sapur.001G131000.1	24.36167536	-0.262281229	0.195048888	-1.33449	0.182043531	0.2284089	grey	-0.127796653	0.193782429				NA
Sapur.010G180900.1	0.18861682	0.812170906	0.60904834	1.333609	0.182164197	0.2288140	grey	0.220316137	0.093875604	GO:0008236;GO:0006508	ATSG22840.1	Serine carboxypeptidase S28 family protein	lysosomal pro-X carboxypeptidase, putative
Sapur.007G126300.1	57.06409479	0.200881361	0.150634037	1.33307	0.182431196	0.2288988	grey	0.112138831	0.162030618	GO:0016758;GO:0008152	ATSG43820.1	ATSAGT1,GT-SAGT1,SAGT1	UDP-glucosyltransferase family
Sapur.016G188200.1	0.303674794	0.577922956	0.43360806	-1.33182	0.182509798	0.2290265	grey	-0.205478188	0.038125626	GO:0005515;GO:0004331	ATSG17080.1	Nucleotidyl cyclase/adenylyl cyclase family protein	TIR-NBS-LRR resistance protein
Sapur.003G058800.1	0.246953347	0.609629852	0.457536048	1.332419	0.182722245	0.2291928	grey	0.043505671	0.588496017	GO:0016787;GO:0008152	ATSG17830.1	Peptidase M20/M25/M40 family protein	M20 peptidase acetylornithine deacetylase
Sapur.015G209300.1	67.28873723	-0.32508114	0.24660366	-1.3323	0.182732	0.2292844	grey	-0.160113824	0.189275555	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATSG44410.1	HSL1	HAESA-like 1	LRR receptor-like kinase
Sapur.013G135200.2	0.553091395	-0.456517652	0.343664601	-1.33226	0.182775427	0.2292839	grey	0.451972718	2.82E-09		ATSG60030.1		hypothetical protein
Sapur.004G182200.1	0.685957884	0.604568842	0.45617872	-1.33209	0.182829119	0.2291863	grey	-0.150609208	0.02080672				NA
Sapur.002G064100.1	3.731277005	-0.185102265	0.139009548	-1.33159	0.182966039	0.2295403	grey	-0.105884363	0.186888871	GO:0005515	ATSG17030.1	ATSWI3C,CHB4,SWI3C	SWITCH/sucrose nonfermenting 3C	chromatin remodeling complex subunit
Sapur.015G054800.1	65.90598876	-0.121379233	0.091455879	-1.3312	0.18319	0.2296804	grey	0.246156168	0.055885863		ATSG18950.1		DOT domain containing protein
Sapur.018G062700.1	49.16024681	0.156662277	0.117688888	1.331189	0.183326868	0.2296804	grey	0.113797771	0.155869318		ATSG20010.2		Protein of unknown function (DUF810)
Sapur.005G045500.1	0.298205259	0.911378536	0.684699682	1.330927	0.18325628	0.2295479	grey	0.187735379	0.03547927		ATSG16360.1	NC domain-containing protein-related	NA
Sapur.016G388000.5	13.78911008	-0.278565548	0.209117658	-1.3303	0.183436669	0.2299052	grey	0.280522463	0.00372874		ATSG56180.2	Sec14p-like phosphatidylinositol transfer family protein	SEC14 cytosolic factor family protein
Sapur.005G197400.2	0.309854247	0.590181006	0.443503244	1.330257	0.183434648	0.2300689	grey	0.080297746	0.317454195	GO:0006468;GO:0005524;GO:0004672	ATSG15780.1	ACT-like protein tyrosine kinase family protein	tyrosine kinase family protein
Sapur.016G205100.1	1.382958371	0.290354394	0.22506625	1.330156	0.183495105	0.2305911	grey	-0.127750224	0.107970078	GO:0008168	ATSG18020.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase PMT2, putative
Sapur.016G107200.1	2.534832249	-0.261071153	0.196281179	-1.33009	0.183849427	0.2305913	grey	-0.11051788	0.181816695		ATSG17630.1	Protein of unknown function (DUF688)	DUF688 family protein
Sapur.016G389200.2	0.454668121	0.537508504	0.424187114	-1.32995	0.183526268	0.2300758	grey	-0.127284241	0.112153846	GO:0046983	ATSG29920.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH protein
Sapur.016G186400.2	1.658264207	0.272607938	0.205043949	1.329761	0.183597103	0.2307664	grey	0.082839559	0.302348036		ATSG10540.1	3-phosphoinositide-dependent protein kinase family protein	NA
Sapur.004G172000.1	0.684979366	0.324568184	0.244388538	1.329208	0.184032128	0.3304453	grey	-0.132284776	0.127004606	GO:0008270;GO:0005515	ATSG7656.1	RING/U-box superfamily protein	RING-H2 type zinc finger protein
Sapur.003G047000.4	4.364612924	0.161412724	0.121475546	1.328769	0.183971561	0.2305463	grey	0.13078266	0.102547663		ATSG47420.1	Tryptophan RNA-binding attenuator protein-like	tryptophan RNA-binding attenuator-like protein
Sapur.001G189400.1	115.6679232	0.112251224	0.084452897	1.328701	0.183836572	0.2305852	grey	0.080400604	0.201577107	GO:0005488	ATSG46800.1	BOU	Mitochondrial substrate carrier family	carnitine/acylcarnitine carrier family
Sapur.016G018200.1	91.90279107	0.101313124	0.076618436	-1.32848	0.184035585	0.2306511	grey	-0.160043604	0.091652502	GO:0005515	ATSG18290.1	Thioredoxin superfamily protein	glutathione S-transferase, zeta class, thioredoxin domain protein
Sapur.016G143300.3	4.171875	-0.176888859	0.131184955	-1.32813	0.184135451	0.2307968	grey	-0.10027274	0.211471866	GO:0005815;GO:0009922;GO:0000226	ATSG17410.1	Spc97 / Spc98 family of spindle pole body (SBP) component	spindle pole body protein
Sapur.015G092000.1	171.4979172	0.067061929	0.047887423	-1.32811	0.184136171	0.2307968	grey	-0.103863111	0.164777912	GO:0003677;GO:0005634;GO:0005634	ATSG21620.1	KNOX/ELK homeobox transcription factor	class I KNOX homeobox transcription factor
Sapur.003G159900.3	0.464384291	0.460591298	0.351888565	1.326931	0.184561402	0.2317566	grey	0.113047512	0.158679979		ATSG02100.2	catalytics	spermatogenesis-associated protein
Sapur.016G154100.1	0.731443164	0.601388874	0.45321764	-1.32682	0.184624254	0.2317566	grey	-0.187562494	0.033632878				NA
Sapur.004G094500.2	1.381735227	-0.203220383	0.152461369	-1.32655	0.184659197	0.2314028	grey	-0.085422423	0.286318751	GO:0004689;GO:0005524;GO:0004672	ATSG48480.1	RKL1	receptor like kinase 1
Sapur.018G261600.1	1.491626441	0.478864622	0.359675169	1.326663	0.184818564	0.2318556	grey	0.118192574	0.193755078		ATSG66570.1		Plant protein of unknown function (DUF247)
Sapur.001G110000.2	0.41796793	0.472842038	0.356533481	1.326146	0.184978281	0.2315093	grey	0.070287411	0.343590678		ATSG65490.1		SGT1-like protein
Sapur.003G063000.1	1.325167938	0.303183233	0.228665125	1.325325	0.185209171	0.2320455	grey	0.037524938	0.648301007	GO:0016491;GO:0008152	ATSG20480.1	NAD(P)-binding Rossmann-fold superfamily protein	short chain dehydrogenase
Sapur.003G132300.1	386.75919	-0.067524194	0.050901945	-1.32499	0.185173365	0.2320124	grey	-0.107564695	0.179992718	GO:0008270;GO:0005524	ATSG54460.1	SNF2 domain-containing protein / helicase domain-containing protein / F-box family protein	chromatin remodeling complex subunit, putative
Sapur.010G102000.1	0.464282129	0.544651037	0.409313141	1.324891	0.185207319	0.2320587	grey	-0.10424536	0.193842546	GO:0055114;GO:0016491	ATSG21660.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.017G080200.1	335.7779179	0.047474807	0.111343033	1.324853	0.185239961	0.2320269	grey	0.11737709	0.1487648		ATSG19010.1		hypothetical protein
Sapur.016G057000.1	914.2975948	-0.050509923	0.038163584	-1.32351	0.185656518	0.2320248	grey	-0.135202232	0.091716441		ATSG12010.1		colon cancer-associated protein Mic1-like containing protein
Sapur.005G088800.1	66.81663008	0.147202619	0.108049425	-1.32266	0.185875056	0.2318129	grey	-0.144408092	0.071172971	GO:0043531	ATSG40190.1	RPM1,RPS3	NB-ARC domain-containing disease resistance protein
Sapur.017G094500.1	1.274887795	0.348067029	0.261910707	1.322475	0.186010117	0.2300756	grey	-0.10664387	0.176161459				NA
Sapur.018G139300.1	1.257978321	0.349212762	0.264036487	1.322233	0.186092167	0.2303964	grey	0.113142218	0.160556111	GO:0006511;GO:0005622;GO:0004843	ATSG65650.1	UCH2	Peptidase C12, ubiquitin carboxyl-terminal hydrolase 1	ubiquitin carboxyl-terminal hydrolase
Sapur.003G070000.1	1.029945881	0.351122394	0.265663378	1.322045	0.186153125	0.2319609	grey	0.106341612	0.185814251		ATSG07840.1		Ankyrin repeat family protein	ankyrin-3 protein
Sapur.013G058600.1	34.89451139	0.212327887	0.176578893	1.321762	0.186277346	0.2317837	grey	0.115278858	0.150526264	GO:0055114;GO:0016702	ATSG68160.1	Protein of unknown function (DUF1637)	NA
Sapur.003G242200.1	4.041678932	0.254787473	0.192801312	1.321503	0.186337171	0.2333732	grey	0.098493208	0.219762623				transmembrane protein, putative
Sapur.006G087700.1	266.3736661	0.149991792	0.112546017	-1.32051	0.186684003	0.2332785	grey	-0.174892927	0.030454114	GO:0008270;GO:0005515	ATSG26800.1	RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.015G077500.4	2.501605505	0.291566728	0.216620729	1.319773	0.186829	0.2340939	grey	0.074032181	0.554969477	GO:0005515	ATSG15470.2	SPIke/Wrneuzin receptor (SPRY) domain-containing protein	Ran-binding protein in the microtubule-organizing centre protein
Sapur.015G122200.1	231.9884947	-0.074599127	0

Sapur.008G051800.3	75.18437249	-0.10704551	0.083761489	-1.27833	0.201133815	0.25680375	grey	0.201352926	0.011446687	GO:0005515	AES05780.1	AE3ATHMDV34,RPN8A	RP non-ATPase subunit 8A
Sapur.017G109700.1	1.558393732	-0.31742467	0.24838703	-1.27793	0.201272363	0.25084399	grey	-0.110373715	0.107278344	GO:0006468,GO:0005524,GO:0004672	AES11050.1		Protein kinase superfamily protein
Sapur.013G309100.1	131.8661163	0.06090294	0.054731967	1.277537	0.201417705	0.25160884	grey	0.076172575	0.142728104	GO:0043565,GO:0006355,GO:0003700	AES04670.1	ATWRKY30,WRKY30	WRKY DNA-binding protein 30
Sapur.016G197000.4	7.904165143	-0.147186102	0.115239763	-1.27744	0.201447662	0.25162953	grey	-0.114745377	0.152431009	GO:0005515	AES02930.1		F-box/LRR-plant protein family
Sapur.015G200900.1	17.05935031	-0.158857518	0.123878188	-1.27716	0.201545205	0.25165585	grey	-0.110372388	0.18917487		AES11132.1		transmembrane protein, putative
Sapur.003G128400.1	1.136587127	-0.485892529	0.380635195	-1.27679	0.201675164	0.25188592	grey	-0.09976076	0.213829182	GO:0008017	AES02720.1	ATEBI1C,ATEBI1H,EBI1C	end binding protein 1C
Sapur.007G128200.1	1.051187657	0.367812938	0.288170308	1.276358	0.201828857	0.25197623	grey	-0.08579116	0.285409752				hypothetical protein
Sapur.016G115300.1	0.180282673	0.707805495	0.556118128	1.27621	0.201839151	0.25198167	grey	-0.279603086	0.00039052	GO:0015743	AES08430.1	ALMT5,ATALMT1	aluminum-activated malate transporter 1
Sapur.15WG127900.1	3.304891783	-0.210947947	0.16529669	-1.27622	0.201878268	0.25215324	grey	-0.135200405	0.09111938	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AES02410.1	RHS18	root hair specific 18
Sapur.013G206700.1	8.160425643	-0.102231169	0.080133169	-1.27615	0.201914785	1.1761	grey	0.068230292	0.201355781	GO:0005515	AES05660.1	ARIP12,RLP33	receptor like protein 33
Sapur.016G143700.4	1.346210126	-0.260296318	0.211040879	-1.27604	0.201941857	0.25173505	grey	-0.101949559	0.203896094	GO:0016798	AES05510.1		indigoidine synthase A family protein
Sapur.007G248100.1	3.180418131	-0.407264675	0.42627815	-1.27585	0.202030556	0.25246896	grey	-0.149420355	0.01782606		AES02930.1		DNAse I-like superfamily protein
Sapur.15WG117300.1	0.99323369	0.381815411	0.299277822	-1.27579	0.202030049	0.25166413	grey	-0.131858108	0.10045161		AES12583.1		TPD1, putative
Sapur.003G208900.2	2.72362037	-0.21372261	0.167428014	-1.27576	0.202064172	0.25166887	grey	-0.141934641	0.11911815		AES04963.1	ATHOL3,HOL3	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.013G303800.1	10.71552571	-0.141046351	0.110559763	-1.27538	0.202175326	0.25181629	grey	-0.105840878	0.187057567		AES05040.1	HST,HST1	ARM-repeat superfamily protein
Sapur.003G264900.1	8.790643984	-0.207239883	0.146305774	-1.27482	0.202360740	0.25230288	grey	-0.084482273	0.282328371	GO:0005543	AES03463.1		ENTH/ANTH/VHS-containing protein
Sapur.018G079900.1	419.9105235	-0.11218081	0.088094998	-1.27341	0.202873558	0.25260524	grey	-0.120888097	0.131482495	GO:0005515,GO:0003723	AES07835.2	eIFiso4G1	MIF4G domain-containing protein / MA3 domain-containing protein
Sapur.009G060600.1	4.82236288	0.184884395	0.145109151	1.27339	0.202879722	0.25260514	grey	-0.352787015	5.85E-06	GO:0005515	AES04910.1	ATPMPD4A,PRPH0A	pre-mRNA-processing protein 40A
Sapur.008G112500.5	4.727171225	-0.76034859	0.597000574	-1.27281	0.203082798	0.25260554	grey	-0.279603086	0.00039052	GO:0005515,GO:0004672,GO:0016702	AES02460.1	LOX5	PLAT/LH2 domain-containing lipoxygenase family protein
Sapur.007G081500.1	12.93828311	-0.164354422	0.129075523	-1.27332	0.202906053	0.25267485	grey	-0.09870327	0.218731066		AES08833.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Sapur.016G149900.1	4.111616344	-0.203017201	0.159523909	-1.27307	0.203147	0.25273736	grey	-0.117836155	0.172738864		AES02770.1		Protein kinase superfamily protein
Sapur.017G069700.5	0.219533823	0.94432927	0.741880979	1.271706	0.203477496	0.2533625	grey	-0.081608864	0.309509942	GO:0004412,GO:0005840,GO:0005622,GO:0003735	AES03175.1		transmembrane protein, putative
Sapur.015G152600.1	0.476617542	0.671885820	0.537661627	1.270804	0.203780609	0.25270821	grey	-0.147341813	0.065545541		AES79915.1		Putative methyltransferase family protein
Sapur.001G142100.1	0.467392775	0.642784695	0.506332601	1.269514	0.204257945	0.25405562	grey	-0.04882068	0.543721329	GO:0055114,GO:0016491	AES02800.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.008G209400.2	0.473834413	0.517721261	0.407528301	1.269475	0.204276128	0.25406477	grey	-0.12373734	0.191118815		AES07630.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.T164800.1	0.212619726	0.570452314	0.449465369	1.26938	0.204305195	0.25436578	grey	0.179423892	0.026450053		AES17020.1	ATCIM1,ATIPOL1HT2,XPO	exportin 1A
Sapur.002G187400.1	0.342038175	0.719633091	0.567402308	-1.26829	0.204302886	0.25481397	grey	-0.212778919	0.007461414	GO:0070551,GO:0005634,GO:0004861	AES48833.1	ICK6,KRP3	inhibitor/interactor with cyclin-dependent kinase
Sapur.003G151105.1	0.250042299	0.467587979	0.410968022	-1.26786	0.204867174	0.25490512	grey	-0.243072634	0.002343179		AES12726.1	ATMYB87,ATYS1,MYB87	myb domain protein 87
Sapur.004G134600.1	35.26779162	0.268395691	0.211692467	1.267854	0.204850259	0.25495012	grey	0.103228053	0.198281664				
Sapur.006G201200.1	141.9682319	0.079105858	0.062557415	1.26781	0.204866146	0.25505184	grey	-0.117432032	0.163452442		AES19890.1		Pentatricopeptide repeat (PPR-like) superfamily protein
Sapur.006G054500.1	0.90148846	-0.406774772	0.32093282	-1.2674	0.205013185	0.25117939	grey	-0.062492312	0.43686641	GO:0009055	AES02230.1	ATBCB,BCS,AAG14	blue-copper-binding protein
Sapur.008G075600.4	88.48167133	-0.098267487	0.063228223	-1.26718	0.205050798	0.25156004	grey	-0.08277964	0.303229969		AES22152.1	ATMTRNAH2.1,RNE2,T30.8N	Ribonuclease H
Sapur.016G092500.1	0.382098885	0.624045143	0.499195746	1.266848	0.205290837	0.25394301	grey	-0.12406153	0.121608869		AES49960.1		transmembrane protein, putative
Sapur.016G126600.1	275.6482931	-0.05858317	0.0466741	-1.26644	0.205356583	0.25407217	grey	-0.152036686	0.082477716		AES76080.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.014G027700.1	0.925561204	0.346565807	0.272123414	1.266212	0.205437357	0.25568851	grey	-0.045686225	0.575611014	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AES19340.1	CYP82C4	cytochrome P450, family 82, subfamily C, polypeptide 4
Sapur.006G206200.2	0.965261988	0.395129403	0.315243403	1.265969	0.205603513	0.25490553	grey	-0.114615451	0.169663463	GO:0006520,GO:0008270,GO:0003871,GO:0009086	AES17920.1	ATCIMS,ATMETS,ATMS1	Cobalamin-independent methionine synthase
Sapur.007G82900.1	2.892.10348	0.072777776	0.057508634	1.26551	0.205688461	0.25594204	grey	-0.047806708	0.518140983	GO:0005515	AES22135.1		5-methylthioribose/methylthioglutamate-homocysteine methyltransferase
Sapur.005G188500.1	226.0883191	0.069188669	0.054677995	1.265384	0.205733646	0.25388662	grey	0.097839476	0.222728024	GO:0006468,GO:0005524,GO:0004672	AES15890.1		Lipase/lipoxygenase, PLAT/LH2 family protein
Sapur.016G202200.1	0.541748504	0.402202131	0.317834884	1.264988	0.205806464	0.25203064	grey	-0.15797818	0.084905684				Protein kinase superfamily protein
Sapur.007G045300.1	73.23597305	0.431844283	0.341472129	1.264858	0.205922268	0.26204081	grey	0.18926607	0.01761048				
Sapur.001G161500.1	1.086056623	0.377164984	0.270736487	1.26475	0.205968019	0.26224237	grey	-0.05116794	0.534988827	GO:0006355,GO:0005634	AES15950.1	IAA18	auxin-responsive protein IAA26
Sapur.013G208000.1	1.08384919	-0.333331088	0.263507914	-1.26454	0.206034937	0.25432697	grey	-0.072188541	0.168937899	GO:0003677,GO:0006355,GO:0005634	AES22180.1	KNAT6,KNAT6L,KNAT6S	KN/STIMPY-like homeobox gene 6
Sapur.013G238400.4	0.501444407	0.427488879	0.34616687	-1.26381	0.206297162	0.25464152	grey	-0.239128042	0.025395932	GO:0016021,GO:0006952	AES08501.1	SR1	STRUBBELIG-receptor family 1
Sapur.007G061200.4	11.66860427	-0.117297968	0.092837105	-1.26362	0.206337136	0.25479196	grey	-0.081339808	0.311202443		AES63680.4		arginine/serine-rich splicing factor, putative
Sapur.006G075700.1	4.24117604	-0.564862771	0.442069322	-1.26308	0.206509378	0.26496327	grey	-0.132783888	0.09973162	emb3153	AES07520.1		cupin family protein
Sapur.15WG121100.1	0.431338721	-0.481663569	0.381412345	-1.26284	0.206645181	0.25706279	grey	-0.183147253	0.02167894		AES61990.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.006G193200.1	0.965702947	-0.150345437	0.119456736	-1.26263	0.206695618	0.25703427	grey	-0.11461501	0.18485035	GO:0005515	AES46820.1		Phosphotriesterase-related family protein
Sapur.017G021200.1	0.99661924	-0.366169638	0.290011565	-1.2626	0.206731686	0.25733759	grey	-0.0428131	0.594464201	GO:0006468,GO:0005524,GO:0004672	AES66980.1	SNC4	suppressor of npr1-1 constitutive 4
Sapur.15WG134400.1	3.649202577	-0.402533518	0.319007199	-1.26183	0.207009216	0.25769027	grey	-0.07232691	0.36801846	GO:0005515,GO:0006488,GO:0005524,GO:0004672	AES35710.1		Protein kinase family protein with leucine-rich repeat domain
Sapur.017G191000.2	0.663616313	-0.415329935	0.329072298	-1.26176	0.207069172	0.25811204	grey	-0.132398628	0.192417511	GO:0003724,GO:0006338	AES79040.3	Dna2 / Sec63-like domain-containing protein	heat shock protein binding protein
Sapur.007G041000.3	0.362149123	0.568354493	0.450609908	-1.26107	0.207285541	0.25798693	grey	0.030576641	0.703832925	GO:0006872,GO:0000166	AES07270.1	ATMHA8,LHMA1	heavy metal atpase 1
Sapur.013G208900.1	0.150889977	0.951604205	0.754390542	-1.26107	0.207285417	0.25796514	grey	0.128886605	0.105757053				
Sapur.005G131000.5	0.454489455	0.435188879	0.345137627	1.26095	0.207326721	0.25785387	grey	0.095257865	0.231330059	GO:0016868,GO:0006096,GO:0004619	AES22170.1		Phosphoglycerate mutase family protein
Sapur.005G130700.2	0.932882634	0.427488879	0.34616687	-1.26083	0.207364188	0.25798284	grey	0.239128042	0.025395932	GO:0016021,GO:0006952	AES08501.1	ATMLO1,MLO1	Seven transmembrane MLO family protein
Sapur.001G136800.1	2.087523272	0.434284168	0.34473686	1.260718	0.207404376	0.25791046	grey	-0.12393261	0.094455195	GO:0003700	AES27950.1	CRF4	cytokinin response factor 4
Sapur.007G060.1	0.386665569	0.878055158	0.696548664	1.26049	0.207517263	0.25797073	grey	-0.237371243	0.004353308		AES24280.1	GMI1	gamma-irradiation and mitomycin c induced 1
Sapur.012G001100.1	2.49015213	0.221452766	0.175707475	1.260349	0.207543439	0.25850079	grey	-0.113715543	0.161953304				
Sapur.016G005200.1	24.40919344	-0.31585726	0.249147261	-1.2597	0.207776611	0.25837922	grey	-0.154270763	0.051715324		AES22630.1	MKA,PDF2	phosphate deficiency response 2
Sapur.014G081400.1	2.075748344	-0.249661486	0.198459523	-1.25951	0.207836205	0.26840515	grey	-0.147388604	0.054447227	GO:0006468,GO:0004672	AES20020.1	ATMAPK6,PBK1	protein kinase family protein
Sapur.15WG064400.1	492.3587828	-0.34281051	0.272193072	-1.25944	0.207971189	0.25845688	grey	-0.16629718	0.037382429		AES22660.2		Protein of unknown function (duplicated DUF1396)
Sapur.005G188000.1	3.317963186	0.223595807	0.176888996	-1.25938	0.207980075	0.25846199	grey	-0.060409372	0.417334551	GO:0004681,GO:0003677	AES2J8	AGL98	AGAMOUS-LIKE 98
Sapur.015G082800.1	0.857144448	0.366186639	0.290015565	-1.2626	0.208066036	0.25846169	grey	-0.085647872	0.26686786				
Sapur.006G201300.1	0.66867863	0.932024924	0.740680745	-1.25942	0.208151131	0.25854681	grey	-0.232624499	0.00345264	GO:0008168,GO:0005875,GO:0003777	AES47520.1		F-box nucleotide triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain
Sapur.15WG092300.1	122.7124513	-0.128381454	0.101976639	-1.25893	0.208556583	0.25850387	grey	-0.08319364	0.307662882				
Sapur.005G072200.1	1.034163642	0.681546169	0.540897604	-1.25889	0.208575145	0.25854969	grey	-0.132023314	0.137872668		AES42090.1		DNAse I-like superfamily protein
Sapur.009G080300.1	66.41376644	-0.154740258	0.123018852	-1.25786	0.208941084	0.2506755	grey	-0.09006528	0.261976737	GO:0055114,GO:0016491,GO:0005507	AES03260.1	LAC11	laccase 11
Sapur.015G084300.1	130.5915704	-0.083287292	0.066188155	-1.25763	0.208043043	0.25807988	grey	0.163624248	0.061841036	GO:0006281,GO:0003676,GO:0000723	AES28178.1		FH1 helicase
Sapur.012G096500.1	558.7696416	0.04765115	0.037886336	1.25774	0.208485932	0.25901293	grey	0.03408805	0.675688283		AES19950.1		transmembrane protein, putative
Sapur.010G190200.1	1.096104608	-0.375435317	0.298543828	-1.25753	0.208561122	0.25937421	grey	-0.120145484	0.133368501	GO:0055114,GO:0020037,GO:0004679,GO:0004601	AES14532.1		Peroxidase superfamily protein
Sapur.013G097500.2	0.243480779	-0.262362241	0.192718805	-1.25723	0.208675171	0.25977421	grey	-0.252892975	0.015889027	GO:0005515	AES02145.3	ALG12,GBS4	homolog of yeast ALG12 mannosyltransferase 12
Sapur.004G079500.2	2.331624117	0.221665627	0.176530866	1.255676	0.209232299	0.26000831	grey	-0.13024806	0.103991263	GO:0046872,GO:0008824,GO:0046137	AES30841.1		Cofactor-independent phosphoglycerate mutase
Sapur.T191400.1	4.19255004	0.172364984	0.137294758	1.25544	0.209310	0.26009182	grey	-0.116442551	0.16441628		AES48503.1		Vacuolar protein sorting-associated protein 26
Sapur.005G007600.2	9.866470737	0.123248521	0.105428436	1.25534	0.209315395	0.26013005	grey	-0.10802119	0.178555428		AES26590.1	ZIP4	Clathrin adaptor complexes medium subunit family protein
Sapur.016G042200.5	5.700049184	-0.140482346	0.112077553	-1.25491	0.209439368	0.26029404	grey	-0.08616063	0.315564465	GO:0005515	AES26132.1	NF-YA10	nuclear factor Y, subunit A10
Sapur.003G001300.1	12.43996279	-0.170634044	0.136196031	-1.25286	0.210205804	0.26134953	grey	-0.08435156	0.290845882	GO:0016021,GO:0006952	AES45290.1	ATMLO3,MLO3	Seven transmembrane MLO family protein
Sapur.006G208300.1	216.7205225	-0.064004184	0.051082184	1.252429	0.210349197	0.26195739	grey	-0.088646491	0.217157102	GO:0004857,GO:0043546,GO:0030599,GO:0005618	AES07950.1		Plant invertase/pectinesterase inhibitor superfamily
Sapur.006G029900.1	17.91854654	0.17061127	0.136100387	1.252442	0.210487725	0.26160253	grey	-0.087274675	0.277087526		AES42150.1		Haloacid dehalogenase-like hydrolase family protein
Sapur.003G298300.1	16.8867782	0.109043283	0.087034589	-1.25185	0.210824183	0.26180037	grey	0.093884665	0.258677683		AES04850.1		
Sapur.004G089700.1	-0.094796574	0.376049982	0.32197025	-1.25476	0.210700712	0.26182034	grey	0.054907684	0.238805916	GO:0016592,GO:0003757,GO:0001104	AES03325.2	GCT	RNA polymerase II transcription mediators
Sapur.15WG077300.1	0.231473639	0.850875271	0.680154652	1.251003	0.210933377	0.26200488	grey	0.162614204	0.041867749		AES33800.1		Protein of unknown function (DUF579)
Sapur.013G257500.1	39.81838825	-0.101125066	0.0808579	-1.25066	0.211058068	0.26216952	grey	-0.117332674	0.143334079				
Sapur.014G069900.1	0.18023697	-0.785907791	0.628499933	-1.25059	0.211082906	0.26230858	grey	-0.31071933	7.48E-05	GO:0005089	AES20460.2	ATROPGEF1,ROPGEF3	RHO guanyl-nucleotide exchange factor 3
Sapur.005G126100.2	0.58075522	-0.419341617	0.34660471	-1.25024	0.211211279	0.26340461	grey	-0.076038632	0.468749652	GO:0055114,GO:0071949	AES02230.1	ABA1,ATABA1,ATZIP,BG1J	zeaxanthin epoxidase
Sapur.018G049500.1	101.2480406	0.195691857	0.2687573	1.250083	0.211269186	0.26240278	grey	0.145087182	0.068429065	GO:0003674			RGH domain protein
Sapur.015G190100.1	7.364814841	-0.221351784	0.097855728	-1.24996	0.211314517	0.26344832	grey	-0.08116693	0.313207271	GO:0016021	AES41705.2		camphor resistance Crc3 family protein
Sapur.003G047900.1	0.300519987	-0.622381893	0.497042491	-1.24991	0.211334158	0.26362648	grey	-0.172342608	0.030893409		AES63850.1		BTB/POZ domain-containing protein
Sapur.003G253700.1	12.13310449	0.152003664	0.122178284	1.249429	0.211450683	0.26379	grey	0.068864491	0.272577202		AES28040.1		Exostosin family protein
Sapur.003G300800.1	14.92057614	-0.117642089	0.094167138	-1.24929	0.211518929	0.26271074	grey	0.086139666	0.283485175	GO:0008270,GO:0005685,GO:0003908,GO:0000187	AES03120.1		CZHC and CZHC zinc fingers superfamily protein
Sapur.003G229800.1	0.224126065	0.855154543	0.524615436	1.248752	0.211575808	0.26294788	grey	-0.193821264	0.055090209	GO:0005643,GO:0046907	AES15970.1		NUP50 (Nucleoporin 50 kDa) protein
Sapur.004G097500.1	0.365327184	-0.626284097	0.501197381	-1.24708	0.212088005	0.26368957	grey	0.162818855	0.056010236	GO:0015297,GO:0015238,GO:0005855	AES16210.2		MATE efflux family protein
Sapur.008G027000.3	11.1124988	0.177479512	0.142318235	1.247063	0.212375154	0.26369657	grey	0.110727271	0.167428302	GO:0006221,GO:0003883	AES12670.1	emb2742	CTP synthase family
Sapur.018G007900.1	1.033467571	-0.295161644	0.23703203	-1.24674	0.212496626	0.26381395	grey	-0.072048035	0.364827169		AES31600.1		UDP-sugar transporter, putative
Sapur.007G040700.1	136.2209902	0.067035315	0.037042085	1.24623	0.212680005	0.26456739	grey	0.08109653	0.22113309		AES07000.1	ACD2,ATRCER	Red chlorophyll catabolite reductase
Sapur.T124700.1	0.146037777	-0.966025754	0.775798833	-1.24584	0.212818654	0.26472711	grey	-0.212819255	0.003539748		AES16080.1	AHCH17,CH17	carboxylesterase 17
Sapur.007G028800.1	16.26868849	0.242388711	0.180251188	1.244491	0.213183733	0.26481849	grey	-0.127529805	0.11278362		AES56145.2		Leucine-rich repeat transmembrane protein kinase
Sapur.002G138300.1	5.824587904	0.173351441	0.139399588	1.243443	0.213764627	0.26528003	grey	-0.125432006	0.117511186		AES01680.1	ATPRD1,PRD3	putative recombination initiation defects 1
Sapur.013G084700.1	0.379937725	0.502335265	0.403996648	1.243414	0.213715153	0.26529159	grey	-0.075666622	0.346256737	GO:0008270,GO:0003676	AES21280.1		
Sapur.013G338000.1	71.48600163	-0.103745684	0.084233882	-1.24326	0.213773187	0.26535889	grey	-0.098913908	0.231243883		AES46210.1		hypothetical protein
Sapur.T052900.2	0.319945523	0.571194166	0.459465036	1.243172	0.213806379	0.26538187	grey	-0.103557112	0.136780427	GO:0046838,GO:0046872,GO:0016756,GO:0010038	AES44070.1	ARA8,ATPCS1,CAD1,PCS1	phytochelatin synthase 1 (PCS1)
Sapur.003G208600.1	29.7026185	-0.327817769	0.263669896	-1.24315	0.213814109	0.26538455	grey	-0.134890543	0.09207086				phytochelatin synthase
Sapur.006G205100.1	0.805413129	-0.355406422	0.28539411	-1.24297	0.213892554	0.26546619	grey	-0.057478356	0.474381299		AES32560.2		paramyosin-related
Sapur.018G089900.1	0.223831791	-0.642621541	0.517168607	-1.24256	0.214030362	0.26562522	grey	-0.245993171	0.001899458				
Sapur.011G141000.2	1.243795666	0.328996017	0.26004149	-1.24111	0.214690306	0.26174225	grey	-0.168574192	0.151663943	GO:0005975,GO:0004553	AES11720.1		Glycosyl hydrolases family 31 protein
Sapur.002G149600.1	4.76805829	-0.45935707	0.3702705	-1.24046	0.214805338	0.2665543	grey	-0.153855687	0.0455145				
Sapur.005G202400.1	411.9857553	-0.054000545	0.047418839	-1.23954	0.215164109	0.26606704	grey	-0.127561165	0.127878318	GO:0004883	AES16430.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.010G079100.3	2.668449951	-0.229183293	0.184902282	-1.23948	0.215166546	0.26682518	grey	-0.08263805	0.303157384	GO:0015770,GO:0005515,GO:0005887	AES02860.1	ATSUC1,ATSUT2,SUC3,SUT1	sucrose transporter 2
Sapur.003G150100.1	166.1858791	-0.082684441	0.066696124	-1.2392	0.215705919	0.26701598	grey	-0.107523566	0.180908331				
Sapur.010G167700.1	28.61399868	0.154863528	0.124667601	1.239003	0.215154398	0.26718127	grey	0.108117664	0.17492629				
Sapur.006G147700.1	0.820385651	0.327050897	0.26408168	-1.23884	0.215492263	0.26736137	grey	0.031937018	0.699587003	GO:0005634	AES21110.1		G10 family protein
Sapur.017G021400.5	0.862926043	0.367125752	0.3045843	-1.23845	0.215677005	0.26743808	grey	-0.04240876	0.261396866	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AES66980.1	SNC4	suppressor of npr1-1 constitutive 4
Sapur.005G052600.1	105.0386847	0.104459315	0.08435324	1.238366	0.215830352	0.26745783	grey	-0.091399382	0.254926772	GO:0005975,GO:0004553	AES03800.1	BGAL6,MUM2	Glycosyl hydrolase family 35 protein
Sapur.016G223204.1	0.352279798	0.622324257	0.502187	1.238	0.215888505	0.26780822	grey	0.100307088	0.213317035	GO:0005515	AES03970.1		F-box protein interaction domain protein
Sapur.010G132004.4	6.339862745	0.174457692	0.140734499	1.238005	0.215917027	0.26784043	grey	-0.081608864	0.309509942	GO:0003676	AES02800.1	TAF15	TBP-associated factor 15
Sapur.T033800.1	0.267905543	0.543831399	0.439546525	1.237	0.215984838	0.26816494	grey	0.11208408	0.192560169	GO:0005515	AES8AFL,FIM1		fimbrin-like protein
Sapur.016G002000.1	12.16548854	0.117963684	0.095387634	1.236677	0.216207054	0.26833023	grey	0.109813573	0.170553928		AES02155.1		Phosphoglycerate mutase family protein
Sapur.003G208500.2	3.717626795	-0.202287122	0.163691918	1.236287	0.216391968	0.26892187	grey	-0.060268439	0.322202272		AES07630.1		hypothetical protein
Sapur.012G181000.1	588.0125416	-0.051377263	0.041572117	-1.23586	0.216511666	0.2685258	grey	-0.123139396	0.124446305	GO:0047761,GO:0016021	AES19130.1		glycosyl phosphatidyl inositol transmembrane-like protein, putative
Sapur.011G154100.2	1.249866613	0.332458517	0.268204149	1.24111	0.216754312	0.26831037	grey	-0.152506461	0.052348883		AES25200.1	CRK35	cysteine-rich RLK (RECEPTOR-like protein kinase) 25
Sapur.008G105200.1	154.4228854	-0.061609083	0.049928289	-1.2405	0.216848054	0.26891524	grey	-0.120624317	0.13236503	GO:0016787	AES30103.2	ATNUDX25,NUDX25	nudix hydrolase homolog 25
Sapur.016G195800.1	0.468845569	-0.515330931	0.417273745	-1.23484	0.216854297	0.26891584	grey	-0.172272337	0.039991424	GO:0005515	AES02520.1	ATGSTF2,ATPHI26,ATRMC4L	glutathione S-transferase PHI 2
Sapur.008G208200.1	270.7540369	0.051608287	0.04184787	1.234479	0.216875769	0.26935513	grey	0.06934674	0.286472667	GO:0004854	AES02870.1	VTC4	Inositol monophosphatase family
Sapur.010G085200.3	3.26057665	-0.17388827	0.140892018	-1.23417	0.217138982	0.26938011	grey	-0.091182271	0.256061892	GO:0016887	AES11560.1		bromo-adjacent homology (BAH) domain-containing protein
Sapur.004G201400.1	944.2331146	0.289270934	0.234516005	1.233	0.217167609	0.26363411	grey	0.068591932	0.38098422		AES46410.1	CPC	Homeodomain-like superfamily protein
Sapur.005G075000.2	0.773822217	0.277207521	0.30587975	-1.23396	0.217216789	0.26391294	grey	-0.064600309	0.422516921				
Sapur.006G165200.1	141.7170362	0.080262325	0.088316402	1.233227	0.217674123	0.26944453	grey	0.09984217	0.227288611				Fimbrin 1
Sapur.006G175500.1	17.06882084	0.135080537	0.110313137	1.232688	0.217868466	0.26987863	grey	0.117626839	0.142326924				
Sapur.003G208800.2	15.18088877	0.094966148	0.077648239	1.232422	0.217764173	0.26996648	grey	0.074161506	0.302882612		AES15220.1		FAMILIA1 protein
Sapur.014G130900.1	344.6262116	0.054993583	0.04502987	1.231885	0.217892153	0.27025101	grey	0.107142249	0.185677261		AES04530.1	CP2,TBZ2	Metallo-hydrolase/oxidoreductase superfamily protein
Sapur.T108400.1	0.118719919	0.847957866	0.688559161	1.231466	0.218127392	0.27028409	grey	0.32885919	2.60E-05		AES26380.1		Melibiase family protein
Sapur.017G053800.1	49.10470663	-0.052122505	0.043195958	-1.23122	0.218245556	0.27052231	grey	-0.188496563	0.017457673				hypothetical protein
Sapur.005G016900.1	780.7954004	0.063769704	0.051835515	1.230825	0.218388485	0.27067589	grey	0.10562768	0.17192216		AES27860.1		hypothetical protein
Sapur.005G090200.1	221.7984654	0.050104555	0.041000242	1.230577	0.218434397	0.27080763	grey	0.052154758	0.51523093	GO:0006355,GO:0003677,GO:0008270,GO:0003676	AES60620.1	CSDP1	cold-shock domain protein 1
Sapur.015G111900.1	21.94597224	0.165893865	0.134638675	1.230074	0.218444579	0.27075188	grey	-0.081832836	0.308240551	GO:0043565,GO:0006355,GO:0003700	AES38470.1	ATWRKY32,WRKY32	WRKY DNA-binding protein 32
Sapur.T015G180.1	1.567263097	0.166376009	0.135138209	1.229962	0.218728345	0.27166445	grey	-0.160079976	0.076024491		AES17920.1		
Sapur.006G206500.1	4.530859613	0.243275677	0.197652904	-1.2268	0.218588485	0.27261325	grey	-0.126915777	0.113141702		AES30180.1		Barwin-related endoglucanase
Sapur.006G231000.1	221.7984654	0.050104555	0.041000242	1.226569	0.218834511	0.27300299	grey	-0.227504168	0.004242143	GO:0006364	AES67352.1		ribosome-binding factor A
Sapur.013G119100.1	64.1862636	0.203415961	0.165265453	1.22921	0.218993205	0.27363985	gr

Sapur.01G0203400.2	32.39077207	-0.09333604	0.07819404	-1.19365	0.23261789	0.28690536	gene	-0.08754934	0.27557647
Sapur.01G0204000.1	12.21684009	-0.28363624	0.23733197	-1.1931	0.23202997	0.28758486	gene	-0.09655029	0.22924755
Sapur.01G0210100.4	0.35456875	0.60202734	0.54183058	1.90255	0.23204384	0.28747062	gene	-0.12753737	0.11149104
Sapur.01G0214500.1	2.77034519	-0.25376772	0.21280373	-1.19306	0.23325783	0.28765583	gene	-0.10624507	0.18538573
Sapur.01G0216100.2	99.01525614	-0.07878124	0.06618231	-1.1917	0.23237653	0.28785091	gene	-0.11616469	0.10280563
Sapur.01G0219080.1	2.38065804	0.21889329	0.18374653	1.19126	0.23155147	0.28801203	gene	-0.26337614	0.00861854
Sapur.01G0282800.1	475.2518674	0.04841571	0.04068088	-1.19099	0.23156548	0.28810757	gene	-0.09897605	0.21734537
Sapur.01G0307200.6	0.50882244	0.39170388	0.32890163	1.19065	0.23267232	0.28833336	gene	0.07775756	0.10249728
Sapur.01G0209800.1	0.79487509	-0.34483225	0.28955624	-1.19061	0.23268721	0.28854742	gene	-0.02164563	0.73560373
Sapur.7075400.1	0.17920164	0.26197348	0.22000349	1.19075	0.23407242	0.28823384	gene	-0.24432864	0.60260324
Sapur.05G1910100.3	2.81570606	0.19466589	0.16352575	-1.19047	0.23383207	0.28834264	gene	0.04059592	0.56235767
Sapur.01G0217000.1	7.10575675	0.27144086	0.23042022	-1.18967	0.23416129	0.28873317	gene	0.11318914	0.15807268
Sapur.01G0407600.1	120.3143903	0.09004704	0.07568782	1.18973	0.23415073	0.28885919	gene	-0.06874208	0.39207383
Sapur.01G0238700.1	5.85019269	0.20738371	0.24908118	-1.18941	0.23325603	0.28884258	gene	-0.07367756	0.33828448
Sapur.01G0260700.1	657.9684328	0.05485751	0.04615562	1.18932	0.23433112	0.28854307	gene	0.08365185	0.29798409
Sapur.01G0287600.1	0.20395579	0.62194224	0.52743688	1.18876	0.23452306	0.28913732	gene	0.10180806	0.16692022
Sapur.7044100.1	1.69118611	-0.28910842	0.24320977	-1.18869	0.23450747	0.28938037	gene	-0.06391749	0.42643854
Sapur.01G0137300.1	516.4898595	-0.04000237	0.03365021	-1.18837	0.23482704	0.29260641	gene	-0.14088343	0.0762101
Sapur.01G0402500.1	146.7276171	0.16329988	0.13739435	1.18837	0.23482642	0.29260641	gene	-0.09663879	0.21928569
Sapur.007G0714000.1	2.72854805	0.19947823	0.16783172	1.18834	0.23488778	0.29260561	gene	0.12241636	0.12688735
Sapur.01G0249500.1	2.34087868	0.27367577	0.23025391	1.18742	0.23746185	0.29349687	gene	-0.1537108	0.69192722
Sapur.09G0182900.1	0.22202223	-0.85260875	0.75146244	-1.18783	0.23480391	0.29349952	gene	-0.2809636	0.00225834
Sapur.01G0268300.1	84.44869075	0.27503138	0.23132147	1.18729	0.23502856	0.29364187	gene	0.07007821	0.18125514
Sapur.01G0192700.1	1569.288622	0.02575703	0.02160784	1.18747	0.23502914	0.29364187	gene	0.09107525	0.25662279
Sapur.01G0212300.1	0.13181118	0.68907703	0.58000522	1.18703	0.23507163	0.29387393	gene	0.30481923	0.05003773
Sapur.09G0131600.1	354.4603777	0.38200122	0.32178883	1.18722	0.23510746	0.29395983	gene	0.18799685	0.03843475
Sapur.09G0240700.1	3.96318288	0.30089586	0.25309556	1.18698	0.23522865	0.29398782	gene	0.10522994	0.18979469
Sapur.05G0367200.1	0.62361354	0.49357646	0.41508322	1.18674	0.23533667	0.29405766	gene	-0.0074596	0.22463344
Sapur.01T0003200.1	0.54496074	-0.43876249	0.36985879	-1.18637	0.23555425	0.29221957	gene	-0.11983727	0.13459997
Sapur.01G0287000.1	13.49759132	0.16329988	0.13739435	1.18565	0.23579347	0.29463261	gene	-0.10363663	0.23834419
Sapur.08G0214800.6	6.13708198	-0.77368248	0.65718884	-1.18468	0.23614584	0.29029349	gene	-0.07416509	0.15609152
Sapur.01G0160800.1	12.09857757	0.61623363	0.51819356	-1.18464	0.23620183	0.29050107	gene	-0.1573108	0.69192722
Sapur.09G0168700.1	19.04619118	0.28460413	0.23929745	1.18455	0.2361936	0.29066445	gene	0.10732009	0.18094583
Sapur.01G0228300.1	19.93563971	0.71032767	0.5996716	-1.18443	0.23628193	0.29082267	gene	-0.28059363	0.03034688
Sapur.7191000.1	0.40594501	0.47164024	0.39843709	1.18726	0.23621656	0.29138873	gene	0.09287318	0.26077652
Sapur.01G0267600.1	2.92438731	0.68025368	0.58238987	1.18398	0.23617132	0.29150663	gene	0.25134288	0.01380593
Sapur.01G0623700.2	4.12685019	0.19807645	0.16759708	-1.18184	0.23708274	0.29235322	gene	0.25134288	0.01380593
Sapur.01G0185500.1	2.19506761	0.23025795	0.19683471	1.18182	0.23727694	0.29235322	gene	0.09960755	0.23453882
Sapur.09G0293600.1	5.25765617	0.11350355	0.10819895	1.18179	0.23728548	0.29235322	gene	0.10285645	0.20354945
Sapur.09G0134900.1	1883.357972	-0.11205366	0.09483862	-1.18175	0.23730927	0.29248404	gene	-0.12178727	0.12861146
Sapur.01G0238100.1	3.05725157	0.32180615	0.29798545	-1.1816	0.23732261	0.29308561	gene	-0.0867553	0.21232606
Sapur.01G0271700.1	0.99172143	0.31475529	0.26648186	1.18107	0.23757235	0.29255816	gene	0.10288178	0.19497841
Sapur.01G0289100.2	0.32760103	0.52180884	0.44201629	1.18017	0.23795224	0.29288606	gene	0.12726421	0.2206132
Sapur.01G0202300.1	86.82451774	0.29671673	0.25144605	1.18009	0.23798482	0.29304295	gene	0.10339149	0.15639274
Sapur.01G0252400.1	255.1691523	0.21341831	0.17923689	-1.1793	0.23834823	0.29368869	gene	0.09516028	0.27439863
Sapur.01G0139000.2	1.88631241	0.25846723	0.19164273	1.17968	0.23860916	0.29376823	gene	0.13652868	0.08195509
Sapur.01G0160500.1	3.70583036	0.32568037	0.27632518	-1.17778	0.23889159	0.29408482	gene	-0.08948835	0.26492151
Sapur.01G0186800.1	1.1821632	0.27968547	0.23682484	1.17693	0.23972897	0.29432898	gene	0.06812186	0.35688651
Sapur.0D2G0187700.1	131.8076661	0.12875912	0.10946938	-1.17751	0.23899524	0.29406228	gene	-0.10651371	0.18426784
Sapur.1H0G0549900.1	0.57263102	0.51268256	0.43511249	1.17665	0.23935146	0.29436508	gene	-0.16848272	0.04976569
Sapur.01G0309600.2	1.17232072	0.39557767	0.25126127	1.17635	0.23964096	0.29476624	gene	0.08737314	0.2765423
Sapur.01G0320100.1	1.83276537	-0.30188665	0.26091112	-1.1624	0.23969706	0.29479765	gene	-0.11367305	0.15327804
Sapur.09G0138800.2	1.20528335	0.29256072	0.24806507	-1.1762	0.23561243	0.29480612	gene	-0.0938569	0.24238618
Sapur.01G0269100.1	1.13039357	0.54882625	0.23126767	-1.17618	0.23564176	0.29480598	gene	0.14394792	0.07207353
Sapur.01G0201900.2	0.28239451	0.66375956	0.56752263	-1.17523	0.23960186	0.29547891	gene	-0.18112718	0.01830316
Sapur.01T0081500.1	51.26617089	0.19114588	0.16274283	-1.17663	0.24013419	0.29523567	gene	0.09763419	0.22473388
Sapur.01G0229900.1	7.70899435	-0.12228667	0.10400293	-1.1746	0.24015466	0.29553761	gene	-0.15365979	0.05468589
Sapur.09G0291300.2	1.8977982	0.21026985	0.17914369	-1.17375	0.24049547	0.29596243	gene	-0.14028975	0.08814396
Sapur.01G0204300.1	4.88782172	-0.30704863	0.26147879	0.10050057	-1.17352	0.24064889	gene	-0.08184403	0.30705453
Sapur.01G0215900.1	165.4914959	0.31443848	0.26795444	1.17322	0.24070734	0.29618178	gene	0.12244857	0.13659579
Sapur.01G0278200.1	11.71778812	0.22164168	0.18882148	-1.1731	0.24075717	0.29626137	gene	0.12709942	0.13288853
Sapur.01G0171400.1	5.18079109	0.19204762	0.18660825	1.17268	0.24076537	0.29628026	gene	0.11032065	0.18898942
Sapur.01G0186100.1	1.15219628	0.56768633	0.48351279	-1.17186	0.24112231	0.29632882	gene	-0.08832253	0.27293735
Sapur.09G0412300.1	0.41658029	0.45366821	0.38710922	1.17708	0.24091007	0.29639384	gene	0.05167291	0.50608213
Sapur.01G0138600.1	2.78654115	0.29368429	0.25018227	1.17153	0.24091973	0.29664324	gene	0.09268756	0.19268118
Sapur.09G0123500.1	1.12081405	0.30883422	0.26345759	1.17269	0.24108899	0.29685584	gene	0.06852088	0.41111258
Sapur.01G0250100.1	0.36094306	0.56738154	0.48614045	-1.17125	0.24159103	0.29685584	gene	-0.14388884	0.07423561
Sapur.08G0115000.1	0.176192	0.98237465	0.83808342	1.17005	0.24191241	0.29689069	gene	-0.24653068	0.00185968
Sapur.05G0266000.1	5.44143972	0.14388613	0.12288249	-1.1709	0.24163143	0.29727427	gene	-0.07561005	0.73093816
Sapur.05G0250100.13	6.80618868	0.21312242	0.18619756	-1.17101	0.24159215	0.29731385	gene	-0.09488612	0.23091193
Sapur.09G1184800.1	0.31171164	0.50185346	0.42858046	1.17066	0.24162168	0.29755872	gene	0.09277508	0.24782787
Sapur.01G0281500.1	12.3270737	0.09087819	0.07770826	1.17069	0.24162183	0.29755917	gene	0.06832742	0.36541174
Sapur.09G0240400.1	15.3358361	0.26707283	0.18599527	1.17028	0.24178246	0.29791088	gene	0.05840871	0.4638822
Sapur.01G0401200.1	5.00022481	0.41208888	0.35197274	-1.17007	0.24179197	0.29715213	gene	0.06874967	0.39197921
Sapur.01G0295800.1	0.17774994	0.82458178	0.70464597	-1.17054	0.24178384	0.29732548	gene	-0.29782538	0.00016921
Sapur.09G0142300.3	2.30073849	0.25342306	0.21658327	1.16731	0.24268075	0.29758864	gene	-0.21161628	0.09781808
Sapur.01G0231900.2	108.2116874	0.05972868	0.05108026	1.17008	0.24188155	0.29753505	gene	0.10933366	0.17285486
Sapur.7028600.1	1.30705396	0.30232807	0.25850647	-1.17003	0.24189038	0.29753968	gene	-0.11105337	0.16595645
Sapur.09G0277500.1	14.11011996	-0.76408376	0.65318793	-1.16974	0.24203163	0.29766068	gene	-0.05165161	0.52298921
Sapur.01G0565000.2	4.85845444	0.15929487	0.13617926	1.16973	0.24239055	0.29766068	gene	0.07408761	0.35642212
Sapur.01T0080000.1	406.8829614	0.05168383	0.04367515	-1.16926	0.24238383	0.29800284	gene	-0.12383171	0.12720117
Sapur.01G0274100.2	2.07795014	0.20533425	0.17578641	-1.1692	0.24232145	0.29795108	gene	-0.11258109	0.10330192
Sapur.7063200.1	1.03429063	0.34657806	0.29647854	1.16892	0.24243569	0.29795356	gene	0.04833656	0.58973334
Sapur.7121900.1	4.76689272	-0.15101945	0.12917433	-1.16868	0.24261283	0.29795306	gene	-0.11894399	0.17075343
Sapur.01T0281600.1	0.01568862	0.97211242	0.83182227	1.16862	0.24264948	0.29817162	gene	0.10764019	0.17842836
Sapur.09G0120400.1	16.28853257	0.16145479	0.13819976	1.16827	0.24269731	0.2883239	gene	-0.05915677	0.40554422
Sapur.09G0280800.1	66.92515779	0.07180147	0.06067774	1.16798	0.24280716	0.28847165	gene	0.06174016	0.41437865
Sapur.05G0813000.2	5.4050674	0.13004087	0.11134867	1.16781	0.24285472	0.28849063	gene	0.10546129	0.17854629
Sapur.01G0292400.3	1.10845118	0.31629589	0.27093831	-1.1678	0.24288775	0.2882287	gene	-0.04262237	0.56506144
Sapur.09G0234300.1	1016.794197	0.02164374	0.01853773	1.16731	0.24278680	0.28744608	gene	0.08444044	0.39202728
Sapur.15W0045600.1	0.76074546	-0.33155299	0.28560769	-1.16625	0.24313323	0.2892487	gene	-0.11257408	0.16039177
Sapur.01G0243800.1	0.12877275	-0.50219582	0.43475029	-1.16615	0.24287323	0.29443884	gene	-0.11692924	0.56469703
Sapur.7060600.1	46.75696828	0.09008487	0.07743834	1.16542	0.24468408	0.3003279	gene	0.11641541	0.14649606
Sapur.01G0260800.2	0.36303826	0.40087366	0.35234128	1.16109	0.24470925	0.30007770	gene	0.22728266	0.00488147
Sapur.01G0294100.1	0.53744458	0.38990216	0.33518528	1.16295	0.24483777	0.3008333	gene	0.05373458	0.48811445
Sapur.01G0313100.1	358.4117015	0.05168383	0.04367515	-1.16204	0.24484906	0.30080244	gene	0.06869455	0.35208865
Sapur.01G0173600.3	7.49451874	0.12964114	0.11469703	1.16259	0.24482742	0.30091807	gene	0.04909578	0.54148964
Sapur.05G0945600.1	3.63162286	0.16487839	0.14073514	1.16097	0.24542457	0.30177532	gene	0.01397969	0.87488227
Sapur.01G0110700.1	0.16899286	0.94025753	0.80054966	1.16073	0.24570637	0.30189392	gene	0.23800559	0.02085307
Sapur.01G0139800.2	24.49862893	-0.17436751	0.15028307	-1.16008	0.24602836	0.30220722	gene	-0.08899183	0.21782007
Sapur.01G0242800.1	27.28805063	-0.10757785	0.09273836	-1.15962	0.24620168	0.30240356	gene	-0.08889106	0.28182448
Sapur.01G0187200.5	4.93838271	0.16174293	0.13948739	-1.15955	0.24620846	0.30241378	gene	-0.11663631	0.14643578
Sapur.01G0186600.1	671.5158269	0.07180147	0.06067774	1.15946	0.24620504	0.30246679	gene	0.09752417	0.23437704
Sapur.01G0131900.1	0.61375248	-0.36659958	0.31653292	-1.1581	0.24682736	0.30314724	gene	-0.14530425	0.08407128
Sapur.01G0177200.1	12.72137736	0.16161653	0.14752689	1.15764	0.24687926	0.30320214	gene	0.07936878	0.33728787
Sapur.01G0269700.1	4.93606435	-0.16307029	0.14083446	-1.15792	0.24686975	0.30314532	gene	-0.08160997	0.27221976
Sapur.01G0275000.1	184.8549105	0.05804968	0.07809669	1.15758	0.24707387	0.30337583	gene	-0.08512142	0.36304559
Sapur.01T0020300.1	3.17781284	-0.26689927	0.23052374	-1.15754	0.24705274	0.30383289	gene	-0.10520728	0.18974131
Sapur.01G0268700.1	301.7099118	-0.03398308	0.03402786	-1.1574	0.24710665	0.30441594	gene	-0.09880114	0.21744801
Sapur.01G0266400.1	7.40029703	0.07365344	0.06365161	1.15705	0.24719391	0.30342861	gene	0.06815121	0.27263754
Sapur.01G0125400.2	0.22680124	0.58642261	0.50708258	1.15482	0.24784851	0.30397922	gene	0.15783878	0.04834629
Sapur.05T0160100.1	0.36953969	0.30275253	0.42317587	-1.15441	0.24751178	0.30401812	gene	0.11617164	0.06137404
Sapur.09G0097600.1	671.4536033	0.03327949	0.02906584	1.15618	0.24763168	0.30401986	gene	0.07008369	0.18348787
Sapur.01G0267900.1	0.57379766	0.37248718	0.32237833	-1.1544	0.24791962	0.30437062	gene	0.10522102	0.18950275
Sapur.01G0292700.1	0.93298375	-0.42920188	0.37196194	-1.15529	0.24797117	0.30443201	gene	-0.08945004	0.91634806
Sapur.01G0285200.1	1.69524909	0.24677464	0.21558664	1.15368	0.24824103	0.30527163	gene	0.10475242	0.18426968
Sapur.01G0291400.1	98.0298506	-0.08506172	0.07367282	-1.15458	0.24822385	0.30476912	gene	-0.08173621	0.30647991
Sapur.01G0111300.1	101.8754151	0.05168383	0.04367515	1.15409	0.24846947	0.30495332	gene	-0.08765431	0.27219919
Sapur.05G0270000.1	196.9614732	-0.07121204	0.06250588	-1.15393	0.24853028	0.30506664	gene	0.08984878	0.26791473
Sapur.08G0391200.1	49.02863023	-0.07046248	0.06118122	-1.15392	0.24853265	0.30506664	gene	-0.08213327	0.30647991
Sapur.01G0204500.1	1.05305645	-0.41429616	0.36296511	-1.15325	0.24887926	0.30539129	gene	-0.10223219	0.20433945
Sapur.01G0398600.1	0.71507715	0.35508594	0.30792965	1.15152	0.24847862	0.30542886	gene	0.12835948	0.12536389
Sapur.08G0257100.1	10.50527177	0.09170664	0.07960154	1.15268	0.24909515	0.30547784	gene	0.10268852	0.16126175
Sapur.01G0136900.3	0.38416574	-0.40870937	0.35462263	-1.15252	0.24910746	0.30572568	gene	-0.16209823	3.16E-06
Sapur.7181600.1	21.04027785	0.12218285	0.10609344	-1.15202	0.24911117	0.30616546	gene	0.07483933	0.31248187
Sapur.01G0184200.2	0.33560065	0.46579116	0.40505553	1.15156	0.24938452	0.30603718	gene	0.04528809	0.57362982
Sapur.01G0278300.1	0.13527266	0.86269964	0.74869267	-1.15123	0.24960966	0.30603279	gene	0.30279155	0.00016474
Sapur.15W0281500.1	26.24867984	0.19521937	0.16954108	1.15168	0.24958018	0.30260379	gene	0.11717867	0.15983548
Sapur.01G0241000.1	82.0329663	0.11956198	0.09726757	-1.15127	0.24962857	0.30629846	gene	-0.10102845	0.20807859
Sapur.01G0164400.2	10.18819947	-0.13597816	0.10576066	-1.15052	0.24993597	0.30649694	gene	-0.08176449	0.30868994
Sapur.03G0427700.4	0.30197451	0.48856994	0.42403312	1.15027	0.25012565	0.30600984	gene	0.07862098	0.33621709
Sapur.08G0282000.1	2.76707088	0.19521937	0.16954108	1.15021	0.25013994	0.30600984	gene	0.07884604	0.33621709
Sapur.01G0413500.1	7.55938413	0.13540553	0.11759192	-1.14971	0.25020261	0.30703258	gene	-0.06514873	0.41760166
Sapur.01G0222101.1	747.6947368	0.03168104	0.02751728	1.14971	0.25020262	0.30703258	gene	0.11984852	0.18517177
Sapur.01G0149700.5	0.30601856	-0.47403617	0.41504853	1.14916	0.25038615	0.30766942	gene	0.15765647	0.04868042
Sapur.01G0461400.1	0.15940024	0.91349204	0.79319494	-1.14905	0.25041584	0.30731302	gene	0.08833664	0.27335591
Sapur.01G0261400.2	6.18175987	0.12849461	0.11760324	1.14897	0.25056767	0.30735732	gene	0.04396436	0.65178163
Sapur.01G0247300.1	75.58153144	0.07180147	0.06250588	1.14885	0.25075385	0.30737985	gene	-0.09352589	0.24324326
Sapur.05G1291000.1	19.38048296	0.08853392	0.07749379	1.14765	0.25118225	0.30800592	gene	0.14329729	0.07946241
Sapur.01G0279100.2	4.64757921	-0.15379121	0.13457197	-1.14755	0.25115806	0.30800592	gene	-0.10363645	0.18731142
Sapur.08G0293600.1	45.74659182	0.08426305	0.07508855	1.14719	0.25133132	0.30820568	gene	0.09872646	0.29072582
Sapur.01T0097500.1	104.4943564	0.06655184	0.05825411	1.14639	0.25160836	0.30832201	gene	0.05414472	0.50262387
Sapur.01G0269300.1	2.28023968	0.48704948	0.42352125	-1.14605	0.25164261	0.30832201	gene	0.10416667	4.32E-05
Sapur.01G0263400.1	291.6318822	0.06230515	0.05438859	1.14592	0.25180056	0.30880279	gene	0.04932685	0.53933429
Sapur.01G0267500.1	1.92726556	0.38875198	0.33958185	1.14569	0.25166051	0.30887318	gene	-0.09343335	0.43538562
Sapur.01T0012800.1	226.2287759	0.42186134	0.36835158	1.14574	0.25201845	0.30900963	gene	0.10397987	0.19498396
Sapur.01G0188400.1	1.87306469	0.26097922	0.22769484	1.14518	0.25205176	0.30940219	gene	0.07200168	0.38237286
Sapur.01G0272100.1	5.81627319	0.29577765	0.18229237	1.14703	0.25232171	0.30937262	gene	0.06939857	0.38778344
Sapur.01G0265300.1	5.58863477	0.09255487	0.08077184	1.14478	0.25267542	0.30387189	gene	0.07471729	0.41368652
Sapur.01G0164000.2	0.26586884	0.47917128	0.41813184	1.14067	0.25255731	0.30967742	gene	0.19383829	0.01967913
Sapur.01G0184000.1	8.40984761	0.13362229	0.11692309	1.14364	0.25297039	0.31009374	gene	0.07664531	0.32814697
Sapur.01T0080200.1	0.37159985	0.97988227	0.85777868	1.14278	0.25297126	0.31045188	gene	0.04624145	0.56045188
Sapur.01G0099400.1	18.21602234	0.07904658	0.06922035	-1.1423	0.25328898	0.31025535	gene	-0.13457671	0.09281005
Sapur.01G0373000.1	5.38268256	0.09255487	0.08077184	1.14122	0.25385196	0.31051198	gene	-0.05334142	0.49146272
Sapur.01G0249000.3	0.19703768	0.58155809	0.50924536	1.14107	0.25392753	0.31070354	gene	0.13406071	0.09413543
Sapur.01G0282200.1	1.43715102	0.38867727	0.34049894	1.14108	0.25392818	0.31088581	gene	0.09581742	0.23238584
Sapur.01G0165800.1	939.3298363	0.04615839	0.04047549	-1.14048	0.25426619	0.31385091	gene	-0.06127358	0.25598446
Sapur.01G0136100.1	1.36956747	0.36147652	0.31673555	-1.14021	0.25439129	0.31402605	gene	-0.06382272	0.42717759
Sapur.01G0141000.1	1.36956704	0.24829381	0.21781675	-1.13958	0.25462305	0.31180386	gene	-0.09389515	0.22023337
Sapur.01G0208300.2	1.29380333	0.27615965	0.23910738	1.13975	0.25462536	0.31201274	gene	0.08932313	0.36481038
Sapur.09G0231200.1	0.15890983	0.94027241	0.78348058	1.13906	0.25467595	0.31265701	gene	0.22367803	0.00604324
Sapur.01G0018300.1	1806.208837	0.11576028	0.10165354	1.13899	0.25471232	0.31207214	gene	0.08573810	0.28566832
Sapur.01G0187100.1	167.6604303	0.05168383	0.04367515	1.13871	0.25482529	0.31268154	gene	0.08895048	0.27152173
Sapur.01G0270800.3	28.18752656	0.17230185	0.11819612	1.13847	0.25492946	0.31231405	gene	0.08716381	0.31492922
Sapur.05G0207700.1	0.46088622	0.37144829	0.33784097	1.13849	0.25497931	0.31235796	gene	0.10316161	0.18782246
Sapur.02G0150700.1	62.06502577	-0.09402287	0.08472673	-1.1378	0.25520358	0.31265527	gene	-0.08834596	0.27121323
Sapur.01G0278800.1	167.6604303	0.05168383	0.04367515	1.13744	0.25534923	0.31270867	gene	0.10629115	0.18-05
Sapur.01G0364000.1	6.24760704	0.30428383	0.24918455	1.13742	0.25536171	0.31280853	gene	0.12121201	0.12477421
Sapur.01G0298300.1	0.16417244	0.73956373	0.60222746	1.13730	0.25537425	0.31280853	gene	0.19474049	0.02106026
Sapur.01G0227000.1	219.0842915	-0.19636028	0.17274741	-1.13674	0.25564108	0.31322223	gene	-0.10033376	0.21195939
Sapur.05G1361000.5	0.30472634	0.61408472	0.54052892	1.13628	0.25592836	0.31349882	gene	0.13148529	0.10697688
Sapur.15W0282800.3	0.49783273	0.46364554	0.40790496	1.13584	0.25606296	0.31362184	gene	0.06009135	0.45163631
Sapur.03G0279000.1	0.1974828	0.68803703	0.60643831	1.13543	0.25614567	0.31370169	gene	0.18007837	0.02602511
Sapur.01T0090300.1	110.8623115	0.06243284	0.05491257	1.13512	0.25657544	0.31402344	gene	0.08224196	0.30549051
Sapur.05G0103400.1	1.38378542	0.27153676	0.20065495	-1.1341	0.25674953	0.31403769	gene	-0.11099945	0.16363282
Sapur.01G0184300.1	2.79445754	0.19508623	0.17278845	1.13388	0.25683004	0.31447709	gene	0.10831136	0.18629729
Sapur.01G0227500.1	0.36960288	0.45471268	0.37535414	1.13367	0.25834363	0.31495258	gene	0.05778167	0.47225498
Sapur.01G0428300.1	11.05137213	0.07801193	0.07000161	1.13316	0.25851681	0.31534993	gene	0.04948831	0.53176543
Sapur.01G0269800.1	19.31623751	0.30303091	0.27149033	-1.1315	0.25757228	0.31529553	gene	-0.15235805	0.05124549
Sapur.01G0270200.1	3.59173261	0.66218739	0.59387599	-1.13196	0.25763096	0.31545837	gene	0.06943706	0.15748868
Sapur.05G1150000.1	109.7357958	-0.05003147	0.04420162	-1.1191	0.25767202	0.31549842	gene	-0.12076646	0.13215617
Sapur.01G0140900.1	0.14823937	0.75131792	0.66391587	1.13164	0.25779740	0.31568592	gene	0.09497301	0.05629409
Sapur.01G0178100.1	0.27448947	0.54189033	0.47896383	1.13143	0.25788321	0.31564457	gene	0.07570307	0.34168475
Sapur.05G1176200.1	9.49431945	0.11958476	0.10570199	1.1134	0.25792157	0.31565623	gene	0.3414554	1.13E-05
Sapur.05G2041300.1	98.97563977	0.05168383	0.04367515	1.11298	0.25796155	0.31712614	gene	-0.39003604	0.00017
Sapur.T0470600.1	838.0026639	0.02438758	0.02155857	1.1132	0.25797016	0.31712613	gene	0.06142588	0.44472365
Sapur.09G1169500.2	1.35282904	0.19521937	0.16954108	1.11316	0.25802939	0.31772627	gene	0.10923268	0.18882122
Sapur.09G0125800.1	4.1474185	0.28344862	0.25072751	-1.13089	0.25802475	0.31580123	gene	-0.10202073	0.21720015
Sapur.01T0298000.1	1.10160979	0.36449353	0.32241188	1.13085	0.25812705	0.31580703	gene	0.02828806	0.72683617
Sapur.01G0127700.3	0.26282627	0.60454734	0.53478236	1.13045	0.25830164	0.31607066	gene	0.09032809	0.3605851
Sapur.01G0257500.1	0.22760386	0.68135784	0.60292529	1.13021	0.25835794	0.31627659	gene	0.14120182	0.08976196
Sapur.01G0130000.1	11.05137213	0.07801193	0.07000161	1.13016	0.25837211	0.31629843	gene	0.05855666	0.35238266
Sapur.01G0190800.1	19.31623751	0.30303091	0.27149033	-1.1215	0.25757228	0.31529553	gene	-0.15235805	0.05124549
Sapur.01G0270200.1	3.59173261	0.66218739	0.59387599	-1.12326	0.25763096	0.31545837	gene	0.06943706	0.15748868
Sapur.05G1150000.1	109.7357958	-0.05003147	0.04420162	-1.1191	0.25767202	0.31

Sapur.006G025800.1	54.75373356	0.167136946	0.15035756	1.111597	0.266311652	0.325198139	grey	0.073490129	0.360345011	GO:0008152,GO:0003824	AT1G66120.1		AMP-dependent synthetase and ligase family protein	acyl-CoA synthetase
Sapur.012G103300.2	2.149216305	0.21921633	0.197243404	1.1114	0.266396189	0.325289358	grey	0.00043652	0.9956708		AT1G16560.1		Per1-like family protein	PERLD1, putative
Sapur.15WG017500.1	0.234894894	0.641159533	0.576912078	1.111364	0.266411539	0.325296092	grey	0.153673126	0.054660946					NA
Sapur.013G143500.1	6.548586187	-0.125805507	0.113262626	-1.11074	0.266679603	0.325611385	grey	-0.103037015	0.199088096		AT5G10860.1		Cystathionine beta-synthase (CBS) family protein	named after animal CBS
Sapur.15WG005800.1	21.92019637	0.089532625	0.080704199	1.109392	0.267260941	0.326309143	grey	0.095769553	0.232812812	GO:0005975	AT5G24400.1	EMB2024,PGL3	NagB/RpiA/CoA transferase-like superfamily protein	6-phosphogluconolactonase, putative
Sapur.15WG142900.1	0.212305789	0.59626841	0.537935874	1.108438	0.267672825	0.326799963	grey	0.133249113	0.096173995		AT5G51840.1			ACI13
Sapur.002G133800.1	8.70904325	-0.314488601	0.283758631	-1.1083	0.267733933	0.32685962	grey	-0.117036497	0.144354391					NA
Sapur.004G035600.1	72.11059395	-0.129135943	0.116519372	-1.10828	0.267741453	0.32685962	grey	-0.090183394	0.261329084	GO:0016020,GO:0004970	AT2G29120.1	ATGLR2.7,GLR2.7	glutamate receptor 2.7	glutamate-gated kainate-type ion channel receptor subunit GluR5
Sapur.001G056600.2	6.23913709	0.130531236	0.117809322	1.107987	0.26786729	0.327001171	grey	-0.098248139	0.220887239		AT5G47890.1		NADH-ubiquinone oxidoreductase B8 subunit, putative	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2
Sapur.002G197300.5	5.56165618	-0.140970566	0.127235932	-1.10795	0.267885057	0.327010791	grey	0.094635703	0.238416403		AT4G28760.2		Protein of unknown function (DUF3741)	DUF4378 domain protein
Sapur.014G116700.2	0.224910378	-0.634173749	0.572464082	-1.1078	0.26794968	0.327072867	grey	-0.220039296	0.005621581	GO:0008270,GO:0004553,GO:0015923,GO:0006013,GO:0005975,GO:0004559	AT5G13980.1		Glycosyl hydrolase family 38 protein	glycoside hydrolase family 38 protein
Sapur.15WG096300.1	0.33063208	-0.498453223	0.449955788	-1.10778	0.267955688	0.327072867	grey	-0.164450532	0.039577946					NA
Sapur.011G012000.2	0.478850953	-0.461501502	0.416715424	-1.10747	0.268089043	0.327223567	grey	-0.116721801	0.1454441		AT4G05530.1	IBR1,SDRA	indole-3-butyric acid response 1	short-chain dehydrogenase/reductase family protein
Sapur.016G018700.1	24.03669113	0.126814929	0.114574317	1.106836	0.268365028	0.32754834	grey	0.094699827	0.238097006	GO:0006355,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AT1G71692.1	AGL12,XAL1	AGAMOUS-like 12	MADS box transcription factor
Sapur.016G209700.1	946.4509984	-0.03479549	0.031444113	-1.10658	0.268474683	0.327670086	grey	-0.065464002	0.415312153	GO:0005515	AT3G27260.1	GTE8	global transcription factor group E8	global transcription factor group protein, putative
Sapur.007G109100.1	0.16283503	1.02900087	0.93013885	1.106287	0.268602153	0.327813565	grey	0.243772426	0.002093751	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT5G15180.1		Peroxidase superfamily protein	peroxidase
Sapur.T000900.1	32.9119529	-0.24454202	0.221077954	-1.10613	0.268668175	0.327882042	grey	-0.115625116	0.149290405	GO:0009052,GO:0004751	AT1G71100.1	RSW10	Ribose 5-phosphate isomerase, type A protein	NA
Sapur.013G061200.1	3.125479704	-0.199702516	0.180665564	-1.10537	0.268998767	0.328261271	grey	-0.065770962	0.413123738	GO:0006468,GO:0005524,GO:0004672	AT1G17910.1		Wall-associated kinase family protein	NA
Sapur.003G121700.1	5.033917083	0.137978301	0.124836633	1.105271	0.269042212	0.328302174	grey	0.078548531	0.32814497		AT2G33540.1	ATCPL3,CPL3	C-terminal domain phosphatase-like 3	RNA polymerase II carboxy-terminal domain phosphatase-like protein, putative
Sapur.007G099900.1	39.20598357	-0.10287509	0.093079721	-1.10524	0.269057197	0.328308346	grey	-0.09502459	0.236483964	GO:0006468,GO:0005524,GO:0004672	AT5G60900.1	RLK1	receptor-like protein kinase 1	tyrosine kinase domain protein
Sapur.012G042800.1	1.470036826	-0.240907557	0.217987686	-1.10514	0.269097649	0.32833348	grey	-0.093349415	0.244886705		AT1G21280.1			NA
Sapur.001G124900.1	201.7605994	-0.047380209	0.042881715	-1.1049	0.269200873	0.32844731	grey	-0.084354694	0.293539561	GO:0004518,GO:0003677	AT5G41150.1	ATRAD1,RAD1,UVH1	Restriction endonuclease, type II-like superfamily protein	DNA repair endonuclease UVH1
Sapur.005G114300.1	0.851263683	0.288519396	0.261145149	1.104824	0.269235911	0.328477942	grey	0.051833	0.519115614	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	AT5G44050.1		MATE efflux family protein	NA
Sapur.004G055800.2	0.284160904	0.513184189	0.464543454	1.104707	0.269286772	0.328527875	grey	0.123492545	0.123342011	GO:0003676	AT5G52545.1			RNA-binding domain protein
Sapur.T033400.1	30.48083396	0.318462262	0.288311285	1.104578	0.26934255	0.328583804	grey	0.161102802	0.043834753		AT4G17900.2		PLATZ transcription factor family protein	NA
Sapur.15WG122500.1	11.4004562	-0.195919683	0.177438704	-1.10415	0.269526271	0.328783679	grey	-0.081104747	0.312599106		AT5G45470.1		Protein of unknown function (DUF594)	NA
Sapur.002G074800.1	2784.621326	-0.040626949	0.036796651	-1.10409	0.269552514	0.328803565	grey	-0.127245088	0.11226419		AT4G08685.1	SAH7	Pollen Ole e 1 allergen and extensin family protein	pollen protein ole E I-like protein
Sapur.001G082700.1	3.33234385	0.236050474	0.21384962	1.103815	0.269673283	0.328938749	grey	0.074319481	0.354935201	GO:0005515	AT5G41380.1		CCT motif family protein	CCT motif protein
Sapur.005G187500.2	0.229704282	0.549413448	0.498205148	1.102786	0.270120296	0.32947185	grey	0.122433318	0.126617124	GO:0008270,GO:0003676	AT1G75560.2		zinc knuckle (CCHC-type) family protein	zinc knuckle protein
Sapur.009G076000.3	0.176340925	-0.817054232	0.741207413	-1.10233	0.27031878	0.329701786	grey	-0.215462119	0.00672699		AT2G01640.2			ribosome biogenesis protein SLX9
Sapur.007G091200.1	9.352536328	-0.132600905	0.120356074	-1.10174	0.27057543	0.329980296	grey	-0.055754546	0.487958431	GO:0001735	AT5G63910.1	FCLY	farnesylcysteine lyase	prenylcysteine lyase
Sapur.018G016500.1	114.5323005	0.102047229	0.092624146	1.101735	0.270577058	0.329980296	grey	0.103569147	0.196765498	GO:0043531	AT3G14460.1		LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.005G083500.1	36.06505358	-0.071172667	0.064608527	-1.1016	0.270636189	0.330028071	grey	-0.099408387	0.215456387	GO:0005515	AT2G17030.1		F-box family protein with a domain of unknown function (DUF295)	F-box protein
Sapur.010G021900.1	2.862285632	0.17646115	0.160300765	1.100813	0.270978098	0.330432829	grey	0.049133478	0.541139791					NA
Sapur.019G052400.1	0.190374302	0.575153101	0.522540679	1.100686	0.271033432	0.330488119	grey	0.158966298	0.046746624		AT4G23160.1	CRK8	cysteine-rich RLK (RECEPTOR-like protein kinase) 8	NA
Sapur.002G174400.1	15.71067705	-0.117486146	0.106750665	-1.10057	0.271085614	0.330539562	grey	-0.092705934	0.248168931	GO:0016020,GO:0006810,GO:0005215	AT3G21670.1		Major facilitator superfamily protein	nitrate transporter
Sapur.006G152700.1	9.567335723	-0.201203092	0.182851535	-1.10036	0.271173926	0.330635053	grey	-0.093209459	0.245598002		AT5G58030.1		Transport protein particle (TRAPP) component	transporter particle protein
Sapur.001G141000.1	175.5494524	0.047199523	0.042910297	1.099958	0.271350439	0.330838074	grey	0.266899452	0.000727431	GO:0008270,GO:0005634	AT5G47430.1		DWNN domain, a CCHC-type zinc finger	DWNN domain, A CCHC-type zinc finger protein, putative
Sapur.014G047200.1	0.164062589	-0.88275945	0.803012536	-1.09931	0.271633013	0.331158181	grey	-0.336542917	1.64E-05					NA
Sapur.002G009700.11	3.616172567	0.169873566	0.154575489	1.098968	0.271781883	0.331315248	grey	0.384803159	6.49E-07	GO:0043169,GO:0005975,GO:0003824	AT1G76130.1	AMY2,ATAMY2	alpha-amylase-like 2	alpha-amylase
Sapur.019G010000.1	0.203707566	0.634833593	0.577999567	1.098329	0.272060924	0.331630966	grey	0.167904768	0.035555457	GO:0008270,GO:0003676				NA
Sapur.017G036800.1	67.34638455	0.084601902	0.077083966	1.097529	0.272410131	0.33202858	grey	0.099211369	0.216371805	GO:0006468,GO:0005524,GO:0004672	AT1G66980.1	SNC4	suppressor of npr1-1 constitutive 4	NA
Sapur.T189500.1	38.42303424	0.073106442	0.066611007	1.097513	0.272417232	0.33202858	grey	0.103072517	0.198932525	GO:0006355,GO:0005739,GO:0003690	AT5G07900.1		Mitochondrial transcription termination factor family protein	NA
Sapur.001G029300.1	0.566078597	0.360307964	0.328413739	1.097116	0.272590691	0.332227753	grey	0.051921729	0.518399571	GO:0034968,GO:0018024,GO:0008270,GO:0005634,GO:0005515,GO:0042393	AT1G73100.1	SDG19,SUVH3	SU(VAR)3-9 homolog 3	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH3 protein
Sapur.006G176300.2	0.189227907	-0.926817024	0.845106283	-1.09669	0.272778267	0.332444115	grey	0.000110203	0.998907057	GO:0008270,GO:0003676	AT2G37340.1	ATRSZ33,RSZ33	arginine/serine-rich zinc knuckle-containing protein 33	RNA recognition motif, a.k.a. RRM%2C RBD protein
Sapur.013G060400.1	0.230130369	0.624800925	0.56992174	1.096292	0.272950794	0.332642122	grey	0.165077126	0.038821108		AT1G32030.1		Domain of unknown function (DUF313)	DUF313 domain protein
Sapur.010G127400.1	0.38085058	0.421296857	0.384363872	1.096089	0.273040004	0.332738582	grey	0.117206982	0.143766637	GO:0016779,GO:0009058	AT4G39210.1	APL3	Glucose-1-phosphate adenylyltransferase family protein	NA
Sapur.008G073100.4	3.533299101	0.22793207	0.207975485	1.095956	0.273097843	0.332796804	grey	0.151889409	0.057565323		AT1G69340.1		appr-1-p processing enzyme family protein	appr-1-P processing enzyme family protein
Sapur.018G025800.1	4997.843702	0.094995327	0.086711663	1.095531	0.273284013	0.333011401	grey	0.092451908	0.249473007		AT5G11420.1		Protein of unknown function, DUF642	plant/F18G18-200 protein
Sapur.019G085300.1	1.230922201	-0.259618026	0.237091803	-1.09501	0.273512015	0.333276954	grey	-0.140944599	0.078286067	GO:0046983	AT1G68810.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	HLH DNA-binding domain protein, putative
Sapur.004G039500.1	0.171415321	-0.706900234	0.646803291	-1.09291	0.274431654	0.334348272	grey	-0.303604321	0.000110909					NA
Sapur.T139500.1	3.328371587	0.229517935	0.210056814	1.092647	0.274548845	0.334478728	grey	0.13767954	0.085517424					hypothetical protein
Sapur.019G077600.1	73.23302751	-0.079814703	0.073061843	-1.09243	0.274645623	0.334584307	grey	-0.086151569	0.283340257	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G20230.1		Ribosomal L18p/L5e family protein	50S ribosomal protein L18
Sapur.002G175600.2	25.73786806	-0.078630096	0.071979579	-1.09239	0.274659743	0.334589183	grey	-0.105927914	0.186706622		AT4G20720.1		dentin sialophosphoprotein-related	hypothetical protein
Sapur.T103600.1	16.15930587	0.187074406	0.171405278	1.091416	0.275090021	0.335101004	grey	0.116851656	0.144993693		AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO:	exportin 1A	NA
Sapur.019G059800.1	1.573370909	-0.290758454	0.266445548	-1.09125	0.275163305	0.33517793	grey	-0.061821159	0.441796574		AT1G24706.2	AtTHO2,THO2	THO2	NA
Sapur.007G058300.1	5.367021892	0.182829261	0.167560155	1.091126	0.275217393	0.335219122	grey	0.058416149	0.467395021		AT1G31320.1	LBD4	LOB domain-containing protein 4	LOB domain protein
Sapur.016G167900.1	43.19865867	0.115346296	0.105718016	1.091075	0.275239833	0.335234109	grey	0.123784078	0.122452189					NA
Sapur.T114400.1	2.105081984	0.279940987	0.256593504	1.09099	0.275277215	0.335267293	grey	0.101479796	0.205998746	GO:0046872,GO:0000166,GO:0016887,GO:0016021,GO:0006812	AT5G23630.1	MIA,PDR2	phosphate deficiency response 2	NA
Sapur.008G038500.1	476.9581008	0.048831783	0.04476093	1.090947	0.275296397	0.335278309	grey	0.087453445	0.276100909	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT3G55320.1	PGP20	P-glycoprotein 20	multidrug/pheromone exporter, MDR family, ABC transporter family protein
Sapur.T085900.1	3.829022662	0.283452992	0.259836769	1.090889	0.275321865	0.335296979	grey	0.098942073	0.217627531	GO:0008270,GO:0003676				NA
Sapur.011G006500.2	1.677269481	-0.215046404	0.197189479	-1.09056	0.275467775	0.33543762	grey	0.146616604	0.066901492	GO:0006629,GO:0006508,GO:0004190	AT1G11910.1	APA1,ATAPA1	aspartic proteinase A1	aspartic protease
Sapur.15WG142700.3	0.41743032	-0.39254087	0.360042455	-1.09026	0.275597428	0.335583143	grey	-0.051293257	0.523482193	GO:0005975,GO:0016868	AT5G51820.1	ATPGMP,PGM,PGM1,STF1	phosphoglucomutase	phosphoglucomutase
Sapur.001G041400.1	1023.336453	-0.036921656	0.033892307	-1.08938	0.275985637	0.336043476	grey	-0.094886463	0.237169077		AT1G04780.1		Ankyrin repeat family protein	GPCR-chaperone protein
Sapur.013G121300.2	5.691226252	-0.126082232	0.115820597	-1.0886	0.276330581	0.336451099	grey	-0.076864812	0.338651321	GO:0055085,GO:0016020,GO:0006811,GO:0005216	AT4G03560.1	ATCCH1.ATTPC1.FOU2.TPC:	two-pore channel 1	two pore calcium channel protein
Sapur.001G053100.1	710.9333705	0.060785337	0.055852016	1.088328	0.276450139	0.336584278	grey	0.057879575	0.471501878		AT1G27440.1	ATGUT1,GUT2,IRX10	Exostosin family protein	secondary cell wall-related glycosyltransferase family 47 protein
Sapur.003G066300.1	96.38278196	-0.127930265	0.117606984	-1.08778	0.27669285	0.336854982	grey	-0.099834633	0.21348535	GO:0016020	AT1G32090.1		early-responsive to dehydration stress protein (ERD4)	early-responsive to dehydration stress protein
Sapur.011G037000.1	0.945336259	-0.3970037	0.365357699	-1.08662	0.277206335	0.337467694	grey	-0.137680762	0.08551462		AT4G32480.1		Protein of unknown function (DUF506)	plant/F8B4-180 protein, putative
Sapur.005G088100.1	274.8676723	-0.053628748	0.049358437	-1.08652	0.277250618	0.337506926	grey	-0.107276301	0.181128226	GO:0055085,GO:0016021,GO:0008324,GO:0006812	AT2G04620.1		Cation efflux family protein	NA
Sapur.008G091900.1	16.23896651	0.125230227	0.115261798	1.086485	0.277264425	0.337506926	grey	0.070428787	0.380754305	GO:0016787	AT1G68760.1	ATNUDT1.ATNUDX1.NUDX:	nudix hydrolase 1	nudix hydrolase
Sapur.002G143000.2	2.183619891	-0.22009771	0.202579754	-1.08647	0.277269175	0.337506926	grey	0.346817231	8.60E-06		AT2G46550.1			transmembrane protein, putative
Sapur.006G214800.1	3.620598153	0.181594223	0.167264153	1.085673	0.277623562	0.337906643	grey	0.115930741	0.148210869					NA
Sapur.010G118700.1	5.965116812	-0.135363853	0.124694342	-1.08557	0.277671353	0.337946727	grey	-0.09451991	0.238993922	GO:0005515,GO:0016787,GO:0005524,GO:0003677	AT5G14610.2		DEAD box RNA helicase family protein	NA
Sapur.002G101300.1	0.204762376	0.611870301	0.564194463	1.084502	0.278142062	0.33850716	grey	0.17457829	0.028757043	GO:0008270,GO:0005515	AT5G42940.1		RING/U-box superfamily protein	zinc finger protein
Sapur.001G069000.1	0.975516712	0.28451415	0.262419594	1.084196	0.278278115	0.338660278	grey	0.076738887	0.339445587		AT4G27745.1		Yippee family putative zinc-binding protein	Fad NAD-binding oxidoreductase, putative
Sapur.010G058500.1	22.39630636	-0.091855401	0.084732853	-1.08406	0.278338697	0.338709079	grey	-0.298881055	0.000143342		AT5G19320.1	RANGAP2	RAN GTPase activating protein 2	Ran GTPase activating protein
Sapur.013G119200.1	2.775959524	-0.467527142	0.431329528	-1.08392	0.278399819	0.338758306	grey	-0.113418842	0.157260435	GO:0010155,GO:0005886,GO:0005783	AT1G10880.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	NA
Sapur.004G103600.1	402.9634357	0.044368758	0.040934252	1.083903	0.278407809	0.338758306	grey	0.093017287	0.246577014		AT5G40340.1		Tudor/PWWP/MBT superfamily protein	PWWP domain protein
Sapur.007G084200.2	25.82261666	0.074660636	0.068881586	1.083898	0.278409877	0.338758306	grey	0.108646446	0.175586312		AT4G39860.1			HN1-like protein
Sapur.003G148200.3	0.69943531	0.312162792	0.288213232	1.083097	0.278765517	0.339156704	grey	0.064493389	0.422276433		AT3G12480.1	NF-YC11	nuclear factor Y, subunit C11	negative cofactor 2 transcriptional co-repressor, putative
Sapur.017G027900.1	1158.50325	0.083827775	0.077419686	1.082771	0.278910171	0.339317111	grey	0.065565986	0.414584326		AT2G46410.1	CPC	Homeodomain-like superfamily protein	MYB transcription factor
Sapur.011G071100.1	0.795764912	-0.2923963	0.270079093	-1.08263	0.278971746	0.339379539	grey	-0.130288608	0.103863253	GO:0006281,GO:0003678,GO:0000723	AT5G28780.1		PIF1 helicase	NA
Sapur.019G098800.1	2.831803582	-0.346393748	0.320139666	-1.08201	0.279248878	0.339704186	grey	-0.077892225	0.332215134		AT4G03500.1		Ankyrin repeat family protein	ankyrin-like protein
Sapur.013G115700.1	1579.926423	-0.051587677	0.047679742	-1.08196	0.279269337	0.339716579	grey	-0.116063964	0.147742146	GO:0055114,GO:0045300,GO:0006631	AT2G43710.1	FAB2,SSI2	Plant stearoyl-acyl-carrier-protein desaturase family protein	acyl-[acyl-carrier] desaturase
Sapur.010G000600.6	8.960488934	-0.107743668	0.099588139	-1.08189	0.279300262	0.339741701	grey	-0.119573741	0.135793801	GO:0008565,GO:0006606,GO:0005737,GO:0005634,GO:0005515	AT3G06720.1	AIMP ALPHA AT-IMP ATKAP	importin alpha isoform 1	importin subunit alpha
Sapur.007G105200.4	0.262005918	0.459805343	0.425071578	1.081713	0.279380188	0.339826079	grey	-0.031987142	0.690853755		AT3G22104.1		Phototropic-responsive NPH3 family protein	root phototropism protein, putative
Sapur.016G281400.1	0.144598094	0.828513142	0.765943047	1.08169	0.279390177	0.339826079	grey	0.218050535	0.006080214		AT5G54930.1		AT hook motif-containing protein	hypothetical protein
Sapur.014G100900.2	0.570910881	-0.354497218	0.327869694	-1.08121	0.279602048	0.340071273	grey	-0.007371827	0.926990549	GO:0005515,GO:0007165,GO:0000155	AT2G40940.1	ERS,ERS1	ethylene response sensor 1	ethylene receptor
Sapur.011G045700.1	29.10110118	-0.217032264	0.200959871	-1.07998	0.280151925	0.340715012	grey	-0.116701029	0.145516247	GO:0009052,GO:0004751				NA
Sapur.002G156500.1	105.5129427	0.074130905	0.068644695	1.079922	0.280176986	0.340732962	grey	0.103001643	0.199243186					NA
Sapur.010G193300.1	217.0216615	0.04751005	0.044002585	1.07971	0.280271146	0.340826226	grey	0.030791287	0.701852162	GO:0008138,GO:0006470				membrane-associated phospholipid phosphatase
Sapur.15WG007700.2	18.65260005	-0.087624342	0.081183439	-1.07934	0.280437237	0.341011845	grey	-0.079962929	0.319482818	GO:0008408,GO:0006139,GO:0003676	AT5G24340.1		3\'-5\' exonuclease domain-containing protein	3'-5' exonuclease
Sapur.007G043800.2	0.200479396	0.555529239	0.514861683	1.078987	0.28059337	0.341186923	grey	0.037409897	0.641815616	GO:0003676	AT2G42240.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif protein
Sapur.019G062600.3	0.126286455	0.943741525	0.874670276	1.078968	0.280601847	0.341186923	grey	0.309038745	8.21E-05		AT3G25030.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.001G137200.1	0.350227789	0.433702768	0.40222661	1.078255	0.280920068	0.341561295	grey	0.110640523	0.167745999	GO:0070072	AT1G05780.1		Vacuolar ATPase assembly integral membrane protein VMA21-like domain	vacuolar ATPase assembly integral membrane protein VMA21-like domain protein
Sapur.004G034600.3	1.744958361	-0.209239641	0.19413888	-1.07778	0.281130478	0.341804559	grey	-0.013897519	0.862846197		AT1G28540.1			transmembrane protein, putative
Sapur.001G110000.1	15.12712791	-0.250193097	0.232186601	-1.07755	0.281233809	0.341917622	grey	-0.093413698	0.24456048					NA
Sapur.002G018400.3	0.870094641	0.350605784	0.325579033	1.076868	0.281539047	0.342276142	grey	-0.077609513	0.333978316		AT1G19835.1		Plant protein of unknown function (DUF869)	myosin heavy chain, striated muscle protein%2C putative
Sapur.002G091600.1	1052.34558	-0.170177373	0.158035325	-1.07683	0.281555671	0.34228377	grey	-0.095064657	0.236285489	GO:0005975,GO:0004553,GO:0016798	AT1G58370.1	ATXYN1,RXF12	glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein	glycosyl hydrolase family 10 protein
Sapur.006G043200.1	1161.443049	0.042797301	0.039747697	1.076724	0.281603572	0.34232942	grey	0.074532608	0.353553224		AT5G19590.1		Protein of unknown function, DUF538	DUF538 family protein
Sapur.018G048200.12	0.369302018	-0.44791843	0.416131204	-1.07639	0.281753986	0.342499682	grey	0.040229095	0.616903544	GO:0006468,GO:0004672	AT5G56890.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.019G023200.1	28.77877703	-0.340019291	0.315953223	-1.07617	0.28185136	0.342605457	grey	-0.144966221	0.070065402		AT5G10350.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif protein, putative
Sapur.011G064300.1	38.01351314	0.093147771	0.08659754	1.07564	0.282088327	0.3428683	grey	0.076779949	0.339186462	GO:0008152,GO:0006741,GO:0003951	AT1G78590.1	ATNADK-3,NADK3	NAD(H) kinase 3	NADH kinase, putative
Sapur.004G094300.1	0.210145755	0.553911446	0.515057241	1.075437	0.28217927	0.342966234	grey	0.156395111	0.050462889					NA
Sapur.T012600.1	4.754774743	-0.133762148	0.124459535	-1.07474	0.282489328	0.343330468	grey	-0.104845449	0.191275035	GO:0006265,GO:0005694,GO:0003917,GO:0003677,GO:0003918	AT5G55300.1	MGO1,TOP1,TOP1ALPHA	DNA topoisomerase I alpha	DNA topoisomerase I
Sapur.001G061600.1	1.236830788	-0.361891735	0.336741031	-1.07469	0.282514186	0.343348063	grey	-0.134640238	0.09272017					hypothetical protein
Sapur.017G043800.1	12.60446145	0.097843973	0.09108905	1.074157	0.282752161	0.343624655	grey	0.071694135	0.372234697					NA
Sapur.005G152100.2	0.711237018	0.301174943	0.280439905	1.073938	0.282850674	0.343731746	grey	0.109643251	0.171633892	GO:0043565,GO:0006355,GO:0003700	AT5G44080.1		Basic-leucine zipper (bZIP) transcription factor family protein	transcription factor, putative
Sapur.018G038200.1	56.32023243	-0.104982011	0.097798761	-1.07345	0.283069579	0.343972729	grey	-0.09021558	0.261158214					hypothetical protein
Sapur.019G106000.2	12.3105197	0.15063999	0.140332714	1.073449	0.283069775	0.343972729	grey	0.087498187	0.275854349	GO:0005515	AT4G03260.2		Outer arm dynein light chain 1 protein	protein phosphatase 1 regulatory subunit, putative
Sapur.010G196700.4	0.194781851	0.662191072	0.617038523	1.073176	0.283192056	0.344108677	grey	0.078548531	0.32814497	GO:0051082,GO:0031072	AT5G22060.1	ATJ2,J2	DNAJ homologue 2	chaperone protein DnaJ
Sapur.006G001600.1	8.229768313	0.2341176	0.218194738	1.072975	0.283282127	0.344205476	grey	0.062742912	0.435006216					transmembrane protein, putative
Sapur.013G130600.1	143.6957372	-0.669107279	0.624142567	-1.07204	0.283701001	0.344689108	grey	-0.216916105	0.006356519		AT3G50150.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.008G065900.1	44.79577601	0.089065375	0.083107678	1.071686	0.283860873	0.344845345	grey	0.087146568	0.277796001		AT1G79510.2		Uncharacterized conserved protein (DUF2358)	plant/F3O9-12 protein
Sapur.004G030300.2	0.196478073	-0.595198484	0.555620221	-1.07123	0.284064864	0.345080487	grey	-0.258025231	0.0011038	GO:0006412,GO:0005840,GO:0003735,GO:0003723	AT2G33800.1		Ribosomal protein S5 family protein	30S ribosomal protein S5
Sapur.017G051000.8	0.2975275	0.509671819	0.476077973	1.070564	0.284365632	0.345420482	grey	-0.090810408	0.258014169	GO:0008152,GO:0003824	AT3G23790.1	AAE16	AMP-dependent synthetase and ligase family protein	long-chain-fatty-acid-CoA ligase
Sapur.006G150300.5	9.399053623	-0.116920389	0.109233032	-1.07038	0.284450208	0.345510529	grey	0.089088078	0.267189532	GO:0016746,GO:0008152	AT4G30580.1	ATS2,EMB1995,LPAT1	Phospholipid/glycerol acyltransferase family protein	1-acyl-sn-glycerol-3-phosphate acyltransferase
Sapur.008G048100.1	390.1458322	-0.050040561	0.046755739	-1.07025	0.284504566	0.345563863	grey	-0.07096873	0.377104449	GO:0009058,GO:0005524,GO:0009396,GO:0004326	AT5G05980.2	ATDFB,DFB	DHFS-FPGS homolog B	folylpolyglutamate synthase
Sapur.012G044200.1	3.233579613	-0.25765091	0.2407656	-1.07013	0.284560014	0.345618519	grey	-0.076309105	0.342165327	GO:0030170,GO:0009058	AT2G22250.2	AAT,ATAAT,MEE17	aspartate aminotransferase	NA
Sapur.T018000.1	0.271242235	0.419565224	0.392164826	1.06987	0.284678011	0.345742154	grey	0.05807411	0.470010659		AT4G23330.2			NA
Sapur.011G040700.1	46.04126078	0.095190503	0.088974799	1.069859	0.284682714	0.345742154	grey	0.087403266	0.276377601	GO:0006355,GO:0003677	AT4G28500.1	ANAC073,NAC073,SND2	NAC domain containing protein 73	NAC transcription factor 096
Sapur.018G021300.1	0.748428442	0.407898076	0.381553708	1.069045	0.285049402	0.346174779	grey	0.072219593	0.368731442		AT2G28690.1		Protein of unknown function (DUF1635)	UPA23, putative
Sapur.008G123000.1	41.16219399	-0.088592771	0.082899597	-1.06868	0.285215901	0.346364264	grey	-0.094576653	0.238710794		AT2G32120.1	HSP70T-2	heat-shock protein 70T-2	heat shock 70 kDa protein
Sapur.005G094800.1	521.6135608	0.103862467	0.097193444	1.068616	0.285242744	0.346384142	grey	0.10292965	0.199559109		AT3G51050.1		FG-GAP repeat-containing protein	NA
Sapur.004G114900.1	45.11404973	0.139933144	0.131000576	1.068187	0.285436057	0.346596304	grey	0.071133109	0.375997557		AT1G49310.1			DUF2775 family protein
Sapur.006G109800.1	148.3402003	0.109732634	0.102728404	1.068182	0.285438415	0.346596304	grey	0.100767896	0.209214857		AT2G37240.1		Thioredoxin superfamily protein	NA
Sapur.006G086800.1	195.473426	-0.048305622	0.045260475	-1.06728	0.285845198	0.347077502	grey	-0.061559657	0.443733894	GO:0008716,GO:0005737	AT3G08840.2		D-alanine--D-alanine ligase family	D-alanine-D-alanine ligase
Sapur.014G073400.1	12.5456806	-0.140696121	0.131861718	-1.067	0.285972973	0.347219901	grey	-0.060865803	0.448897469					NA
Sapur.006G151300.3	1.569813134	0.223459167	0.20952728	1.066492	0.286201294	0.347484365	grey	0.060258005	0.453448241	GO:0045905,GO:0045901,GO:0043022,GO:0006452,GO:0003746,GO:0003723	AT1G13950.1	ATELF5A-1,EIF-5A,EIF5A,ELF	eukaryotic elongation factor 5A-1	eukaryotic translation initiation factor 5A
Sapur.013G083800.1	0.540232018	-0.387437964	0.363317385	-1.06639	0.286247457	0.347527656	grey	-0.152927952	0.055859225					NA
Sapur.008G075200.2	0.220668503	0.576660154	0.541005933	1.065904	0.286467236	0.347768954	grey	0.102464111	0.201610763		AT2G03510.1		SPFH/Band 7/PHB domain-containing membrane-associated protein family	SPFH domain/band 7 family protein
Sapur.005G104800.2	15.46997485	0.090340802	0.084794498	1.065421	0.286685306	0.348020915	grey	0.066551221	0.407591567		AT3G50430.1			lines amino-terminus protein
Sapur.014G065600.4	3.365509739	0.173972696	0.163332976	1.065141	0.286811998	0.348161932	grey	-0.036942443	0.64598618	GO:0006468,GO:0005524,GO:0004672	AT2G45910.1		U-box domain-containing protein kinase family protein	tyrosine kinase family protein
Sapur.017G060200.1	31.01839183	0.352081885	0.330711521	1.064619	0.287048219	0.348435894	grey	0.131813632	0.099844029		AT5G40020.1		Pathogenesis-related thaumatin superfamily protein	thaumatin-like protein
Sapur.002G038100.1	5.072365686	0.189054808	0.177603682	1.064476	0.287113248	0.348502039	grey	0.090861229	0.257746759		AT3G04810.1	ATNEK2,NEK2	NIMA-related kinase 2	Serine/Threonine kinase domain protein
Sapur.017G128000.1	5.955667514	-0.198501649	0.186493847	-1.06439	0.287153364	0.348537941	grey	-0.071274078	0.375049885					NA
Sapur.15WG151900.3	6.434705404	0.113007441	0.106193613	1.064164	0.287254325	0.34864769	grey	0.103821464	0.195671102	GO:0006468,GO:0005524,GO:0004672	AT1G63700.1	EMB71,MAPKKK4,YDA	Protein kinase superfamily protein	MAP kinase kinase kinase
Sapur.004G108200.1	4.941637979	-0.143678236	0.135020076	-1.06412	0.287272083	0.348656448	grey	-0.116631343	0.145758482	GO:0005515	AT3G19080.1		SWIB complex BAF60b domain-containing protein	upstream activation factor protein, putative
Sapur.009G000200.1	610.2785897	0.049546375	0.046601282	1.063198	0.28769232	0.349140857	grey	0.125687059	0.116765406					NA
Sapur.011G097700.2	0.174360664	0.565704635	0.532378367	1.062599	0.287963914	0.349457639	grey	0.011198262	0.889294541		AT5G54660.1		HSP20-like chaperones superfamily protein	small heat-shock protein, putative
Sapur.T162500.1	0.360173564	-0.405793914	0.381909293	-1.06254	0.287990593	0.349466888	grey	-0.171049567	0.032199161		AT1G43760.1		DNAse I-like superfamily protein	NA
Sapur.005G077300.2	0.664886592	0.372118685	0.350217662	1.062535	0.287992668	0.349466888	grey	0.027738879	0.730202561	GO:0055114,GO:0016491	AT3G12900.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	leucoanthocyanidin dioxygenase, putative
Sapur.011G093900.1	20.79088715	0.305218722	0.287330096	1.062258	0.288118531	0.349597633	grey	0.125688759	0.116760418	GO:0048544	AT4G27290.1		S-locus lectin protein kinase family protein	NA
Sapur.002G039300.1	3.542122629	0.158000728	0.148741364	1.062251	0.288121554	0.349597633	grey	0.058011711	0.470488701	GO:0005515	AT3G63220.1		Galactose oxidase/kelch repeat superfamily protein	F-box/kelch-repeat protein SKIP30
Sapur.009G032800.1	0.196470172	-0.643174128	0.60603875	-1.06128	0.288564679	0.350122462	grey	-0.238568414	0.002621643		AT5G11050.1	AtMYB64,MYB64	myb domain protein 64	NA
Sapur.T001700.1	2.547649312	0.182555688	0.172133531	1.060547	0.28889585	0.350511421	grey	0.101724724	0.204900513					hypothetical protein
Sapur.005G172500.3	1.542206802	0.220647638	0.208112803	1.060231	0.289039537	0.350660026	grey	-0.110512132	0.16824283	GO:0008080	AT3G54610.1	BGT.GCN5.HAC3.HAG01.HA	histone acetyltransferase of the GNAT family 1	NA
Sapur.001G056300.1	10.70445528	-0.238906028	0.225396542	-1.05994	0.289173475	0.350809651	grey	-0.080299215	0.317445313		AT3G50170.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.019G112300.2	11.86036261	-0.122771007	0.115919616	-1.0591	0.289552113	0.351243228	grey	-0.071198342	0.375558841	GO:0008270,GO:0003677	AT4G32010.1	HSI2-L1,HSL1,VAL2	HSI2-like 1	B3 domain transcription repressor
Sapur.008G016300.2	37.79967256	-0.096463723	0.091106495	-1.0588	0.289690042	0.351397655	grey	-0.091073981	0.256629364	GO:0035267,GO:0032777,GO:0006357	AT5G04670.1		Enhancer of polycomb-like transcription factor protein	enhancer of polycomb-like protein
Sapur.001G099800.2	6.523241467	0.129464637	0.122333792	1.05829	0.289923219	0.351667604	grey	0.076050296	0.343809762		AT1G62530.1		Plant protein of unknown function (DUF863)	hypothetical protein
Sapur.005G199300.1	0.191344074	-0.642508119	0.607409291	-1.05778	0.290153712	0.351908466	grey	-0.225152797	0.004581011		AT2G17080.1		Arabidopsis protein of unknown function (DUF241)	NA
Sapur.012G049300.3	12.64895257	0.136689403	0.129227605	1.057742	0.290173303	0.351909192	grey	0.069829203	0.384832391		AT5G07980.1		dentin sialophosphoprotein-related	hypothetical protein
Sapur.008G166900.1	14.50838954	-0.132646327	0.125405834	-1.05774	0.29017559	0.351909192	grey	-0.045562227	0.570968727		AT2G39080.1		NAD(P)-binding Rossmann-fold superfamily protein	hypothetical protein
Sapur.018G068500.13	0.660487016	-0.385400874	0.364390336	-1.05766	0.290210738	0.351938912	grey	0.078548531	0.32814497		AT4G26965.1		NADH:ubiquinone oxidoreductase, 17.2kDa subunit	NA
Sapur.T163000.1	1.261010264	0.233223476	0.220650331	1.056982	0.290519704	0.352287762	grey	0.157745023	0.048482333		AT3G28455.1	CLE25	CLAVATA3/ESR-RELATED 25	NA
Sapur.005G066200.1	17.19795586	-0.136509968	0.129170895	-1.05682	0.29059522	0.352366413	grey	-0.078715924	0.327112013					NA
Sapur.001G003700.1	1081.133358	0.050163115	0.047478452	1.056545	0.290719357	0.352504015	grey	0.0880993	0.272556265	GO:0005515	AT5G19820.1	emb2734	ARM repeat superfamily protein	importin beta-3, putative
Sapur.007G102500.4	7.711926837	0.138725329	0.131352281	1.056132	0.290907977	0.35270686	grey	0.107255067	0.18121511	GO:0008270,GO:0004089	AT4G33580.1	ATBCA5,BCA5	beta carbonic anhydrase 5	carbonic anhydrase
Sapur.002G027600.4	0.40431675	0.410418272	0.388821138	1.055545	0.291176065	0.353018958	grey	-0.019391499	0.809511859		AT5G28850.2		Calcium-binding EF-hand family protein	serine/threonine-protein phosphatase 2A regulatory subunit B protein
Sapur.012G084300.1	15.3884061	0.097236367	0.092131553	1.055413	0.291236486	0.353079269	grey	0.106771747	0.183201087	GO:0006508,GO:0004197	AT1G02170.1	AMC1.ATMC1.ATMCPB1.LO	metacaspase 1	metacaspase-1 protein
Sapur.002G164100.1	4.576578502	0.134547947	0.127499485	1.055282	0.291296244	0.353138772	grey	0.048147966	0.549293743	GO:0005524,GO:0003676	AT2G47330.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.006G206700.2	2.180611128	0.205548286	0.194812082	1.055111	0.29137476	0.353221009	grey	0.087760352	0.27441265	GO:0008152,GO:0003824,GO:0016114,GO:0008661	AT5G11380.1	DXPS3	1-deoxy-D-xylulose 5-phosphate synthase 3	1-deoxy-D-xylulose-5-phosphate synthase
Sapur.005G087100.1	24.50835344	-0.170639706	0.161859597	-1.05451	0.2916514	0.35354341	grey	-0.09099572	0.257040009	GO:0016020,GO:0006810,GO:0005215	AT2G16850.1	PIP2;8,PIP3B	plasma membrane intrinsic protein 2;8	plasma membrane intrinsic protein PIP2
Sapur.010G099700.1	28.47899597	-0.26033653	0.246930669	-1.05429	0.291750174	0.353637516	grey	-0.05910064	0.462184651	GO:0006355,GO:0003700,GO:0003677	AT1G25560.1	EDF1,TEM1	AP2/B3 transcription factor family protein	AP2/ERF and B3 domain transcription factor
Sapur.002G118300.2	0.255894846	-0.548963093	0.520694854	-1.05429	0.291750416	0.353637516	grey	-0.159894457	0.045462403	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	Plant-specific transcription factor YABBY family protein	YABBY transcription factor
Sapur.005G159400.1	12.10543332	-0.139361079	0.132309205	-1.0533	0.292204234	0.354174619	grey	-0.095228941	0.235472917		AT1G06320.1			NA
Sapur.013G136800.2	0.495018443	-0.404013675	0.383609861	-1.05319	0.292254392	0.354222433	grey	-0.266869785	0.000728463		AT5G58450.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR repeat protein R13F6.10, putative
Sapur.004G135100.2	0.166828384	0.728133475	0.691376064	1.053166	0.29226511	0.354222443	grey	0.174376303	0.028945241	GO:0006468,GO:0004672	AT4G38470.1		ACT-like protein tyrosine kinase family protein	tyrosine kinase domain protein
Sapur.010G094100.2	0.284829272	0.491124128	0.466354139	1.053114	0.292288693	0.354238044	grey	0.104085167	0.194532051		AT1G68260.1		Thioesterase superfamily protein	thioesterase, putative
Sapur.005G056500.1	349.4454736	0.0380568	0.036142851	1.052955	0.29236156	0.354313372	grey	0.053830828	0.503116587		AT5G65250.1			transmembrane protein, putative
Sapur.009G038800.2	2.111699497	-0.178530004	0.169640978	-1.0524	0.292616505	0.354596735	grey	-0.161227162	0.043670039	GO:0005515	AT1G51450.1	TRO	TRAUCO	SPRY domain protein
Sapur.010G205400.1	1.677198938	0.223940281	0.212790411	1.052398	0.292616819	0.354596735	grey	0.109091884	0.173811881					NA
Sapur.019G107300.1	0.214839998	-0.617289072	0.586742555	-1.05206	0.292771476	0.354771151	grey	-0.186762577	0.019176912	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G08850.1		Leucine-rich repeat receptor-like protein kinase family protein	receptor kinase, putative
Sapur.004G017500.1	51.74229927	0.138891621	0.132096906	1.051437	0.293057769	0.355105062	grey	0.069589745	0.386468431	GO:0016491	AT4G27270.1		Quinone reductase family protein	quinone oxidoreductase
Sapur.008G078800.2	0.231305747	0.675967579	0.643076961	1.051146	0.293191681	0.35525431	grey	0.194282489	0.014761498	GO:0055114,GO:0051920,GO:0016491,GO:0016209	AT1G48130.1	ATPER1,PER1	1-cysteine peroxiredoxin 1	1-cys peroxiredoxin
Sapur.008G087200.2	0.257467988	0.480007871	0.456711246	1.05101	0.293254214	0.355317064	grey	0.140581784	0.079064429		AT1G69060.1		Chaperone DnaJ-domain superfamily protein	heat shock protein-binding protein, putative
Sapur.002G098000.1	0.359591979	-0.471604216	0.448762369	-1.0509	0.293304682	0.355365193	grey	-0.171985922	0.031253339		AT5G43120.1		ARM-repeat/Tetratricopeptide repeat (TPR)-like protein	heat shock protein 70 (HSP70)-interacting protein, putative
Sapur.001G002900.4	0.267434375	0.459533694	0.437383568	1.050642	0.293422889	0.355482367	grey	0.078548531	0.32814497		AT1G55340.1		Protein of unknown function (DUF1639)	DUF1639 family protein
Sapur.016G056900.3	0.587983768	0.366677874	0.349121784	1.050286	0.29358644	0.355667482	grey	0.085983645	0.284283217	GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT5G06670.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	kinesin motor domain protein
Sapur.016G218400.3	7.648786855	0.103426973	0.098478248	1.050252	0.293602283	0.355673647	grey	-0.075395026	0.347995535	GO:0006468,GO:0005524,GO:0004672	AT5G40440.1	ATMKK3,MKK3	mitogen-activated protein kinase kinase 3	dual specificity MAP kinase kinase
Sapur.006G191100.1	2.591938452	-0.166208416	0.158353097	-1.04961	0.293899137	0.356020219	grey	-0.133268191	0.096125949					NA
Sapur.006G226100.1	1.658760249	0.193129656	0.184071981	1.049207	0.294082745	0.356216543	grey	0.09065661	0.258824586					NA
Sapur.003G021000.4	3.570426228	-0.133888304	0.127683464	-1.0486	0.294364337	0.356532098	grey	-0.116375666	0.146649865	GO:0006468,GO:0005524,GO:0004672	AT4G26100.1	CK1,CKL1	casein kinase 1	casein kinase I-like protein
Sapur.014G144300.1	0.294749655	-0.62235412	0.593732863	-1.04821	0.294543884	0.356735917	grey	-0.442031207	6.80E-09	GO:0003723,GO:0032259,GO:0008168	AT3G25470.1		bacterial hemolysin-related	TlyA family rRNA methyltransferase/hemolysin protein, putative
Sapur.003G072700.3	0.225483908	0.488965258	0.466711209	1.047683	0.294784822	0.357014654	grey	0.125640534	0.116901945		AT5G61500.1	ATATG3,ATG3	autophagy 3 (APG3)	autophagy-related protein
Sapur.019G023300.1	6.065267393	-0.148264886	0.141541902	-1.0475	0.294869865	0.357104574	grey	-0.027780767	0.729810928					NA
Sapur.003G010800.1	0.31874253	-0.44831898	0.428085813	-1.04726	0.294977707	0.357222096	grey	-0.229335012	0.003862158		AT1G10780.1		F-box/RNI-like superfamily protein	cyclin-like F-box protein
Sapur.016G198000.1	1.74105063	0.32921182	0.314527078	1.046688	0.29524335	0.357530703	grey	0.076864924	0.338650615		AT5G13200.1		GRAM domain family protein	PH-GRAM-GEM domain protein
Sapur.016G149700.1	4.130852456	-0.138164879	0.132081797	-1.04606	0.295535449	0.357871323	grey	-0.143286245	0.073409863		AT1G16820.1		vacuolar ATP synthase catalytic subunit-related / V-ATPase-related / vacuolar proton pump-related	NA
Sapur.017G008200.1	0.966484417	0.34757092	0.332394077	1.045659	0.295718413	0.358079768	grey	0.09056279	0.259319819					NA
Sapur.008G015600.1	8.959441706	0.349758336	0.335161678	1.043551	0.296693128	0.35924688	grey	0.147069048	0.066054766	GO:0046872,GO:0030001	AT1G66240.1	ATATX1,ATX1	homolog of anti-oxidant 1	copper chaperone
Sapur.011G103600.3	25.42073926	0.081795862	0.078397045	1.043354	0.296784417	0.35934426	grey	0.101382934	0.206434233	GO:0055114,GO:0016671,GO:0005783,GO:0003756	AT1G72280.1	AERO1,ERO1	endoplasmic reticulum oxidoreductins 1	endoplasmic oxidoreductin protein
Sapur.15WG053100.1	0.630102619	0.30851008	0.295882363	1.042678	0.297097374	0.35969685	grey	0.077904164	0.332140807	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT3G47570.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.010G165000.1	0.298008361	0.483368006	0.463651001	1.042526	0.297168095	0.359769303	grey	0.105542569	0.188323684		AT5G13660.1			DNA-binding protein, putative
Sapur.013G019200.2	0.257490489	0.438296167	0.420447043	1.042453	0.297201831	0.359796975	grey	0.092717377	0.248110299		AT3G50700.1	AtIDD2,IDD2	indeterminate(ID)-domain 2	zinc finger protein
Sapur.010G053100.1	124.813154	-0.095659227	0.091767168	-1.04241	0.297220556	0.359806474	grey	-0.09474019	0.237896111		AT1G67590.1		Remorin family protein	remorin, carboxy-terminal region protein
Sapur.008G073900.1	5.939636386	-0.123806274	0.118904502	-1.04122	0.297771393	0.360433723	grey	0.284202744	0.000309437		AT1G26520.1		Cobalamin biosynthesis CobW-like protein	CobW/P47K family protein
Sapur.006G167600.10	1.092948064	-0.258602465	0.248467493	-1.04079	0.297973055	0.360655627	grey	-0.044627333	0.578903525		AT3G28430.1			hypothetical protein
Sapur.T035800.1	7.717113038	-0.121206549	0.116457142	-1.04078	0.297976527	0.360655627	grey	-0.066413712	0.408563345					NA
Sapur.012G088700.2	22.62231655	-0.092744269	0.089137213	-1.04047	0.298123295	0.360820063	grey	-0.103279079	0.19802911	GO:0005515	AT5G45110.1	ATNPR3,NPR3	NPR1-like protein 3	regulatory protein NPR1
Sapur.004G177000.1	40.66227057	-0.08199363	0.078838219	-1.04002	0.298328808	0.361055583	grey	-0.085020997	0.289729445		AT3G54220.1	SCR,SGR1	GRAS family transcription factor	GRAS family transcription factor
Sapur.009G082200.1	7.253496355	0.173673205	0.167001727	1.039949	0.298363801	0.361084721	grey	0.056582249	0.481512337	GO:0016787,GO:0008152	AT1G19190.1		alpha/beta-Hydrolases superfamily protein	alpha/beta hydrolase fold protein
Sapur.004G063800.1	2043.191522	0.038509456	0.037040402	1.039661	0.298497494	0.361233302	grey	0.072315527	0.368094043		AT2G01570.1	RGA,RGA1	GRAS family transcription factor family protein	DELLA domain GRAS family transcription factor GAI/RGA1
Sapur.016G229000.1	1.362891286	0.248772919	0.23932051	1.039497	0.298573718	0.361312325	grey	0.106913504	0.182616954		AT2G34680.1	AIR9	Outer arm dynein light chain 1 protein	protein phosphatase 1 regulatory subunit
Sapur.006G142500.1	726.3237143	0.063718147	0.061329098	1.038955	0.298825864	0.361604223	grey	0.065123962	0.417744307	GO:0016021	AT2G23810.1	TET8	tetraspanin8	tetraspanin protein
Sapur.T115900.1	3.789509993	-0.218313214	0.210215685	-1.03852	0.299027984	0.361835566	grey	-0.086411988	0.28188205					NA
Sapur.016G249200.1	2.345241588	-0.227075199	0.218698265	-1.0383	0.299128727	0.361944228	grey	-0.046389914	0.563986911	GO:0055114,GO:0004097,GO:0016491,GO:0008152				polyphenol oxidase
Sapur.002G188600.1	1.560817203	-0.216938461	0.209006471	-1.03795	0.299292901	0.362129629	grey	-0.190384905	0.01692466		AT5G48730.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.004G097600.1	274.7294691	-0.048420799	0.046654261	-1.03786	0.299333169	0.362165102	grey	-0.112711298	0.159882855		AT1G67050.1			hypothetical protein
Sapur.006G223000.1	370.3826137	0.063276676	0.061035	1.036728	0.299862776	0.362766066	grey	0.094726508	0.237964194					NA
Sapur.002G087800.2	4.768256824	-0.162036074	0.156341403	-1.03642	0.300004104	0.362923764	grey	-0.031040119	0.699558437	GO:0007165	AT4G24400.2	ATCIPK8.CIPK8.PKS11.SnRK:	CBL-interacting protein kinase 8	CBL-interacting Serine/Threonine-kinase
Sapur.019G052000.2	0.778754989	-0.414164432	0.399672498	-1.03626	0.300081084	0.363003612	grey	-0.102724225	0.200462558		AT3G14750.1			structural maintenance of chromosomes domain protein, putative
Sapur.010G060500.1	0.227879343	0.594248922	0.573495139	1.036188	0.300114329	0.363030329	grey	0.147907064	0.064509569		AT5G43150.1			hypothetical protein
Sapur.15ZG046000.1	31.99702263	0.19409786	0.187323293	1.036165	0.300125122	0.363030329	grey	0.096616011	0.228690302		AT1G67140.3	SWEETIE	HEAT repeat-containing protein	NA
Sapur.013G024400.1	63.85939077	-0.079851565	0.077074573	-1.03603	0.300188174	0.363093317	grey	-0.068966056	0.390749333		AT5G64330.1	JK218,NPH3,RPT3	Phototropic-responsive NPH3 family protein	NA
Sapur.T107400.1	0.783210296	0.310813329	0.300124362	1.035615	0.300381731	0.363300862	grey	0.086396872	0.281966551					NA
Sapur.019G004200.1	0.146818612	0.63271702	0.61115189	1.035286	0.300535348	0.363471177	grey	0.17551329	0.027899411	GO:0007165,GO:0005515	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.014G090100.1	19.16427442	-0.121743605	0.117596406	-1.03527	0.300544529	0.363471177	grey	-0.095513911	0.234068063	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT1G02520.1	PGP11	P-glycoprotein 11	NA
Sapur.005G184600.1	621.8046385	-0.052870622	0.051072431	-1.03521	0.30057148	0.363477189	grey	-0.115263604	0.150575004	GO:0016773,GO:0016020,GO:0005524	AT1G10210.1	ATMPK1,MPK1	mitogen-activated protein kinase 1	MAP kinase
Sapur.15ZG031100.1	9.425014328	-0.255112182	0.246470986	-1.03506	0.300641036	0.36354801	grey	-0.098825189	0.218174173		AT3G17950.1			NA
Sapur.004G088900.1	0.216012898	-0.629302334	0.608030232	-1.03499	0.30067579	0.363576743	grey	-0.205521438	0.009816586	GO:0043565,GO:0006355,GO:0003700	AT4G24240.1	ATWRKY7,WRKY7	WRKY DNA-binding protein 7	NA
Sapur.016G264800.1	54.1637556	-0.086908076	0.083987703	-1.03477	0.300775663	0.363684213	grey	-0.058753279	0.464824757	GO:0003677,GO:0043531	AT4G10780.1		LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.010G053300.1	0.161801174	-0.743580104	0.718798851	-1.03448	0.300913727	0.363837853	grey	-0.505377141	1.47E-11	GO:0005524,GO:0003676	AT1G27880.1		DEAD/DEAH box RNA helicase family protein	ATP-dependent DNA helicase RecQ
Sapur.005G070300.2	0.613313122	-0.345581659	0.334170209	-1.03415	0.301066691	0.363996189	grey	-0.118583905	0.139086089	GO:0005515,GO:0016459,GO:0005524,GO:0003774	AT3G19960.1	ATM1	myosin 1	NA
Sapur.006G225800.1	0.165545681	0.788441663	0.76242549	1.034123	0.301078709	0.363997413	grey	0.216289236	0.006513953					NA
Sapur.016G040600.1	2.754681257	0.171664521	0.166085408	1.033592	0.30132702	0.364270984	grey	-0.25511336	0.001261736					hypothetical protein
Sapur.013G077200.1	0.414831178	0.375548246	0.363356844	1.033552	0.30134558	0.364280107	grey	0.047272006	0.556591298					NA
Sapur.013G098600.1	7.046443622	0.180094917	0.174409602	1.032597	0.301792304	0.364806792	grey	0.061752747	0.442302937		AT1G75280.1		NmrA-like negative transcriptional regulator family protein	NA
Sapur.017G091700.1	0.195349752	0.571701003	0.553707914	1.032496	0.301839992	0.364851104	grey	0.158862268	0.046892428					hypothetical protein
Sapur.011G062300.1	488.0032711	-0.069410211	0.067247618	-1.03216	0.301997795	0.365028508	grey	-0.085474731	0.287153814	GO:0008270,GO:0005622	AT1G78600.1	DBB3,LZF1,STH3	light-regulated zinc finger protein 1	B-box zinc finger protein
Sapur.007G079200.1	74.87940369	-0.125831716	0.121948545	-1.03184	0.302145812	0.365194072	grey	-0.092107397	0.251249161		AT5G65207.1			hypothetical protein
Sapur.003G154800.1	4.389191561	-0.148434657	0.143893139	-1.03156	0.302277473	0.365339855	grey	-0.082864256	0.302182343		AT1G76390.1		ARM repeat superfamily protein	U-box protein
Sapur.007G098400.1	3.787645858	-0.370770843	0.359508269	-1.03133	0.302387164	0.365459076	grey	-0.101705304	0.204987438	GO:0008270,GO:0005515	AT3G13228.1		RING/U-box superfamily protein	zinc-RING finger protein
Sapur.006G049900.2	8.189807498	0.110004893	0.106680248	1.031165	0.302463646	0.365538153	grey	0.057092373	0.477562504	GO:0007165	AT1G30270.1	ATCIPK23.CIPK23.LKS1.SnRK	CBL-interacting protein kinase 23	CBL-interacting Serine/Threonine-kinase
Sapur.15WG125300.2	0.208895513	-0.641428161	0.622069491	-1.03112	0.30248465	0.36555018	grey	-0.206116938	0.009601202		AT5G45470.1		Protein of unknown function (DUF594)	transmembrane protein, putative
Sapur.006G004500.1	9.866445106	-0.123406789	0.119731224	-1.0307	0.302682245	0.365762242	grey	-0.099713329	0.214044965		AT5G47630.1	mtACP3	mitochondrial acyl carrier protein 3	acyl carrier protein

Sapur.002G003800.1	0.17502246	0.6807627	0.660585829	1.030551	0.30275158	0.36582661	grey	0.16598433	0.03778955	GO:0006355;GO:0003677	AT5G42630.1	ANAC031,CUC3,NAC368	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	CUP-shaped COTYLEDON protein	
Sapur.013G077400.1	0.86045822	0.31541429	0.306182209	1.030153	0.30298331	0.36601577	grey	0.08621836	0.28291506						NA
Sapur.012G069600.1	12.52607935	0.22605624	0.194446106	-1.0263	0.32398563	0.36690376	grey	-0.11480568	0.15261075	GO:0003968	AT1G14790.1	ATRDRP1,RDR1	RNA-dependent RNA polymerase 1	RNA-dependent RNA polymerase	
Sapur.006G051500.2	0.81835227	0.29172816	0.283330384	1.029657	0.30371075	0.36286002	grey	0.39363977	0.3.96-07	GO:0016157;GO:0005985	AT5G20280.1	ATSPS1F,SPS1F	sucrose phosphate synthase 1F	sucrose phosphate synthase	
Sapur.019G015600.2	83.86289655	-0.15969362	0.154953232	1.029552	0.30319703	0.36235002	grey	-0.07963416	0.12267524	GO:0051892;GO:0003824	AT1FPA	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	trehalose-phosphate phosphatase	trehalose-phosphate phosphatase	
Sapur.019G029300.1	208.6653459	0.05053329	0.049130347	1.028957	0.30349974	0.3466294	grey	0.12549957	0.11758122		AT5G2930.1	Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein	PPR containing plant protein	
Sapur.016G120300.7	1.75391358	-0.28382173	0.275738253	-1.02882	0.30356528	0.36709431	grey	-0.09639951	0.25891245		AT4G27290.1	ARM repeat superfamily protein	armadillo repeat protein, putative	armadillo repeat protein, putative	
Sapur.007G051700.1	1907.641834	0.04876137	0.047486713	-1.02862	0.30372416	0.36692179	grey	-0.09340691	0.24444073	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT5G62320.1	CYP71B36	cytochrome P450, family 71, subfamily B, polypeptide 36	NA	NA
Sapur.013G078000.2	4.99246661	-0.12363763	0.120246537	-1.02819	0.30385888	0.36700584	grey	-0.04534468	0.58166375	GO:0016020	AT4G27630.2	GTG2	GPCR-type G protein 2	GPCR-type G protein	
Sapur.017G007700.1	2.38058334	-0.36368604	0.353670219	-1.02739	0.30407398	0.36760588	grey	0.13517189	0.36700588	GO:0006488;GO:0005634;GO:0004672	AT5G66930.1		Protein kinase superfamily protein	NA	NA
Sapur.004G105100.1	0.34687314	0.38413649	0.374015475	1.02706	0.30430268	0.36763773	grey	0.07201663	0.37082195						
Sapur.003G025700.1	191.6113831	-0.07964237	0.077488227	-1.02687	0.30446999	0.36774047	grey	-0.12629796	0.11794196	GO:0017004;GO:0017003;GO:0005886	AT1G17190.1	ATLTG1	cytochrome C-type biogenesis protein CcmE	cytochrome C-type biogenesis protein CcmE	
Sapur.010G051700.5	0.70087825	0.28694238	0.279484223	1.026684	0.30456071	0.36794066	grey	0.10537357	0.18945659	GO:0017004;GO:0030198					NA
Sapur.003G022600.1	5.85820193	0.28178161	0.274531271	1.026646	0.30458167	0.36796414	grey	0.07624894	0.34763163	GO:0006029;GO:0019762	AT1G71715.3		Mannose-binding lectin superfamily protein	jacalin-like lectin domain protein	
Sapur.003G029700.4	0.18683207	0.58933487	0.574331623	1.026157	0.30481724	0.36810558	grey	0.10589895	0.18293926	GO:0005515;GO:0030117;GO:0016192;GO:0006886;GO:0005198	AT5G23160.1		Coatomer, beta'-1 subunit	coatomer beta subunit, putative	
Sapur.014G070300.1	418.3620999	0.03475304	0.034526438	1.025707	0.30528039	0.36870139	grey	-0.09995758	0.13293429		AT5G61620.1	RRP41	3'-5'-exoribonuclease family protein	exosome complex exonuclease RRP41	
Sapur.013G105100.1	10.97987602	0.10381418	0.101264289	1.025555	0.30532458	0.36870139	grey	0.08482156	0.29086409		AT1G77855.1				hypothetical protein
Sapur.009G105700.1	517.8650246	0.02861747	0.027917383	1.024964	0.30538941	0.36875106	grey	0.04564722	0.63245597		AT4G38640.1		Plasma-membrane choline transporter family protein	plasma-membrane choline transporter	
Sapur.005G105500.1	12.69492166	0.04184876	0.13388503	-1.02464	0.30552248	0.36890664	grey	-0.11945353	0.11755343		AT2G19180.1			DUF4228 domain protein	
Sapur.013G085900.2	0.44652223	0.37968505	0.370603987	1.024339	0.30567525	0.36905455	grey	0.07545858	0.34763124		AT4G27610.3			hypothetical protein	
Sapur.019G027400.1	0.15413829	0.36358134	0.354541276	-1.02415	0.30574928	0.36947068	grey	-0.34773928	8.08-06	GO:0003677	AT2G33810.3	AP2/B3-like transcriptional factor family protein		B3 DNA-binding domain protein	
Sapur.002G075800.1	12.46708014	0.28646055	0.280144358	-1.02253	0.30653046	0.37060403	grey	-0.12755552	0.11149828						NA
Sapur.004G120300.1	0.30221524	0.60195981	0.591968819	-1.02224	0.3066195	0.37014883	grey	-0.25917041	0.05031121	GO:0009733	AT4G34730.1	SAUR-like auxin-responsive protein family		auxin-induced SAUR-like protein, putative	
Sapur.019G092400.1	0.16632308	0.84534174	0.82743671	-1.02164	0.30691677	0.37043287	grey	-0.32284824	2.05E-05	GO:0046983;GO:0003677	AT2G37330.1	AGL15,SEP4	K-box region and MADS-box transcription factor family protein	AGL6-like MADS-box transcription factor	
Sapur.013G085300.1	8.35261148	0.24135271	0.236117175	1.021512	0.30697214	0.37066147	grey	0.06150654	0.44138629	GO:0005975;GO:0016798	AT4G28610.1		Glycosyl hydrolase family protein with chitinase insertion domain	glycosyl hydrolase family 18 protein	
Sapur.012G044100.1	4.05299238	0.25309514	0.247819374	1.021323	0.30710269	0.37069588	grey	0.08719986	0.28016393						NA
Sapur.010G029500.9	5.27929836	-0.14379039	0.140883941	-1.02065	0.30742813	0.37105452	grey	0.07522605	0.34907651	GO:0043565;GO:0006355;GO:0003700;GO:0006351	AT5G12150.1	BZIP45,TGA6	TGACG motif binding factor 6	transcription factor TGA6	
Sapur.003G013500.1	2188.306664	-0.01452301	0.014229163	-1.02016	0.30758549	0.37108579	grey	-0.15973918	0.04649546		AT5G15545.1		Mov34/MPN/PAD-1 family protein	26S proteasome non-ATPase regulatory subunit	
Sapur.004G148500.1	104.9777944	0.06658669	0.064746613	1.02015	0.30752613	0.37108579	grey	0.07078884	0.3781178		AT5G10370.1			glycosyl hydrolase, putative	
Sapur.019G180200.2	2.69824214	0.19174227	0.187927188	1.020127	0.30765477	0.37126144	grey	0.07063906	0.38739655	GO:0016757;GO:0047262	AT2G26210.1	GALT1D1;GT4	galactosyltransferase 10	CAZy family GT8 glycosyltransferase	
Sapur.019G070800.2	1.56591861	-0.25328771	0.248513629	-1.01921	0.30810941	0.37181178	grey	-0.11301893	0.16248395	GO:0052689;GO:0006482	AT4G10050.1		esterase/lipase/thioesterase family protein	protein phosphotase methylesterase	
Sapur.011G124100.2	27.32383101	0.06838194	0.067138156	1.01882	0.30816035	0.37210981	grey	0.07507748	0.36825119		AT5G64810.1		RNA-binding (RRM/RBD/RNP motifs) family protein	lactic acid-binding protein, putative	
Sapur.004G142800.1	0.55677537	-0.36548289	0.358877183	-1.01843	0.30844837	0.37255729	grey	-0.06865182	0.45537701		AT3G28120.1		Major facilitator superfamily protein		NA
Sapur.004G152600.1	0.26663343	-0.36760454	0.357156628	-1.01832	0.30857434	0.37261982	grey	-0.08674218	0.3767767	GO:0009733	AT4G27860.1	SAUR-like auxin-responsive protein family		auxin-induced SAUR-like protein, putative	
Sapur.001G137900.1	0.48823678	0.33712485	0.331185349	1.017922	0.30870387	0.37292274	grey	0.06228182	0.43834634	GO:0016151;GO:0006807	AT3G55035.1	URED	urease accessory protein D	urease accessory protein UreD	
Sapur.006G204600.3	0.47404869	0.39212665	0.384000176	1.017508	0.30905622	0.37296678	grey	0.07185791	0.37327465	GO:0005524	AT1G80370.1	EDA16	DNA2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related	chromatin remodeling complex subunit	
Sapur.005G188000.1	634.6776643	0.05389795	0.052846155	1.01615	0.30957896	0.37349766	grey	0.03523694	0.66138507		AT4G05320.1	emb1273	embryo defective 1273	embryo defective 1273	
Sapur.006G118300.2	1.25601524	0.23948786	0.235080795	1.016108	0.30957992	0.37350832	grey	0.04029334	0.61689308	GO:0008152;GO:0005824	AT5G24360.2		ATP-dependent caseinolytic (Clp) protease/crotonase family protein	3-hydroxybutyryl-CoA dehydratase, putative	
Sapur.002G027700.1	11.15839191	0.14319648	0.141054243	1.016051	0.30959174	0.37350832	grey	0.06663242	0.28051626		AT5G48670.1		Ankyrin-repeat family protein	NA	NA
Sapur.004G171100.2	2.57024725	0.18000461	0.177331765	1.015055	0.31007637	0.37408227	grey	0.07937888	0.32308354	GO:0019773;GO:0006511;GO:0047475;GO:0051603;GO:0005839;GO:0004298	AT5G42640.2	PAA2	20S proteasome subunit PAA2	proteasome subunit alpha type-6 protein	
Sapur.005G190600.1	10.80662764	0.12188055	0.119604602	1.014895	0.31015614	0.37451195	grey	0.07734686	0.33434119						NA
Sapur.016G119500.5	15.52087761	-0.09664870	0.095234546	-1.01485	0.31017719	0.37416311	grey	-0.07913308	0.22427418	GO:0007165	AT3G26980.4	CIP63,SnRK3.17	CBL-interacting protein kinase 3	CBL-interacting Serine/Threonine-kinase	
Sapur.003G028300.2	11.46485441	0.07025047	0.069256347	1.014663	0.31030837	0.37470217	grey	0.08253176	0.60404812	GO:0016042;GO:0006629	AT1G14575.1		Mono- /di-acylglycerol lipase, N-terminal;Lipase, class 3	triacylglycerol lipase, putative	
Sapur.005G089300.1	1160.143237	-0.05382714	0.053190465	1.014429	0.31037808	0.37470829	grey	-0.09314577	0.23150243	GO:0003676	AT5G58670.1	U1-70K,U1SNRNP	U1 small nuclear ribonucleoprotein 70 kDa protein	U1 small nuclear ribonucleoprotein 70 kDa protein	
Sapur.012G035300.1	1142.464883	0.05272412	0.050008256	1.014081	0.31049198	0.37564707	grey	0.10334176	0.20404269	GO:0005515;GO:0003723	AT5G44190.1		DNA-binding;zinc ion binding;nucleic acid binding;nucleic acid binding	nuclear receptor-binding set domain protein 1, red protein;H3C protein	
Sapur.014G051300.1	0.56699171	-0.39950459	0.394030876	-1.01389	0.31063448	0.37469945	grey	0.12762607	0.11118454		AT1G76240.1			transmembrane protein, putative	
Sapur.013G130200.1	34.60664991	0.11762488	0.116032157	-1.01379	0.31088485	0.37470787	grey	-0.07849616	0.13278324	GO:0005468;GO:0006672	AT2G14481.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein	
Sapur.008G028200.1	0.27391857	0.45651836	0.450513882	-1.01329	0.31092249	0.37500608	grey	0.07377724	0.27268053	GO:0019901;GO:0006355;GO:0003779	AT3G46430.1	ATRCY,LRCY1	arginine-rich cyclin 1	cyclin-T1 protein	
Sapur.016G039900.2	2.90675245	-0.17416588	0.171911322	-1.01283	0.31141737	0.37520696	grey	-0.09708636	0.23551431	GO:0004843	AT1G05290.1	ATUBP5,PDE323,UBP5	ubiquitin-specific protease 5	ubiquitin carboxyl-terminal hydrolase	
Sapur.015G071200.1	5.47179707	0.02877826	0.028378924	1.012667	0.31174279	0.37526257	grey	0.10883248	0.19763816	GO:0016853;GO:0003824	AT4G08670.1	ATUR1/UPRT1,UR1/UPRT1,UR	uridine monophosphate phosphoribosyltransferase 1	NA	NA
Sapur.006G185000.2	21.2157884	-0.06742444	0.066520878	-1.01206	0.31158733	0.37520595	grey	-0.10896417	8.25E-05	GO:0006457;GO:0003755;GO:0004313	PAA2		20S proteasome subunit PAA2	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein	
Sapur.016G035300.1	0.35708846	0.64461404	0.636756231	-1.01058	0.31171571	0.37520595	grey	-0.14395095	0.09261172	GO:0008168;GO:0008152				S-adenosyl-methionine-dependent methyltransferase, putative	
Sapur.010G191000.1	0.99482713	-0.2469231	0.244135285	-1.01146	0.31176083	0.37595285	grey	-0.11896196	0.13782209		AT5G22450.1			hypothetical protein	
Sapur.016G130100.2	1.62022004	0.07758249	0.076736133	1.011638	0.31180083	0.37597614	grey	0.05786438	0.47197927	GO:0006355;GO:0005634;GO:0003700	AT5G28120.1	AGL7,AP1	K-box region and MADS-box transcription factor family protein	ARCTALA-like MADS-box PTAF1 protein	
Sapur.013G136100.2	1.82364809	-0.20170148	0.199053751	-1.01114	0.31194719	0.37609646	grey	-0.13042518	0.18857925	GO:0006367;GO:0005672	AT3G07480.1		Transcription factor 84, alpha/beta sushi	transcription factor 84, alpha/beta sushi	
Sapur.006G097500.1	1.01306169	0.10038452	0.099238552	1.010118	0.31195581	0.37609646	grey	0.04080245	0.52723511		AT2G31440.1		MATE efflux family protein	DNA-damage-inducible protein 1, putative	
Sapur.002G070000.1	27.42647848	-0.15547954	0.154058907	-1.01111	0.31196505	0.37610014	grey	-0.09083251	0.25790266		AT5G08760.1		Plant protein of unknown function (DUF936)	DUF936 family protein	
Sapur.T028700.1	13.88261543	0.06570985	0.066000165	1.010664	0.31217719	0.37634239	grey	0.13868512	0.08061811						NA
Sapur.010G192800.1	1705.002214	0.01882503	0.019056029	1.009777	0.31230216	0.37686366	grey	0.09543704	0.23431543		AT5G01600.1	RmlC-like cupins superfamily protein		cupin protein	
Sapur.018G056500.1	0.36316089	0.48127959	0.476641854	1.00973	0.31236455	0.3682837	grey	0.19000621	0.07148705	GO:0055114;GO:0016491;GO:0008152	AT4G24503.1	ALDH2A,ALDH2C4,RER1	aldehyde dehydrogenase 2C4	NA	NA
Sapur.005G199100.1	195.1818073	0.01588251	0.015694891	1.009262	0.31268868	0.37214188	grey	0.06483084	0.43873397	GO:0016592;GO:0006357;GO:0003104	AT4G26661.1		Transcriptional factor, subunit Med10	mediator of RNA polymerase II transcription subunit 10	
Sapur.006G053000.1	35.20549233	0.11127489	0.110178228	1.008089	0.31341954	0.37734384	grey	0.06371724	0.42789365						hypothetical protein
Sapur.008G028200.1	1947.26223	0.02846331	0.028248775	1.007595	0.31369384	0.37795512	grey	0.04509846	0.61932211	GO:0055114;GO:0046872;GO:0008801;GO:0004784	AT3G10920.1	ATMSD1,MEE33,MSD1	manganese superoxide dismutase 1	superoxide dismutase [Mn] protein	
Sapur.012G091600.6	0.45145468	-0.43026564	0.427393781	-1.00673	0.31406315	0.37846785	grey	-0.15130704	0.05853872					zinc finger protein, putative	
Sapur.014G140300.1	0.16319884	0.37842202	0.371284251	1.006606	0.31409636	0.37884202	grey	0.10308209	0.15308532					transmembrane protein, putative	
Sapur.003G084800.1	0.29360815	0.56302228	0.550723404	1.005753	0.31543185	0.37897653	grey	0.10493612	0.19276195	GO:0006508;GO:0004252	AT5G59190.1		subtilase family protein	cucumisin, putative	
Sapur.003G084300.1	0.47265329	0.04375238	0.04275238	-1.005	0.31583713	0.37934053	grey	-0.13157664	0.10329903	GO:0003677	AT5G54560.1	HTA11	histone H2A 11	histone H2A	
Sapur.019G130800.1	12.00692547	0.17624097	0.175573124	1.004845	0.31497713	0.37947574	grey	-0.07245568	0.36715808						NA
Sapur.002G100900.1	0.21057744	0.69882471	0.695857165	1.004491	0.31514181	0.37967136	grey	0.14880744	0.06135751	GO:0006355;GO:0003700	AT4G27688.1	RAP2.1	related to AP2 1	dehydration-responsive element-binding protein, putative	
Sapur.013G075200.1	74.51974	0.07244004	0.072146396	1.004244	0.31526322	0.37976861	grey	0.11070645	0.18723126						NA
Sapur.003G042100.1	21.5630953	-0.09915854	0.098740631	-1.0042	0.31527998	0.37985686	grey	-0.08467733	0.29160492		AT5G27320.1	APUM23,PUM23	pumilio 23	pumilio domain protein C4orf21	
Sapur.004G208300.1	2.11248122	0.10766313	0.107167334	-1.0041	0.31532637	0.37985164	grey	-0.08415267	0.29470511	GO:0005515	AT5G07680.1		Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein	anthranilate phosphoribosyltransferase-like protein	
Sapur.005G076500.1	330.0879331	-0.06837795	0.068153923	-1.00321	0.31575851	0.38055506	grey	-0.07520928	0.34920941		AT5G76160.1				NA
Sapur.008G100300.1	-0.36229329	0.42765153	0.426287752	-1.00288	0.31593984	0.38053457	grey	-0.18549865	0.03004807						NA
Sapur.019G070000.1	157.5466818	-0.04791819	0.047786387	-1.00279	0.31596099	0.38070938	grey	-0.13601843	0.08941084	GO:0016597;GO:0008152;GO:0055114;GO:0050661;GO:0016491;GO:0006520	AT4G19710.2	AK-HSDH,AK-HSDH II	aspartate kinase-homoserine dehydrogenase II	aspartokinase/homoserine dehydrogenase	
Sapur.006G207000.1	0.16177938	0.70088261	0.699021617	-1.0024	0.31615225	0.38078063	grey	-0.28217762	0.02980584	GO:0005515;GO:0003723;GO:0016070;GO:0051028;GO:0045292;GO:0005846;GO:0000933	AT4G11540.1	ABHD11,ATSPB5,LSP8EIEN5	Alpha/beta-hydrolase family protein	nuclear cap-binding protein	
Sapur.T061600.1	0.17654976	0.55608758	0.554756349	1.00223	0.31618482	0.38078063	grey	0.14980798	0.06115067		AT1G70320.1	ATCRM1,ATXPO1,HET2,XPO1	exportin 1A	exportin 1A	
Sapur.001G077100.1	14.03368864	0.08600386	0.085823446	1.002097	0.31629875	0.38093753	grey	0.09917666	0.21494926		AT4G01100.2	ADNT1	adenine nucleotide transporter 1	grave disease carrier protein, putative	
Sapur.002G082800.1	726.1957507	-0.05584891	0.055845859	-1.00187	0.31647543	0.38102586	grey	-0.07456156	0.35742184		AT5G47595.1			synaptotagmin-like protein-carboxy-terminal protein	
Sapur.016G172800.2	3.11703157	0.15395259	0.15312139	-1.00146	0.31682111	0.38137603	grey	-0.04533411	0.57289753	GO:0005515	AT1FMHDA,PRMDA	pre-mRNA-processing protein 40A		FF domain protein	
Sapur.016G000500.1	0.49147534	0.38263239	0.380515365	0.999877	0.31683622	0.38152631	grey	-0.14650594	0.07890947	GO:0006355;GO:0003700	AT4G05010.1	MCM9	minichromosome maintenance 9	minichromosome maintenance protein MCM, putative	
Sapur.018G063800.1	423.1156151	0.16773831	0.167571647	1.000968	0.31684249	0.38155302	grey	0.09548326	0.23398806	GO:0055114;GO:0016491	AT5G15190.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA	NA
Sapur.010G092300.1	19.7918884	0.12486499	0.124694538	-1.00048	0.31709132	0.38185153	grey	-0.08962136	0.12484439	GO:0005515;GO:0006468;GO:0005634;GO:0004672	AT5G18190.2		Protein kinase superfamily protein	Protein kinase superfamily protein	
Sapur.010G060600.1	261.0541724	-0.03379081	0.033768568	-1.00003	0.31724667	0.38199556	grey	-0.10631591	0.18494057		AT2G38970.1			Zinc finger (C3HC4-type RING finger) family protein	WAV4;C3HC4-type: Von willebrand factor type A (VWA) domain was originally proposed
Sapur.010G130300.1	0.96025151	0.35582023	0.355082029	0.99967	0.31727886	0.38317866	grey	0.02506662	0.75317521	GO:0055114;GO:0016491	AT5G63260.1	EMB3004,MEE32	dehydroquinate dehydratase/shikimate dehydrogenase, putative / shikimate dehydrogenase, putative	dehydroquinate dehydratase/shikimate dehydrogenase	
Sapur.016G021300.1	32.9829665	0.16026374	0.160330495	-0.99975	0.31743034	0.38217684	grey	-0.10303564	0.19908884	GO:0055015	AT2G29490.1	ATGSTU1,GST19,GSTU1	glutathione S-transferase TAU 1	NA	NA
Sapur.004G208600.1	2119.410353	0.12728362	0.127285167	-0.99967	0.31743456	0.38217684	grey	0.09863695	0.23833125	GO:0017108;GO:0016020;GO:0005524	AT4G01850.1	ABH1,Arp5acA	Alkino or Clpx-like	Sno/Sin-like family protein	
Sapur.L052G91500.2	2.55157569	0.17630886	0.176439364	0.999392	0.31760496	0.38255885	grey	0.10723251	0.18138994	GO:0006397;GO:0005634;GO:0004721	AT5T8820.1		Sno/Sin-like family protein		NA
Sapur.001G150500.5	3.97069984	0.13878083	0.138898523	-0.99925	0.31767774	0.38242518	grey	-0.05930272	0.46213675	GO:0004488;GO:0055114;GO:0046872	AT2G16100.1	CKL2,CK1	casein kinase I-like protein	casein kinase I-like protein	
Sapur.002G080600.2	0.21655156	0.48436883	0.484816035	0.999135	0.31773905	0.38247609	grey	0.10400419	0.19471661	GO:0003723	AT4G13270.1	BTR1,BTR1L1,BTR1S	binding to TTNTR/C motif DNA 1L (long form)	RNA-binding protein regulator of pre-mRNA splicing	
Sapur.009G087400.1	0.25731281	0.52702033	0.527488557	0.999117	0.31778174	0.38247609	grey	-0.38895167	2.27E-07		AT5G66800.1		Protein of unknown function, DUF547	termany complex factor MPS1 leucine-zipper protein	
Sapur.016G067000.1	2.88243869	0.38246733	0.382515365	0.998974	0.31780742	0.38264116	grey	0.02266856	0.75827511	GO:0008793	AT5G09910.1	SAUR-like auxin-responsive family protein		auxin-responsive family protein	
Sapur.008G062700.2	0.39169255	0.35941429	0.358122105	-0.99889	0.31785794	0.38275307	grey	-0.17853631	0.02587911	GO:0005515;GO:0016491	AT5G48380.1	BIR1	BAK1-interacting receptor like kinase 1	inactive LRR receptor-like kinase, putative	
Sapur.015G087100.1	1.54863515	0.25169259	0.251369464	0.99786	0.31797192	0.38260564	grey	0.05617595	0.48467468		AT5G66270.1		Guanylate binding family protein	NA	NA
Sapur.013G109700.1	29.00383209	0.11130456	0.111395958	-0.99828	0.3181423	0.38289186	grey	-0.07829706	0.33877621	GO:0008270;GO:0005515	AT5G47630.1		RING/U-box superfamily protein	RING-H2 zinc finger protein	
Sapur.003G082800.1	0.98879444	0.52738763	0.528222222	0.99804	0.31825921	0.38318896	grey	-0.13832827	0.08403811		AT5G27570.1		Polyketide cyclase/dehydrase and lipid transport superfamily protein	NA	NA
Sapur.013G107900.1	1.37810948	0.24007539	0.240647353	-0.99762	0.31846216	0.38348648	grey	-0.07317646	0.36903062		AT2G42430.1		Protein of unknown function (DUF679)	transmembrane protein, putative	
Sapur.T033700.1	0.37931506	0.32188646	0.322071463	0.996582	0.31873435	0.38395143	grey	0.11314106	0.15693693		AT4G27960.1		PLATZ transcription factor family protein	NA	NA
Sapur.004G004100.1	4.54928866	0.16383525	0.164185166	0.996945	0.31879168	0.38302768	grey	0.07751904	0.33458204	GO:0016021	AT5G57535.1		Auxin-responsive family protein	eukaryotic cytochrome b561 protein	
Sapur.008G162600.2	0.56056167	0.34884823	0.349543093	0.996915	0.31880587	0.38305922	grey	0.05485905	0.49048229	GO:0018242;GO:0006470;GO:0004722	AT5G18560.1		Protein phosphatase 2C family protein	protein phosphatase 2C	
Sapur.009G081300.1	0.15162249	0.64165098	0.640455718	0.996653	0.31885232	0.38345319	grey	0.05853237	0.42693717		AT5T7120.1			transmembrane protein, putative	
Sapur.003G054100.1	16.02761698	0.06604676	0.066256772	0.9968	0.31886158	0.38365319	grey	0.06079618	0.44945217					hypothetical protein	
Sapur.003G135000.1	2.34824283	0.42328833	0.423769111	0.996544	0.31889604	0.38378124	grey	0.11884604	0.16340305	GO:0005975;GO:0004553	AT5T8060.1		Glycosyl hydrolase family protein	NA	NA
Sapur.006G135900.1	595.7.67681	0.05184033	0.05209532	0.994984	0.31974928	0.3846793	grey	0.05349792	0.55769555	GO:0006096;GO:0004332	AT2G36460.1		Aldolase superfamily protein	fructose-bisphosphate aldolase	
Sapur.003G130100.2	20.18550223	0.11537531	0.116331882	0.994422	0.31980153	0.38488163	grey	-0.05329551	0.53889974	GO:0055114;GO:0045333	AT2T7220.1		NB-ARC domain-containing disease resistance protein	NA	NA
Sapur.012G129300.1	12.43191931	0.13214462	0.132963514	0.994427	0.32004479	0.38501588	grey	Ran BP2/NZF zinc finger-like superfamily protein			AT2G26695.1			zinc finger-like protein	
Sapur.013G041100.2	0.80050483	0.32748642	0.329577173	0.994184	0.32030583	0.38519133	grey	0.04338672	0.63444446	GO:0016491;GO:0016614;GO:0016491;GO:0019104;GO:0005524;GO:0004012;GO:0000028	AT5T9410.1		ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	phosphoglycerol transporting ATPase, putative	
Sapur.012G060600.1	8.52191557	-0.12585368	0.125565571	-0.99399	0.32027246	0.38520464	grey	0.10217997	0.20397028	GO:0055114;GO:0032542	AT3G13170.4	ATSRX,SRX	sulfiredoxin	NA	NA
Sapur.013G130300.2	0.17195	0.37136687	0.37380788	-0.99369	0.32037542	0.38536387	grey	-0.03025763	0.6629183					hypothetical protein	
Sapur.003G138000.1	41.46678694	0.07970773	0.080476362	-0.99339	0.32056578	0.38569207	grey	0.06595521	0.41848168	GO:0016020;GO:0008150	AT4G10380.1	NIPS1,1NLMB,NLMB	NODZ-like intrinsic protein 5;1	nodulin-like intrinsic protein NIPS-1	
Sapur.017G118300.1	40.5451386	0.12104428	0.121935753	0.992688	0.32082228	0.38506152	grey	0.3608751154	4.17E-07		AT5G37360.1			RNA-splicing endonuclease subunit sen54 amino-terminal protein	
Sapur.003G088500.1	121.7505126	0.09588314	0.096724624	0.99168	0.32089716	0.38546131	grey	0.16796878	0.05488104		AT4G08530.1	Major facilitator superfamily protein		nodulin-like protein	
Sapur.016G090100.1	0.11658829	0.87135971	0.832275457	0.992564	0.32092245	0.38597266	grey	0.29853984	0.00014998						NA
Sapur.013G104300.1	0.31247024	0.46423315	0.458138884	0.992372	0.32103164	0.38606822	grey	0.05361858	0.56380722		AT5G58270.1			hypothetical protein	
Sapur.010G130200.1	1.38267747	-0.25701765	0.25900369	-0.99227	0.32106548	0.38614148	grey	0.14377614	0.07248882	GO:0005634;GO:0003677	AT4G37010.1	SPL1	squamosa promoter binding protein-like 1	squamosa promoter-binding protein	
Sapur.010G086400.2	2.26854736	0.19132491	0.192905562	-0.99211	0.32108223	0.38617879	grey	-0.06098914	0.21872658	GO:0006888;GO:0005484;GO:0006886	AT2G17760.1		Eukaryotic synaptosomal-associated protein family	NA	NA
Sapur.012G038300.1	141.510558	0.03609941	0.036408737	0.990341	0.32202727	0.38734897	grey	0.08700604	0.29155852	GO:0006468;GO:0004672	AT4G21390.1	BL10	S-locus lectin protein kinase family protein	tyrosine kinase domain protein	
Sapur.003G078300.1	80.59813104	0.07239853	0.073000219	0.98821	0.32204178	0.38740703	grey	0.07278232	0.32363764	GO:0016853;GO:0005975	AT5G14180.1		Galactose mutarotase-like superfamily protein	aldose 1-epimerase family protein	
Sapur.012G016600.2	11.01070364	-0.09542441	0.0964843	-0.9891	0.32261531	0.38795145	grey	-0.07543541	0.33752625	GO:0006468;GO:0004672	AT5G10270.1	CDKC;1	cyclin-dependent kinase C;3	cyclin-dependent kinase C	
Sapur.013G089900.1	0.13069528	0.86915251	0.879104462	0.988581	0.32288434	0.38841548	grey	0.26017016	0.00074384		AT4G26120

Sapur.002G037600.1	65.16102639	-6.36649371	0.386153064	-0.94908	0.34257527	0.40966872	grey	-0.07462983	0.152923592		AT3G18670.1		Ankyrin repeat family protein		NA
Sapur.003G162100.1	5.78056816	-0.12001153	0.126451464	-0.94907	0.34256837	0.40966872	grey	-0.04717731	0.237283207	GO:0003723,GO:0046872	AT3G21130.1		KH domain-containing protein / zinc finger (CCCH type) family protein		zinc finger C-x8-C-x5-C-x3-H type protein
Sapur.005G071400.1	3.76302468	0.165112984	0.175987966	0.946991	0.34252148	0.4097044	grey	-0.04710242	0.347834381						NA
Sapur.005G062700.1	256.3203741	0.039533867	0.041672454	0.946881	0.34229359	0.40987265	grey	0.08609298	0.283656008		AT5G10070.1		RNase L inhibitor protein-related		ribosome biogenesis protein, putative
Sapur.005G077200.1	5.56072884	0.424261304	0.447436286	0.946364	0.34204415	0.41003918	grey	-0.10329181	0.33354145						transmembrane protein, putative
Sapur.013G079000.1	12.7588696	0.092146686	0.097165972	0.946343	0.34204781	0.41008189	grey	0.08042413	0.316690609						NA
Sapur.006G238300.2	2.116885612	0.162693808	0.171602439	-0.94809	0.34208586	0.41008081	grey	-0.12253641	0.126215589	GO:0005515	AT5G76900.2	AT1LP1,TLP1	tubby like protein 1		tubby-like F-box protein
Sapur.005G032200.1	0.18789893	0.626260462	0.660632833	0.94797	0.34184798	0.41022876	grey	-0.22423854	0.032291135						NA
Sapur.003G166800.1	1.06163663	0.230261529	0.243343239	-0.94768	0.34192052	0.41037942	grey	-0.04661474	0.142098885	GO:0016021,GO:0006820,GO:0016020,GO:0005452	AT5G62270.1		HCO3- transporter family		boron transporter
Sapur.008G207500.1	1.08659763	0.083288897	0.088126849	0.939472126	0.34182638	0.41040682	grey	0.09047228	0.380104015	GO:0008370	AT3G70180.1		SAUR-like auxin-responsive protein family		auxin-responsive family protein
Sapur.006G047100.1	71.88263179	0.223825233	0.235149488	0.947578	0.34184417	0.41041783	grey	0.04234393	0.598506239						NA
Sapur.006G082500.1	0.80262629	0.304068525	0.320261714	0.94748	0.34195158	0.41060867	grey	-0.01234674	0.515852728						NA
Sapur.006G175500.1	13.62410612	0.102705888	0.108436167	0.947386	0.34344228	0.41052244	grey	-0.10329299	0.196026996						NA
Sapur.004G134600.4	2.36373338	0.127377041	0.134344606	0.947329	0.34357722	0.41052547	grey	0.04877209	0.504114767		AT5G48160.1	OBE2	Protein of unknown function (DUF1423)		polyprotyl Vfg interacting protein
Sapur.005G135800.1	5.81412505	-0.15275322	0.161391975	-0.94655	0.34388998	0.41082664	grey	-0.07040163	0.189383763		AT5G77700.1		Pathogenesis-related thaumatin superfamily protein		thaumatin-like protein
Sapur.016G254700.1	71.04873971	0.093836651	0.099124562	-0.94642	0.34389739	0.41100306	grey	-0.07964003	0.123521207		AT3G37610.1		Nucleic acid binding, OB-fold-like protein		NA
Sapur.014G049200.1	0.1123518	0.864393021	0.913772231	0.946008	0.34414645	0.41127258	grey	-0.28348858	0.000286642	GO:0004857	AT4G00080.1	UNE11	Plant invertase/pectin methylesterase inhibitor superfamily protein		pectin methylesterase inhibitor, putative
Sapur.007G045400.1	0.210287332	-0.52895247	0.559728182	-0.94502	0.34450359	0.41856993	grey	-0.16407425	0.040038149		AT1G67240.1	SDN3	small RNA degrading nuclease 3		small RNA degrading nuclease
Sapur.005G132600.4	0.323053997	-0.027263366	0.029677279	-0.9397816	0.34435745	0.41908296	grey	-0.15542774	0.016228059		AT5G02600.1		DHAK2		ATP-binding protein, putative
Sapur.017G086400.1	1482.061462	-0.061921427	0.065543976	-0.94478	0.34477281	0.41974116	grey	-0.08179338	0.308577989	GO:0033321	AT5G30360.1		Transmembrane amino acid transporter family protein		amino acid transporter
Sapur.003G160800.2	13.33738735	0.064166447	0.069854462	-0.94462	0.34484214	0.41985632	grey	-0.04153429	0.656407197		AT5G58190.1	EMB2358,MAN_VC1	Mannosyltransferase family protein		vacuolar protein sorting-associated protein
Sapur.018G045400.2	0.48644139	0.394824248	0.417304053	0.944353	0.34488162	0.41220289	grey	0.30468451	0.001045526	GO:0016773,GO:0005975,GO:0005524,GO:0046835,GO:0005516,GO:0004396,GO:0005167	AT3G18860.1	ATHKR2,HKR2	hexokinase 2		NA
Sapur.008G288100.2	11.51834361	0.064189117	0.122957662	-0.9443	0.34501727	0.41220331	grey	-0.10002752	0.132860128	GO:0055115	AT5G25290.1	DHAK2	dehydroascorbate reductase 2		glutathione S-transferase DHAR2
Sapur.005G032200.1	816.924627	0.054347274	0.05748888	0.945599	0.34524772	0.41261837	grey	0.03320632	0.67921828		AT4G15880.1	RALR.13	ralF-like 13		rapid alkalinization factor
Sapur.013G030700.2	8.41044907	0.095166125	0.101052212	0.945444	0.34543883	0.41274612	grey	0.06082745	0.384843763	GO:0007264,GO:0005525	AT5G64840.2	ATSGP1,SGP1	Ras-related small GTP-binding family protein		GTP-binding family protein
Sapur.002G118500.1	9.36016491	-0.096320366	0.102153158	-0.9429	0.34573128	0.41301436	grey	-0.05237883	0.514718786						NA
Sapur.005G148900.2	0.28890727	-0.402165993	0.426631036	-0.94266	0.34585261	0.41349964	grey	-0.13927085	0.091668838		AT1G47730.1		RING/FYVE/PHD zinc finger superfamily protein		hypothetical protein
Sapur.006G188700.4	4.00599673	0.120374041	0.136406604	0.945579	0.34588610	0.41381476	grey	0.06105137	0.447513824		AT5G11810.1		THO2		Mos2/BRL1 protein
Sapur.005G118900	0.15800573	0.869327138	0.921431765	0.942446	0.34596246	0.41267973	grey	0.27084535	0.00060162						NA
Sapur.019G012500	13.58327217	0.112700579	0.119622512	0.942189	0.34612449	0.41348377	grey	0.10027187	0.208492129						NA
Sapur.012G010000.1	0.08070823	-0.27020758	0.286089924	-0.94212	0.34613229	0.41348777	grey	-0.09438185	0.236687105	GO:0003677,GO:0000786,GO:0000723,GO:0043047	AT5G06330.1	AtPOT1b	Nucleic acid-binding, OB-fold-like protein		protection of telomeres protein 1a, putative
Sapur.003G107700.1	25.6155604	0.093805053	0.100998806	0.941651	0.34627173	0.41387958	grey	0.06223646	0.41872084						NA
Sapur.006G031800.1	180.4315215	0.055432157	0.058858538	0.941643	0.34637558	0.41397458	grey	0.07238199	0.367648834	GO:0005515	AT4G31370.1	BDP2	Ankyrin repeat family protein / BTB/POZ domain-containing protein		BDP/NPR1/NIM1-like protein 2
Sapur.003G181200.1	116.9412298	0.060322177	0.073564961	-0.94124	0.34660249	0.41406671	grey	-0.07613038	0.32454717	GO:0016491,GO:0008152	AT5G24520.1		NADP(H)-binding oxidoreductase family protein		short-chain dehydrogenase TIC 32
Sapur.007G081000.4	3.23582044	0.148362693	0.157523151	0.94122	0.34659242	0.41408471	grey	0.00779904	0.223439322		AT3G70080.3		Protein of unknown function, DUF647		ternary complex factor MIP1 leucine-zipper protein
Sapur.005G146800.1	19.2508004	0.051387197	0.057138409	0.94	0.34703632	0.41482192	grey	-0.07869842	0.152171294	GO:0003824,GO:0070017,GO:0005874,GO:0031122,GO:0007030,GO:0000930	AT5G56320.1	ATGCP2,GCP2,TUBGCP2	gamma tubulin complex protein 2		NA
Sapur.010G098100.1	33.11005431	-0.16872868	0.179425514	-0.94038	0.34730176	0.41491387	grey	0.08362825	0.207776366	GO:0004857	AT1G27760.1		Plant invertase/pectin methylesterase inhibitor superfamily protein		plant invertase/pectin methylesterase inhibitor protein
Sapur.005G142200.2	0.62659958	0.337353389	0.358694521	-0.9399	0.34727419	0.41493552	grey	-0.06418946	0.42466752		AT5G77405.1		Pentatricopeptide repeat (PPR) superfamily protein		PPR containing plant protein
Sapur.711088.1	2.82087678	0.153166153	0.162918346	-0.93975	0.34734806	0.41470163	grey	-0.06939781	0.38811242		AT4G30670.2	AtTHO2,THO2	THO2		NA
Sapur.007G028800.1	0.16962672	0.803178009	0.855127011	0.93921	0.34762288	0.41596249	grey	0.13051166	0.101135726		AT2G18630.1		Protein of unknown function (DUF677)		transmembrane protein, putative
Sapur.003G056400.1	1.20068734	0.154238379	0.24606027	0.93921	0.34767674	0.41599714	grey	0.08839104	0.270352264		AT3G07960.1				hypothetical protein
Sapur.016G042000.2	0.47001603	-0.33994516	0.362058843	-0.93892	0.34777598	0.41595621	grey	-0.08012627	0.318492105	GO:0005509	AT3G10300.4		Calcium-binding EF-hand family protein		EF-hand calcium-binding protein, putative
Sapur.003G264600.1	148.3178872	0.045334427	0.056410522	0.938692	0.34782024	0.41646614	grey	0.06287024	0.434027184		AT5G08530.1		Major facilitator superfamily protein		nodulin-like protein
Sapur.006G129400.1	85.13329256	0.253461147	0.270325588	0.938186	0.34814876	0.41546895	grey	0.11657509	0.145464324	GO:0055114,GO:0016616,GO:0051287,GO:0000287	AT5G26260.1	IDH-I,IDH1	Isocitrate dehydrogenase 1		NAD-dependent isocitrate dehydrogenase
Sapur.003G165200.1	1.02450003	0.294188623	0.313609495	0.937803	0.34854481	0.41836047	grey	-0.09080617	0.242575551	GO:0005829,GO:0006765,GO:0016787,GO:0005524,GO:0003677	AT5G22180.1		DEAD-box ATP-dependent RNA helicase family protein		DEAD-box ATP-dependent RNA helicase
Sapur.018G106100.1	37.13943303	0.095115329	0.101475114	0.937327	0.34859554	0.41611584	grey	0.08846705	0.270551755	GO:0006468,GO:0006672	AT3G17220.1		Protein kinase superfamily protein		Serine/Threonine kinase domain protein
Sapur.011G071900.1	16.11290897	0.109617388	0.116757571	0.937307	0.34880708	0.41611584	grey	-0.07860228	0.337813064	GO:0006270,GO:0005515	AT5G59370.1		RING/U-box superfamily protein		RING finger protein
Sapur.008G067200.1	706.8287994	-0.024936466	0.045978925	-0.93725	0.34881111	0.41622858	grey	-0.08105669	0.312050427		AT3G19670.1				hypothetical protein
Sapur.7095400.1	0.37191854	-0.46141366	0.492388436	-0.93709	0.34874198	0.41620991	grey	-0.12453272	0.12163497		AT5G28455.1	CLE25	CLAVATA/ESR-RELATED 25		NA
Sapur.008G137400.1	2.74094621	0.142408251	0.152192527	-0.937	0.34875247	0.41628351	grey	0.26246152	0.00031811						hypothetical protein
Sapur.010G160400.1	2.79008691	-0.077710043	0.211136146	-0.93651	0.34903836	0.41651047	grey	-0.31921937	4.60E-05		AT5G36055.1				transmembrane protein, putative
Sapur.003G056400.1	0.50749524	0.161616984	0.180152486	0.936562	0.34904621	0.41656182	grey	-0.16903083	0.016606411	GO:0071805,GO:0016020,GO:0015079	AT4T2,ATKUP2,KT2,KUP2.9	AT4T2	potassium transporter 2		potassium transporter 2
Sapur.15W0G051200.1	2.47480969	-0.257884921	0.275628869	-0.93588	0.34928148	0.41684286	grey	-0.00299946	0.249740345	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G47530.1		Leucine-rich repeat protein kinase family protein		NA
Sapur.003G078800.1	1.94618883	0.227509179	0.244755171	-0.93539	0.34967571	0.41751889	grey	-0.08813816	0.273423281	GO:0016758,GO:0008152	AT2G21160.1	AtUGT85A2,UGT85A2	UDP-glycosyltransferase family protein		UDP-glucosyltransferase family protein
Sapur.008G072800.1	0.27472894	0.418112761	0.447365199	0.934611	0.34968648	0.41761797	grey	0.06852661	0.391796518	GO:0016757	AT3G03240.1		Glycosyltransferase family 61 protein		glycosyltransferase, putative
Sapur.005G137300.1	0.36868309	0.177127197	0.198004514	0.93606705	0.35045158	0.35200373	grey	0.15534865	0.052068489		AT1G64780.2				histone chaperone domain CAF2 protein
Sapur.006G035500.1	0.15833857	0.862908491	0.921511436	0.934225	0.35182543	0.4178181	grey	0.17463896	0.028700778		AT4G20960.1	ACA4,ATACA4	alpha carbonic anhydrase 4		eukaryotic-type carbonate dehydratase
Sapur.016G147800.1	0.20866214	0.710682354	0.76082291	-0.93407	0.35202748	0.41789384	grey	-0.26329091	0.00086335						NA
Sapur.004G204500.1	274.3014965	0.045607029	0.04638307	0.934084	0.35207072	0.41798384	grey	0.05593931	0.400153778		AT5G46030.1				heat- and acid-stable phosphoprotein
Sapur.003G196600.1	2.34547465	0.162884844	0.17239656	-0.93323	0.35370315	0.41835245	grey	-0.07544662	0.347662484		AT4G28820.1		HIT-type Zinc finger family protein		HIT zinc finger protein, putative
Sapur.009G082100.1	0.10750159	0.875164882	0.917891059	0.932768	0.35369509	0.41867065	grey	0.02348353	0.686325511		AT3G19190.1		alpha/beta-hydrolases superfamily protein		NA
Sapur.001G184900.1	24.8519502	0.088351149	0.094764291	0.932522	0.35166746	0.41877629	grey	0.20281975	0.01984094	GO:0016021,GO:0006665,GO:0004348	AT5G49900.1		Beta-glucosidase, GBA2 type family protein		Non-lysosomal glucosylceramidase
Sapur.008G184400.1	1.68148766	0.070842159	0.076076314	0.932513	0.35187528	0.41877629	grey	0.08752125	0.275342511		AT5G54481.1		DEAD/DEAH box helicase		NA
Sapur.013G079100.1	2.70375144	0.144442553	0.155016623	-0.93179	0.35146351	0.41920575	grey	-0.27840089	0.134787482		AT4G13070.1		RNA-binding CRS1 / YhbY (CRM) domain protein		NA
Sapur.003G139500.4	2.22782464	0.432139604	0.477122984	0.931711	0.35161609	0.41937765	grey	-0.06111609	0.474092917	GO:0016747	AT5G48830.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase		hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase
Sapur.7001200.1	162.0697266	0.060341203	0.064860603	-0.93143	0.35182922	0.41939371	grey	-0.06771019	0.39945433		AT5G50660.1				NA
Sapur.008G051000.4	1.30450828	0.208205104	0.225608831	-0.93088	0.35193836	0.41952887	grey	0.07310534	0.362872915	GO:0016192,GO:0016020	AT5G55530.2		transducin family protein / WD-40 repeat family protein		syntaxin-binding protein 5 (tomosyn)
Sapur.019G092800.1	183.4497322	-0.40883441	0.439776042	-0.92964	0.35256339	0.42066095	grey	-0.10623649	0.185306045	GO:0071345,GO:0005515,GO:0043531	AT5G17680.1		disease resistance protein (TIR-NBS-LRR class), putative		TIR-NBS-LRR resistance protein
Sapur.7124200.1	0.26484818	-0.405278379	0.436790778	-0.92888	0.35284994	0.42092214	grey	-0.20105062	0.01157437		AT5G28455.1	CLE25	CLAVATA/ESR-RELATED 25		CLAVATA/ESR-RELATED 25
Sapur.7168400.1	4.90126864	0.218202828	0.234738866	0.928811	0.35287007	0.42092421	grey	-0.08892048	0.279392134						NA
Sapur.019G094200.1	16.57509607	0.275119365	0.296253207	0.928663	0.35308381	0.42101572	grey	0.07562139	0.34756536		AT5G49960.1				NA
Sapur.7107900.1	137.4561934	0.027205432	0.029324262	-0.92862	0.35308659	0.42102188	grey	0.06044957	0.411476578						NA
Sapur.005G047000.1	25.25402911	-0.49175591	0.52957516	-0.928	0.35360662	0.42130023	grey	-0.15815638	0.046957905	GO:0006355,GO:0003677					NA
Sapur.011G171300.1	1.13287134	0.351810754	0.378275563	0.928067	0.35347249	0.42145344	grey	0.08017926	0.317090456		AT3G03730.1	ATFLA11,FLA11	Fasciclin-like arabinogalactan-protein 11		fasciclin-like AGP protein
Sapur.005G002200.1	308.6227783	0.053131408	0.059535019	0.927783	0.35352033	0.42149686	grey	0.08094074	0.31338346		AT5G05790.1		O-Glycosyl hydrolases family 17 protein		glycoside hydrolase family 17 protein
Sapur.006G200300.1	5.54896249	0.362723284	0.388502795	-0.92767	0.35357931	0.42153032	grey	-0.08327622	0.297739491		AT2G25640.1	emb2410	embryo defective 2410		NA
Sapur.003G164200.1	27.72042408	0.562009627	0.605939873	-0.92751	0.35362682	0.42229155	grey	-0.16322416	0.043149964		AT1G52230.1		Family of unknown function (DUF736)		proteinase inhibitor I4, serpin
Sapur.005G037400.1	0.61287869	-0.329066291	0.354788574	-0.9275	0.35388276	0.42229155	grey	-0.12288119	0.127096312		AT1G04940.1	AT1CYS1,CYSD1	cysteine synthase D1		cysteine synthase
Sapur.004G054045.1	36.34013871	-0.206862266	0.218581638	0.927102	0.35387829	0.42187882	grey	0.06869323	0.279536786		AT5G9370.1	AT5RL1	PRP38 family protein		pre-mRNA-splicing factor 38-associated hydrophilic carboxy-terminal protein
Sapur.7134400.1	0.82818798	-0.24800089	0.242531165	-0.92689	0.35382840	0.42197255	grey	-0.13181595	0.098839455						NA
Sapur.005G087000.1	0.15669854	0.618518529	0.667410304	0.92674	0.35409344	0.42266614	grey	-0.43050614	1.89E-08		AT5G66030.3		Protein of unknown function, DUF547		electron transporter, putative
Sapur.7154600.1	2.36485438	0.146506225	0.158095056	-0.9267	0.35408341	0.42265528	grey	-0.07561758	0.358839758	GO:0004648,GO:0005524,GO:0004672	AT5G50860.1		Protein kinase superfamily protein		NA
Sapur.004G208300.2	49.16287047	0.072054152	0.078875202	-0.9262	0.35454199	0.42269551	grey	-0.06627606	0.40931597		AT5G27760.3	AT5ART32,5ART32	Interferon-related developmental regulator family protein / IFRD protein family		interferon-related developmental regulator
Sapur.7111900.1	202.5712037	0.273345912	0.295253172	0.925802	0.35454003	0.42253163	grey	0.14285605	0.075048648	GO:0016853,GO:0005975	AT5G57330.1		Galactose mutarotase-like superfamily protein		NA
Sapur.7195600.1	0.10176264	0.725874645	0.784606447	0.92579	0.35453127	0.42253163	grey	0.10063138	0.206-05						NA
Sapur.7141900.1	4.31370007	0.134603637	0.145416104	0.925645	0.35463075	0.42267482	grey	0.07364048	0.331786868						NA
Sapur.016G048400.3	0.66551853	0.272187931	0.294127284	0.28606295	0.35516	0.42548713	grey	-0.07342675	0.367189469		AT3G75530.2	AGA1,GK-2	guanylate kinase		guanylate kinase
Sapur.019G101700.1	4.45087076	0.15064027	0.162846862	0.925453	0.35483534	0.42294156	grey	0.08619342	0.364335994	GO:0003899,GO:0003677,GO:0003249	AT4G18090.1	NRPD28	nuclear RNA polymerase D28		NA
Sapur.7115900.1	0.16884135	0.763792381	0.8224216	0.925052	0.35483959	0.42294156	grey	0.21347709	0.007842564						NA
Sapur.017G051100.1	11.01076368	0.088511592	0.096796475	0.924572	0.35513975	0.42364588	grey	-0.20045215	0.018122276		AT2G33490.1		hydroxyproline-rich glycoprotein family protein		hydroxyproline-rich glycoprotein family protein, putative
Sapur.016G082200.1	21.06208683	-0.079532079	0.086067372	-0.92407	0.35541071	0.42387825	grey	-0.06904155	0.390197955	GO:0005515	AT4G30040.2	Igd2	IQ-domain 2		IQ calmodulin-binding motif protein
Sapur.006G053600.3	1.08283908	0.277788549	0.246767458	0.923015	0.35599338	0.42432127	grey	0.05234229	0.515155371		AT5G25810.1		Protein of unknown function, DUF547		RuBisCO/ATP-BC domain-containing protein
Sapur.006G116700.3	0.97015703	0.254500553	0.275876623	0.923523	0.35625088	0.42491797	grey	0.05709262	0.47756885		AT4G39235.1				hypothetical protein
Sapur.15W0G051200.1	1.49811814	0.162319306	0.176108834	-0.9174	0.35684649	0.42482945	grey	-0.09281915	0.245717616		AT3G60160.1		Plant protein of unknown function (DUF247)		NA
Sapur.003G127700.3	7.30018515	-0.09379825	0.105671356	-0.9215	0.35678989	0.42495979	grey	0.07854831	0.321487448	GO:0016787	AT3G09970.1		Calcineurin-like metallo-phosphoesterase superfamily protein		calcineurin-like metallo-phosphoesterase
Sapur.003G071300.1	14.11650000	0.127907451	0.139067253	0.92365203	0.35682607	0.42528117	grey	-0.07028275	0.224532044		AT5G18670.1		Ankyrin repeat family protein		serine/threonine protein phosphatase 6 regulatory ankyrin repeat subunit A, putative
Sapur.016G127200.1	0.20733415	0.502728571	0.545712096	0.921234	0.35683238	0.42531125	grey	0.14117386	0.077797361	GO:0005515	AT3G44430.1		DNA-binding bromodomain-containing protein		bromodomain protein
Sapur.003G078800.1	29.60256339	-0.176486784	0.191635534	-0.92087	0.35718473	0.42542516	grey	-0.08083234	0.318758394		AT4G21490.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein		proteinase inhibitor/seed storage/LTP family protein
Sapur.012G289000.1	0.89519287	0.130968248	0.142235597	0.920784	0.35763242	0.42580545	grey	0.03893116	0.628353643						hypothetical protein
Sapur.006G077200.1	0.26487905	0.590768202	0.641729152	0.920588	0.35725533	0.42587022	grey	0.14573406	0.08576692	GO:0055114,GO:0016491,GO:0005507	AT5G60220.1	LAC7	laccase 7		laccase
Sapur.006G031600.1	0.54855159	0.303416575	0.329609794	0.91906	0.35771873	0.42637074	grey	0.08052612	0.315493788		AT4T9320.1	ATGLDH,GLDH	L-galactono-1,4-lactone dehydrogenase		NA
Sapur.15W0G091600.1	728.4967441	0.028193134	0.03065731	0.91602	0.35770305	0.42605787	grey	0.03701579	0.641331829	GO:0005454	AT1T8780.1	ATHIP2,ATTIDX,HIP,TIDX	tetratocopeptide domain-containing protein		TPR repeat thioredoxin
Sapur.005G165600.2	11.91512522	0.07	0.076224156	0.91605	0.35809762	0.42696062	grey	-0.06017626	0.456577712	GO:0102376,GO:0005798	DGL1	DGL1	dichtyl diphosphoglycosyltransferase-phosphoglycosyltransferase 48kDa subunit family protein		dolichyl-diphosphoglycosyltransferase-protein glycosyltransferase, putative
Sapur.006G125100.16	0.24386098	0.468042569	0.509443052	0.916698	0.35825377	0.42602437	grey	0.13361147	0.095261488		AT5G58550.1				hypothetical protein
Sapur.7131200.1	27.13769664	0.047877774	0.058724483	0.916253	0.35846164	0.42633344	grey	0.06979748	0.382406397	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT3G19570.1	CYP82C2	cytochrome P450, family 82, subfamily C, polypeptide 2		cytochrome P450 family protein
Sapur.012G088800.1	55.0809292	0.071813834	0.078280266	-0.91733	0.35871719	0.42742671	grey	-0.06829431	0.391918862		AT5T61300.1,CLL8	CLL8			CLL8 protein
Sapur.012G088500.1	2.16788557	0.180288444	0.203041587	0.916063	0.35895125	0.42781068	grey	-0.06569602	0.386692245	GO:0006355,GO:0005739,GO:0003690	AT5G65620.1		Mitochondrial transcription termination factor family protein		mTERF protein
Sapur.007G088100.3	65.80603658	0.084953367	0.092602789	0.915526	0.35930984	0.42795079	grey	0.04806677	0.549968216	GO:0009231,GO:0009235,GO:0008686	AT5G65300.1	ATGCH,ATRIBA3,GCH_RFD1	GTP cyclohydrolase II		3%2C4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II
Sapur.001G037500.1	0.43559704	0.443509661	0.483758587	0.916472	0.35961644	0.42830226	grey	0.07683857	0.339785552						NA
Sapur.7124000.1	0.36880505	0.321168661	0.3504473	0.91646	0.35961786	0.42831294	grey	-0.16180866	0.042918863		AT5G54750.3				NA
Sapur.7145400.1	3.98309528	0.164951942	0.18004889	0.915946	0.35969532	0.42821118	grey	0.10554568	0.188309884	GO:0071651,GO:0055115,GO:0043531	AT5G14080.1		Disease resistance protein (TIR-NBS-LRR class) family		NA
Sapur.016G039600.2	7.09043625	0.174441449	0.190251191	0.915819	0.35970997	0.42827471	grey	0.05797287	0.470836497	GO:0016021,GO:0008840	AT4G19810.1	GPT	UDP-glucose:hexadecanoate dihydroxyacetone phosphate acyltransferase		UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase
Sapur.006G107800.3	2.10805042	0.161841408	0.176476934	-0.91567	0.35984163	0.42854205	grey	0.10595737	0.18658434		AT4G16660.1		heat shock protein 70 (Hsp 70) family protein		heat shock 70 kDa protein
Sapur.003G191300.1	6.15863107	0.185444449	0.203082614	0.915663	0.35987267	0.42857564	grey	-0.05817865	0.468767522	GO:0016887,GO:0005524,GO:0005085,GO:0046626,GO:0016021,GO:0008810	AT5G27940.1	PGF13	F-glycosyltransferase 13 protein		ABC transporter family protein, group MDR/PGP protein PgAbCB1B protein
Sapur.003G169800.1	190.2398882	0.034612443	0.037808819	0.915435	0.35963156	0.42868345	grey	0.06038829	0.412395597		AT3G21190.1		Chaperonin Cmo1-domain superfamily protein		chaperone protein Dnaj
Sapur.006G085700.1	66.84792984	0.083403179	0.091128429	0.915268	0.35964051	0.42879076	grey	0.05189463	0.513845391	GO:0016758,GO:0008152	AT2G29210.1		Exostosin family protein		enhancyanidin 3-O-galactosyltransferase
Sapur.003G105400.1	2.00144869	0.029392023	0.032028221	0.914663	0.36038652	0.42904704	grey	-0.01001856	0.900891012	GO:0006508,GO:0005138	AT4G45520.1	RPN12a	regulatory particle non-ATPase 12A		26S proteasome non-ATPase regulatory subunit
Sapur.003G165200.1	74.5748882	0.062401729	0.069479205	0.914466	0.36047666	0.42918869	grey	-0.04846256	0.545177118		AT1G49530.1		Vacuolar protein sorting-associated protein 26		NA
Sapur.002G094400.1	0.17609583	0.570707616	0.624116607	-0.91442	0.36069749	0.42922714	grey	-0.27631363	0.00045137		AT1G75150.1				hypothetical protein
Sapur.006G054000.1	83.19837633	0.153295547	0.169853391	0.914292	0.36058228	0.42908997	grey	0.08174705	0.387809943		AT1G51810.1		Protein of unknown function (DUF567)		tubby C 2 protein
Sapur.7059000.1	5.28607197	0.114261407	0.152095657	0.914022	0.36075137	0.42943396	grey	0.1045256	0.192639094	GO:0016757	AT3G18180.1		Glycosyltransferase family 61 protein		NA
Sapur.013G031000.1	3.76284752	0.184653891	0.201938784	-0.91342	0.36109625	0.42992183	grey	-0.06719138	0.455101295	GO:0010468,GO:0005777	AT5G62200.1		Putative endonuclease or glycosyl hydrolase		NYN domain protein
Sapur.016G097200.1	10.72606469	0.107329304	0.117396293	0.913407343	0.36167363	0.43005574	grey	-0.07445677	0.354508812		AT4G34170.1		ankyrin repeat family protein		NA
Sapur.008G172200.1	0.16214704	0.583233401	0.63915168	-0.91256	0.36147236	0.4301097	grey	-0.25422742	0.00119277						NA
Sapur.016G039300.1	39.89000344	0.070076627	0.08137107	0.912424	0.36154147	0.43075121	grey	0.07697929	0.337936475		AT1T1583.3		LETM1-like protein		NA
Sapur.006G189800.1	280.585276	0.060352021	0.066090389	0.911664	0.36195818	0.43026856	grey	-0.05868174	0.4653665	GO:0016020,GO:0008378,GO:0004886	AT3G26100.1		Galactosyltransferase family protein		beta-1%2C3-galactosyltransferase, putative
Sapur.006G030300.1	0.11614794	0.760270553	0.832156661	0.910662	0.36205727	0.43070074	grey	0.31275458	1.66E-05		AT5G20250.1		Exostosin family protein		exost

Sapur.008G171800.3	0.380780565	0.315555149	0.358779846	0.879523	0.379117735	0.448845216	grey	0.038655155	0.63076034		AT4G03000.2		RING/U-box superfamily protein	E3 ubiquitin-protein ligase RF4, putative
Sapur.010G175400.1	1490.574616	-0.04877826	0.055470158	-0.87936	0.3792059	0.448933527	grey	-0.060615865	0.450765716		AT3G52250.1		Duplicated homeodomain-like superfamily protein	nuclear receptor corepressor, putative
Sapur.001G162800.1	54.77290633	0.081972777	0.09325934	0.878977	0.379413969	0.449147701	grey	0.039366218	0.624483898		AT1G79770.1		Protein of unknown function (DUF1677)	DUF1677 family protein
Sapur.008G069800.1	2.248299784	-0.157700301	0.179569242	-0.87821	0.379827357	0.449605268	grey	-0.105457858	0.188680532	GO:0003723	AT5G15270.2		RNA-binding KH domain-containing protein	K-like RNA-binding domain protein
Sapur.008G009400.1	788.1953397	-0.058363565	0.066457123	-0.87821	0.379827683	0.449605268	grey	-0.073227282	0.362070189		AT3G10650.1			hypothetical protein
Sapur.004G123000.1	0.877134473	-0.249007333	0.283560197	-0.87815	0.379864339	0.449632566	grey	-0.049673748	0.536695248		AT2G21240.1	ATBPC4,BBR,BPC4	basic pentacysteine 4	GAGA-binding transcriptional activator BBR/BPC4-like protein
Sapur.017G125500.1	3.036606195	0.231630232	0.263825571	0.877967	0.379961449	0.449731416	grey	0.092333916	0.250080344	GO:0060236,GO:0032147,GO:0005874,GO:0005819	AT5G37478.1		TPX2 (targeting protein for Xklp2) protein family	microtubule-associated protein
Sapur.002G021400.1	5889.117105	0.046035456	0.052471246	0.877346	0.380298547	0.450114305	grey	0.04696033	0.559199089	GO:0008234,GO:0006508	AT4G39090.1	RD19,RD19A	Papain family cysteine protease	cysteine protease-like protein, putative
Sapur.006G221500.1	0.211307701	0.507512347	0.579294825	0.876086	0.380983039	0.450876052	grey	0.09103384	0.256839931	GO:0016020,GO:0004970	AT2G29110.1	ATGLR2.8,GLR2.8	glutamate receptor 2.8	glutamate receptor
Sapur.016G144400.1	319.2241544	-0.049831722	0.056885766	-0.876	0.381032029	0.450917895	grey	-0.078726991	0.327043793	GO:0016773.GO:0005975.GO:0005524.GO:0046835.GO:0005536.GO:0004396.GO:000167	AT1G50460.1	ATHKL1,HKL1	hexokinase-like 1	NA
Sapur.018G079300.2	0.206632622	0.500468732	0.571453562	0.875782	0.381148568	0.45103967	grey	0.160483687	0.044662512		AT3G18430.1		Calcium-binding EF-hand family protein	calcineurin subunit B
Sapur.017G036900.1	12.39108494	0.455885569	0.520573128	0.875738	0.381172588	0.451051956	grey	0.150595948	0.059749951		AT5G09450.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.15WG013300.1	0.958518953	0.252952629	0.288856195	0.875704	0.381190776	0.451057341	grey	0.038268893	0.634180936	GO:0008270,GO:0005515	AT5G53110.1		RING/U-box superfamily protein	RING finger protein
Sapur.001G046000.1	277.2411207	0.03593608	0.04105227	0.875374	0.38137057	0.451253944	grey	0.045531969	0.571224728		AT1G27385.1			DUF493 family protein
Sapur.017G011400.1	18.67616633	0.129753146	0.148262907	0.875156	0.381489129	0.451361932	grey	0.067343019	0.402022543		AT5G67550.1			transmembrane protein, putative
Sapur.004G164000.2	0.405063376	-0.303770702	0.347241978	-0.87481	0.381677378	0.451568507	grey	-0.110027483	0.17012812		AT5G22875.1			transmembrane protein, putative
Sapur.005G204200.1	324.0424552	0.085809742	0.098114058	0.874592	0.3817961	0.451692811	grey	0.010785982	0.893345736	GO:0008270,GO:0005515	AT1G20823.1		RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.019G004900.1	7.772350875	0.247007701	0.28263331	0.873951	0.382144867	0.452073085	grey	0.061287805	0.445752964		AT4G15093.1		catalytic LigB subunit of aromatic ring-opening dioxygenase family	NA
Sapur.005G123300.1	3.023374739	0.150489585	0.172216768	0.873838	0.382206393	0.452129698	grey	0.065265909	0.416728011	GO:0016567,GO:0004842,GO:0005515	AT2G23140.1		RING/U-box superfamily protein with ARM repeat domain	U-box protein
Sapur.003G128800.1	202.2621393	-0.061139013	0.070006355	-0.87334	0.382480408	0.452437662	grey	-0.114387039	0.153724427		AT5G43260.1		chaperone protein dnaJ-related	drought-induced protein
Sapur.013G035700.1	574.6315257	-0.047405558	0.054306577	-0.87292	0.38270406	0.452686029	grey	-0.058886187	0.463813612	GO:0006468,GO:0005524,GO:0004672	AT3G04910.1	ATWNK1,WNK1,ZIK4	with no lysine (K) kinase 1	Serine/Threonine-kinase WNK1
Sapur.005G011800.1	47.20797973	-0.122005061	0.139910973	-0.87202	0.383197879	0.453253939	grey	-0.072665904	0.365771874	GO:0048544,GO:0006468,GO:0004672	AT4G21390.1	B120	S-locus lectin protein kinase family protein	NA
Sapur.018G046100.1	657.2988937	-0.028488492	0.032674477	-0.87189	0.383269343	0.453322257	grey	-0.082292903	0.305539532	GO:0005634	AT2G26460.1	SMU2	RED family protein	Red-like protein amino-terminal region protein
Sapur.018G051400.2	5.345807319	-0.107714602	0.123603026	-0.87146	0.383505206	0.453585009	grey	-0.045592522	0.57071246	GO:0016787	AT5G20070.1	ATNUDT19.ATNUDX19.NUI	nudix hydrolase homolog 19	nudix hydrolase superfamily protein
Sapur.003G009100.1	0.431054248	-0.345108598	0.396109849	-0.87124	0.38362057	0.453705229	grey	-0.099497572	0.215042907					NA
Sapur.013G120200.1	3.751973039	0.198322272	0.227778659	0.87068	0.383929025	0.454037565	grey	0.066477343	0.408113495					NA
Sapur.007G086000.1	30.15864498	0.064399192	0.073970771	0.870603	0.383970831	0.454070769	grey	0.075639297	0.34643143	GO:0030247	AT1G10380.1		Putative membrane lipoprotein	wall-associated receptor kinase galacturonan-binding protein
Sapur.018G033700.1	197.6892339	-0.055900595	0.064215246	-0.87052	0.384016808	0.454108903	grey	-0.072569068	0.366412762	GO:0016020,GO:0006810,GO:0005215	AT1G52190.1		Major facilitator superfamily protein	nitrate transporter, putative
Sapur.016G011700.1	611.4201853	-0.064918632	0.074593131	-0.8703	0.384134793	0.454232183	grey	-0.06892942	0.39100168		AT3G51970.1	ASAT1,ATASAT1,ATSAT1	acyl-CoA sterol acyl transferase 1	NA
Sapur.006G152800.1	126.6600302	0.05782783	0.066458362	0.870136	0.384225953	0.454323734	grey	0.062440521	0.437227267					NA
Sapur.012G003600.3	1.71856597	0.181031631	0.208145035	0.869738	0.38444364	0.454548635	grey	0.055077272	0.4932671		AT3G49490.1			NA
Sapur.017G002400.1	0.136641843	0.757994697	0.872248887	0.869012	0.3848406	0.454973624	grey	0.224081527	0.004783472	GO:0055114,GO:0016491,GO:0008270	AT5G16970.1	AER,AT-AER	alkenal reductase	NADP-dependent alkenal double bond reductase
Sapur.15WG084300.1	11.58545278	-0.109961692	0.12656817	-0.86879	0.384959706	0.455093731	grey	-0.060763839	0.449659111		AT1G07400.1		HSP20-like chaperones superfamily protein	Hsp20/alpha crystallin family protein
Sapur.012G039200.2	11.77224524	-0.091954355	0.105859144	-0.86865	0.385039585	0.455171893	grey	-0.082286418	0.305577774		AT5G16110.1			hypothetical protein
Sapur.006G062400.1	1.641972697	0.216281561	0.249005769	0.868581	0.385076612	0.455199395	grey	0.022618513	0.778572048		AT2G19090.1		Protein of unknown function (DUF630 and DUF632)	transcription factor bZIP106, putative
Sapur.006G223400.1	0.179575557	0.55260711	0.636272893	0.868506	0.385117145	0.455231038	grey	0.113312276	0.157653332		AT2G24580.1		FAD-dependent oxidoreductase family protein	sarcosine oxidase
Sapur.010G151600.2	0.975941869	-0.225287894	0.259415332	-0.86844	0.385150882	0.455254647	grey	-0.019812204	0.805460371	GO:0003993	AT2G39920.2		HAD superfamily, subfamily IIIB acid phosphatase	acid phosphatase, putative
Sapur.010G013000.2	0.572388079	-0.28192787	0.324645086	-0.86842	0.38516515	0.455255242	grey	-0.108645746	0.175589111	GO:0008270,GO:0006355	AT3G06250.1	FRS7	FAR1-related sequence 7	FAR1-related sequence protein
Sapur.018G008500.1	569.7620558	0.043510284	0.050109177	0.86831	0.385224812	0.455309489	grey	0.079410005	0.322851276	GO:0043531	AT3G14470.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.003G120600.7	12.18667577	0.085862945	0.09889277	0.868243	0.385261377	0.455336434	grey	0.089972993	0.262447944	GO:0042393	AT5G13960.1	KYP,SDG33,SUVH4	SU(VAR)3-9 homolog 4	SAD/SRA domain protein
Sapur.003G163100.5	0.612118442	0.308115107	0.35495644	0.868036	0.385374411	0.455453752	grey	0.042496562	0.597177245		AT3G45240.2	ATSNAK2,GRIK1	geminivirus rep interacting kinase 1	Serine/Threonine kinase domain protein
Sapur.017G051200.1	0.310870828	-0.371366017	0.427852346	-0.86798	0.385406896	0.455466157	grey	-0.142733525	0.074538063		AT3G18790.1			Isy1-like splicing factor
Sapur.018G017800.1	3.43326459	0.223443087	0.257432726	0.867967	0.385412449	0.455466157	grey	0.07965788	0.321338372	GO:0000160	AT2G25180.1	ARR12,RR12	response regulator 12	NA
Sapur.009G043800.1	236.4823692	-0.042955527	0.049513852	-0.86755	0.385643112	0.455718825	grey	-0.0703266	0.381447468		AT5G13720.1		Uncharacterised protein family (UPF0114)	structural constituent of ribosome protein, putative
Sapur.005G184200.8	0.67415762	-0.252472647	0.291025993	-0.86753	0.385653812	0.455718825	grey	-0.088316157	0.271373038	GO:0004518	AT1G75380.2	ATBBD1,BBD1	bifunctional nuclease in basal defense response 1	wound responsive protein, putative
Sapur.T107200.1	1.384054569	0.218431226	0.251977014	0.86687	0.386013435	0.456111191	grey	0.097850417	0.22277106					NA
Sapur.001G093800.1	523.343508	-0.044423581	0.051251268	-0.86678	0.386062491	0.456129637	grey	-0.10208056	0.203312503		AT4G22850.1		SNARE associated Golgi protein family	SNARE associated family protein
Sapur.T116600.1	1.647658486	-0.165328723	0.190739814	-0.86678	0.386064667	0.456129637	grey	-0.048980785	0.542399217		AT4G38620.1	ATMYB4,MYB4	myb domain protein 4	NA
Sapur.002G074500.2	0.228364558	-0.457003997	0.527443716	-0.86645	0.38624303	0.456317269	grey	-0.139697117	0.080988488	GO:0005525	AT1G78010.1		tRNA modification GTPase, putative	tRNA modification GTPase MnmE
Sapur.005G017400.3	0.958586393	-0.22070614	0.254735282	-0.86641	0.386263329	0.456324951	grey	-0.103593881	0.196658021	GO:0006355	AT3G06250.1	FRS7	FAR1-related sequence 7	FAR1 DNA-binding domain protein
Sapur.010G018000.1	1.674042988	-0.258683188	0.29868557	-0.86607	0.386450716	0.456530021	grey	-0.068443364	0.394358891		AT1G67700.2			oligopeptidase, putative
Sapur.010G188600.2	32.82728029	0.065783439	0.075971085	0.865901	0.386544454	0.456608983	grey	0.074628114	0.352935037					XS domain protein
Sapur.005G106000.1	1.019584571	0.210607355	0.243223731	0.8659	0.386545169	0.456608983	grey	0.061553418	0.443780172	GO:0006468,GO:0005524,GO:0004672	AT5G66850.1	MAPKKK5	mitogen-activated protein kinase kinase kinase 5	MAP/ERK kinase kinase-like Serine/Threonine kinase family protein
Sapur.016G146700.2	1.317950502	0.189751998	0.21941184	0.864821	0.387136965	0.457275382	grey	0.086587421	0.280902567	GO:0016021,GO:0015031,GO:0008565	AT3G20920.1		translocation protein-related	translocation protein Sec62
Sapur.008G149200.1	14.78082827	-0.159759126	0.184747185	-0.86474	0.387178998	0.457308699	grey	-0.069931895	0.384132053		AT3G26380.1		Melibiase family protein	alpha-galactosidase
Sapur.005G066400.2	0.16322621	-0.557176585	0.644710408	-0.86423	0.387462825	0.457627593	grey	-0.232307272	0.003414764		AT2G21960.1			transmembrane protein, putative
Sapur.001G130200.2	1.205776456	0.204390776	0.236519308	0.864161	0.387499421	0.457654473	grey	0.064042454	0.425534871		AT5G47420.1		Tryptophan RNA-binding attenuator protein-like	tryptophan RNA-binding attenuator-like protein
Sapur.006G134400.1	3.336580213	0.14837667	0.171716987	0.864077	0.387545686	0.457692769	grey	0.072998473	0.363576124					NA
Sapur.006G199000.1	0.308139759	0.356356736	0.412447211	0.864006	0.387584766	0.45772258	grey	0.031259909	0.697534664		AT5G11530.1	EMF1	embryonic flower 1 (EMF1)	EMBYO flowering-like protein, putative
Sapur.004G130000.2	1.59402901	0.195722179	0.226542879	0.863952	0.387614244	0.457741048	grey	0.04114478	0.608903263	GO:0008540,GO:0006511	AT4G38630.1	ATMCB1.MBP1.MCB1.RPN1	regulatory particle non-ATPase 10	26S proteasome non-ATPase regulatory subunit, putative
Sapur.013G084300.4	0.246509312	0.401772201	0.46546393	0.863165	0.388046721	0.458235406	grey	0.311354288	7.21E-05	GO:0015969	AT3G14050.1	AT-RSH2,ATRSH2,RSH2	RELA/SPOT homolog 2	guanosine-3'%2C5'-bis(diphosphate) 3'-pyrophosphohydrolase, putative
Sapur.006G009300.1	4.731513041	-0.148645516	0.172265353	-0.86289	0.388199654	0.458399635	grey	-0.064395884	0.422979767		AT5G45480.1		Protein of unknown function (DUF594)	transmembrane protein, putative
Sapur.011G116000.2	74.02055681	0.046864543	0.054329341	0.862601	0.388356888	0.45856893	grey	0.051654773	0.520555424	GO:0055114,GO:0016491	AT1G06650.2		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase-like protein
Sapur.003G139100.1	34.07353568	0.059733541	0.069251603	0.862558	0.388380398	0.458580318	grey	0.056661761	0.480895529		AT1G16000.1			GAG1At protein
Sapur.013G023500.1	25.71838354	-0.069886224	0.080000852	-0.86232	0.388512207	0.458719575	grey	-0.084529035	0.292539428		AT3G05327.1		Cyclin family protein	cyclin-dependent kinase, putative
Sapur.008G030600.1	2.043692542	0.16195901	0.187859649	0.862128	0.388617242	0.45882721	grey	0.067060182	0.404006636	GO:0016021,GO:0004252	AT3G07950.1		rhomboid protein-related	NA
Sapur.005G148300.7	0.172710062	0.57868934	0.671272744	0.862078	0.388644699	0.458843249	grey	0.131770683	0.099955517	GO:0051861,GO:0046836,GO:0017089,GO:0005737	AT3G21260.3	GLTP3	Glycolipid transfer protein (GLTP) family protein	pleckstrin domain protein
Sapur.T071600.1	0.728018451	0.25269778	0.293159299	0.861981	0.388697909	0.458889689	grey	0.096485911	0.229320558					NA
Sapur.006G005500.1	0.22675067	-0.527905714	0.612547912	-0.86182	0.388786872	0.458965007	grey	-0.150995565	0.059067854	GO:0016758,GO:0008152	AT3G21760.1	HYR1	UDP-Glycosyltransferase superfamily protein	UDP-glucose flavonoid 3-O-glucosyltransferase, putative
Sapur.003G015400.1	0.217477424	0.436265803	0.506217603	0.861815	0.38878946	0.458965007	grey	0.078026849	0.331377626	GO:0005515	AT2G19210.1		Leucine-rich repeat transmembrane protein kinase protein	LRR receptor-like kinase
Sapur.017G011900.1	0.688173618	-0.321955483	0.373657808	-0.86163	0.388890117	0.459067447	grey	-0.109816758	0.170952713		AT3G60470.1		Plant protein of unknown function (DUF247)	NA
Sapur.016G194400.1	0.361434217	0.325881168	0.378370483	0.861275	0.389086412	0.459249991	grey	-0.239006252	0.002572981	GO:0003676	AT3G23900.1		RNA recognition motif (RRM)-containing protein	RNA recognition motif (RRM) containing protein
Sapur.014G137900.1	1.361605783	-0.203043383	0.235894118	-0.86074	0.38938154	0.459581937	grey	-0.086716273	0.280184611	GO:0008152,GO:0003824	AT2G04350.2	LACS8	AMP-dependent synthetase and ligase family protein	long-chain fatty acyl CoA ligase, putative
Sapur.15WG142400.1	2.536436433	-0.193981656	0.225402036	-0.8606	0.389456763	0.459654319	grey	-0.080929066	0.313651891	GO:0046983,GO:0003677	AT4G25410.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	helix loop helix DNA-binding domain protein
Sapur.016G070000.1	0.752560025	-0.30273709	0.351793205	-0.86055	0.389483667	0.459669669	grey	-0.012513557	0.876389675		AT2G36100.1		Uncharacterised protein family (UPF0497)	casparian strip membrane protein
Sapur.T121000.1	4.298306825	-0.098804307	0.114842419	-0.86035	0.389597904	0.459771679	grey	-0.060279083	0.453289991	GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT3G43210.1	ATNACK2,NACK2,TES	ATP binding microtubule motor family protein	NA
Sapur.016G099100.1	29.22567111	-0.062409517	0.072568243	-0.86001	0.389782747	0.459973404	grey	-0.053784089	0.503487914					NA
Sapur.012G035300.1	0.204417432	0.412564521	0.479736858	0.859981	0.389799587	0.459976864	grey	0.063789419	0.427369643	GO:0005515	AT3G28890.2	AtRLP43,RLP43	receptor like protein 43	NA
Sapur.013G039700.1	112.7030445	-0.068815619	0.080101654	-0.8591	0.390283359	0.460514871	grey	-0.063383189	0.430324762		AT1G54460.1		TPX2 (targeting protein for Xklp2) protein family	targeting protein for Xklp2 protein
Sapur.003G089800.1	0.175248281	-0.601308042	0.70011345	-0.85887	0.390410978	0.460649021	grey	-0.273740893	0.000522287		AT5G23850.1		Arabidopsis thaliana protein of unknown function (DUF821)	glycosyltransferase family 90 protein
Sapur.007G121700.1	29.4991569	0.121136803	0.141114527	0.858429	0.390655614	0.460909216	grey	0.05405155	0.501364963	GO:0006355,GO:0003677	AT4G28500.1	ANAC073,NAC073,SND2	NAC domain containing protein 73	NA
Sapur.010G143800.1	350.4787764	0.061740949	0.071924535	0.858413	0.390664501	0.460909216	grey	0.038323355	0.633698172		AT2G40320.1	TBL33	TRICHOME BIREFRINGENCE-LIKE 33	PmrS/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.005G025700.1	33.30007287	-0.223210088	0.260031313	-0.8584	0.390673307	0.460909216	grey	0.193267777	0.015300059	GO:0007165,GO:0005515,GO:0043531	AT5G17680.1		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.018G064000.4	2.826179544	-0.131657753	0.153415815	-0.85818	0.390795349	0.461036754	grey	-0.058292065	0.468342994	GO:0043399,GO:0019988	AT2G40570.1		initiator tRNA phosphoribosyl transferase family protein	initiator tRNA phosphoribosyl transferase
Sapur.018G072300.1	502.4296731	-0.307321257	0.358336062	-0.85763	0.391094492	0.461373207	grey	-0.110416912	0.168612004		AT4G11650.1	ATOSM34,OSM34	osmotin 34	thaumatin-like protein
Sapur.001G026700.2	8.966735861	-0.109431552	0.127603241	-0.85759	0.391117649	0.461381872	grey	-0.032945094	0.682089611	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G46950.1	CYP709B2	cytochrome P450, family 709, subfamily B, polypeptide 2	cytochrome P450 family protein
Sapur.017G026100.1	1.979511155	0.1965022	0.229138278	0.85757	0.391129737	0.461381872	grey	0.09083451	0.257887326	GO:0030247,GO:0006468,GO:0005524,GO:0004672	AT1G66980.1	SNC4	suppressor of npr1-1 constitutive 4	NA
Sapur.008G039000.3	1.466954912	0.196232051	0.228853645	0.857457	0.391192631	0.461439605	grey	0.071473257	0.373713384	GO:0030127,GO:0008270,GO:0006888,GO:0006886	AT3G07100.1	ERMO2,SEC24A	Sec23/Sec24 protein transport family protein	protein transporter Sec24-like protein
Sapur.007G080300.3	1.58977536	0.208858832	0.2436063	0.857362	0.391244746	0.461484619	grey	-0.084003466	0.295561326	GO:0005515	AT2G22125.1	CSI1	binding	cellulose synthase-interactive protein
Sapur.001G103600.3	0.328352081	-0.399141327	0.465692493	-0.85709	0.391394022	0.461644231	grey	0.150639953	0.059674524		AT5G61450.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	2-phosphoglycerate kinase, putative
Sapur.005G031200.1	0.158796407	0.563023623	0.656924639	0.85706	0.391411901	0.461648856	grey	0.335123026	1.78E-05	GO:0055085,GO:0022857,GO:0016021	AT1G08930.2	ERD6	Major facilitator superfamily protein	NA
Sapur.013G015600.1	110.9744773	-0.156982352	0.183391862	-0.85599	0.392001042	0.462327228	grey	-0.074812898	0.35174089	GO:0005515,GO:0043531	AT4G26090.1	RPS2	NB-ARC domain-containing disease resistance protein	NA
Sapur.012G036000.1	138.8912415	-0.042895475	0.050141544	-0.85549	0.392281196	0.462624648	grey	-0.055856214	0.487164175	GO:0007165,GO:0005515,GO:0043531	AT1G27170.1		transmembrane receptors;ATP binding	TIR-NBS-LRR resistance protein
Sapur.017G128200.4	1.604409693	0.203793687	0.238422004	0.85476	0.392683806	0.463066431	grey	0.078548531	0.32814497		AT1G73390.3		Endosomal targeting BRO1-like domain-containing protein	BRO1-like domain protein
Sapur.019G014800.1	0.42369098	0.421676243	0.493537836	0.854395	0.392886184	0.463288564	grey	0.040656446	0.613164122	GO:0016829,GO:0010333,GO:0008152,GO:0000287	AT5G23960.2	ATTPS21,TPS21	terpene synthase 21	NA
Sapur.019G036200.1	10.86542011	-0.143057597	0.167611724	-0.85351	0.393378813	0.463836394	grey	-0.050312992	0.531460078		AT3G20898.1			cyclin-dependent kinase inhibitor siamese protein, putative
Sapur.008G033200.1	4.70673533	0.12491673	0.146393453	0.853295	0.393496003	0.463958033	grey	-0.100887261	0.208673113		AT5G63220.1			DUF410 family protein
Sapur.010G104600.1	310.3721718	0.033418027	0.039165172	0.853259	0.393515812	0.46396485	grey	0.042964422	0.593142622	GO:0005515	AT1G13570.1		F-box/RNI-like superfamily protein	F-box/FBD/LRR protein
Sapur.016G146100.1	129.0272731	-0.108733908	0.127485293	-0.85291	0.39370736	0.464174142	grey	-0.099771702	0.213775543					NAD(P)H-quinone oxidoreductase chain, putative
Sapur.001G080200.1	6.956000838	-0.10514534	0.123289014	-0.85284	0.393750121	0.46420801	grey	-0.064484079	0.422343556		AT2G46150.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.010G089400.1	4.821893146	0.160523588	0.188284186	0.85256	0.393903285	0.464372028	grey	0.055236133	0.492019154					NA
Sapur.002G034600.2	0.241920295	-0.419830843	0.492453017	-0.85253	0.39392014	0.464375346	grey	-0.182769986	0.021955615	GO:0006568,GO:0004834	AT3G54640.1	TRP3,TSA1	tryptophan synthase alpha chain	indole-3-glycerol phosphate lyase IGL1
Sapur.012G093500.1	0.198685275	0.504382078	0.591648485	0.852503	0.393935003	0.464376316	grey	0.141000608	0.078166461					NA
Sapur.017G026000.1	2.209697667	-0.148324597	0.174014329	-0.85237	0.394008755	0.464446702	grey	-0.046194957	0.565627765	GO:0006468,GO:0005524,GO:0004672	AT1G66980.1	SNC4	suppressor of npr1-1 constitutive 4	NA
Sapur.004G077700.2	15.75071148	-0.112142593	0.131585852	-0.85224	0.394081459	0.464515848	grey	-0.046477376	0.56325153	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT5G16000.1	NIK1	NSP-interacting kinase 1	NA
Sapur.014G049700.1	386.5523479	0.043997199	0.051633793	0.852101	0.39415812	0.464589653	grey	0.037530165	0.640744397	GO:0016765	AT2G45300.1		RNA 3\'-terminal phosphate cyclase/enolpyruvate transferase, alpha/beta	NA
Sapur.016G067400.2	0.242696942	-0.392991125	0.46122813	-0.85205	0.394184299	0.464597176	grey	-0.156587419	0.050176704	GO:0006355,GO:0005667,GO:0003700	AT2G36010.1	ATE2FA,E2F3	E2F transcription factor 3	transcription factor E2F
Sapur.017G037400.1	0.284105164	-0.370355095	0.434669321	-0.85204	0.394192597	0.464597176	grey	-0.149131265	0.062305516		AT5G09450.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.003G161100.1	3.944769355	-0.215692475	0.253180475	-0.85193	0.394251995	0.464650625	grey	-0.093994947	0.241624449	GO:0016758,GO:0008152	AT5G49690.1		UDP-Glycosyltransferase superfamily protein	NA
Sapur.001G073600.1	0.53447588	0.287850188	0.338225206	0.851061	0.394735623	0.465204033	grey	0.071419279	0.374075285	GO:0046872,GO:0005515	AT4G10930.1			PHD-finger protein
Sapur.011G024000.1	8.207894421	-0.122631603	0.144244815	-0.85016	0.395234476	0.465775345	grey	-0.076493927	0.340994055	GO:0048544,GO:0006468,GO:0004672	AT1G11340.1		S-locus lectin protein kinase family protein	NA
Sapur.15WG024500.1	246.6733354	0.103289184	0.121514165	0.850018	0.395315275	0.465853966	grey	0.054801939	0.49543396	GO:0016021,GO:0006886,GO:0005783	AT1G48440.1		B-cell receptor-associated 31-like	erwinia induced protein
Sapur.001G058200.1	59.85559928	0.053861139	0.06336797	0.849974	0.395339433	0.465854226	grey	0.089104644	0.267100236	GO:0006367,GO:0005634	AT4G20280.1	TAF11	TBP-associated factor 11	NA
Sapur.006G200700.1	5.111860748	0.121651171	0.143124652	0.849967	0.395343666	0.465854226	grey	0.080112875	0.31857327		AT5G25630.2		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.010G181600.2	0.137446866	0.673259393	0.792244902	0.849812	0.395429499	0.465938767	grey	0.17597629	0.027482869		AT2G39170.1			hypothetical protein
Sapur.15WG069700.3	0.13891007	-0.735762235	0.866361771	-0.84926	0.395739306	0.466287204	grey	-0.310091367	7.74E-05		AT5G07980.1		dentin sialophosphoprotein-related	hypothetical protein
Sapur.016G166800.1	0.12691779	-0.733792602	0.864117778	-0.84918	0.395780453	0.466319073	grey	-0.339359297	1.37E-05					NA
Sapur.003G166000.1	1.645927163	0.231737482	0.273040589	0.848729	0.396032073	0.466598916	grey	0.068334892	0.39511046	GO:0055114,GO:0051537,GO:0016491	AT4G25650.2	ACD1-LIKE,PTC52,TIC55-IV	ACD1-like	NA
Sapur.006G072200.3	0.229517798	-0.546238922	0.643624849	-0.84869	0.396052991	0.46660694	grey	-0.171300233	0.031943611	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G02560.1		Ribosomal protein S7e family protein	40S ribosomal protein S7, putative
Sapur.15WG048000.1	0.122009013	-0.696407614	0.820909052	-0.84834	0.396250255	0.466822717	grey	-0.360655179	3.48E-06	GO:0005515	AT5G42150.1		Glutathione S-transferase family protein	NA
Sapur.001G078200.1	5.508494799	-0.1023152	0.120618705	-0.84825	0.396296988	0.466861143	grey	-0.249014475	0.001661434	GO:0016020,GO:0008378,GO:0006486	AT5G53340.1		Galactosyltransferase family protein	beta 1%2C3-glycosyltransferase-like protein, putative
Sapur.002G135000.1	75.14755518	-0.247953947	0.292329302	-0.8482	0.396326153	0.466865959	grey	-0.11494593	0.151710703		AT4G34160.1	CYCD3,CYCD3;1	CYCLIN D3;1	NA
Sapur.010G105000.1	0.405181949	0.299027201	0.352545292	0.848195	0.396329308	0.466865959	grey	0.042810845	0.594465641	GO:0016021,GO:0005783	AT1G13580.2	LAG13	LAG1 longevity assurance homolog 3	LAG1 longevity assurance-like protein
Sapur.012G021000.1	9.592984063	-0.138199126	0.162943645	-0.84814	0.396359656	0.466885079	grey	-0.093395399	0.24465331	GO:0005975,GO:0004553	AT5G24090.1	ATCHIA,CHIA	chitinase A	acidic endochitinase
Sapur.017G108100.2	0.986457354	-0.218384285	0.257515152	-0.84804	0.396413238	0.466931565	grey	-0.080935998	0.313610308	GO:0043531	AT3G14460.1		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.017G107200.2	13.05617024	-0.124279208	0.146558428	-0.84794	0.396470802	0.466977162	grey	0.103940605	0.195155882	GO:0003676	AT1G66260.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif, a.k.a. RRM%2C RBD protein
Sapur.008G086700.1	6.476218541	-0.110254723	0.130028985	-0.84792	0.396480186	0.466977162	grey	-0.043016822	0.592691513		AT5G49320.1		Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.016G122400.1	2.39259687	-0.225416465	0.265943647	-0.84761	0.396655265	0.467166735	grey	-0.049524479	0.537921394	GO:0005975,GO:0004553	AT2G44480.1	BGLU17	beta glucosidase 17	glycoside hydrolase family 1 protein
Sapur.002G149600.2	0.328752228	0.353116114	0.416731032	0.847348	0.396801304	0.467322093	grey	0.024023308	0.765207963		AT1G14620.1	DECOY	decoy	decoy
Sapur.006G060900.2	14.03477771	0.109650274	0.129488394	0.846796	0.39710875	0.46765982	grey	0.092634492	0.24853521	GO:0005515	AT2G19260.1		RING/FYVE/PHD zinc finger superfamily protein	PHD-finger protein
Sapur.002G041400.1	0.552801705	-0.281880924	0.332884671	-0.84678	0.397116347	0.46765982	grey	-0.117153401	0.143951165		AT3G63120.1	CYCP1;1	cyclin p1;1	cyclin-dependent kinase, putative
Sapur.013G096300.1	236.9054687	-0.049286297	0.058220895	-0.84654	0.397251753	0.467802623	grey	-0.079465435	0.32251256	GO:0008168,GO:0008152	AT1G22800.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NA
Sapur.016G265300.1	0.366734022	0.346646552	0.409514733	0.846481	0.397284318	0.467824315	grey	0.039328147	0.624819272		AT5G54300.1		Protein of unknown function (DUF761)	NA
Sapur.006G185400.3	4.330989039	0.218307372	0.258070046	0.845923	0.397595733	0.468141021	grey	0.079769596	0.320658016	GO:0018342,GO:0008318	AT4G24490.1	ATRGTA1,RGTA1	RAB geranylgeranyl transferase alpha subunit 1	NA
Sapur.003G054200.3	0.716824486	0.265491996	0.313901418	0.845781	0.397674678	0.468217304	grey	-0.135766557	0.089996661		AT5G47020.1			transmembrane protein, putative
Sapur.009G070100.1	0.142581399	0.76907453	0.909335185	0.845755	0.397689586	0.468218189	grey	0.253327536	0.001368552					NA
Sapur.002G099500.1	0.589321409	-0.342022753	0.404423011	-0.84571	0.397717071	0.46823388	grey	-0.052576302	0.513132854					transmembrane protein, putative
Sapur.T006500.1	24.21742107	-0.42309655	0.500535445	-0.84529	0.397950121	0.468491575	grey	-0.131272108	0.101256919	GO:0003677	AT3G42170.1		BED zinc finger ;hAT family dimerisation domain	NA
Sapur.013G094600.1	0.156084004	0.613202993	0.725903185	0.844745	0.3982533	0.468831808	grey	0.177892474	0.025814983	GO:0006355,GO:0003700	AT1G71520.1		Integrase-type DNA-binding superfamily protein	ethylene-responsive transcription factor ERF019
Sapur.007G094000.1	24.39908361	0.109226375	0.129323784	0.844596	0.398336339	0.468912873	grey	0.045156536	0.57440568	GO:0006355,GO:0003677	AT5G64530.1	ANAC104,XND1	xylem NAC domain 1	NAC transcription factor protein
Sapur.004G008000.1	9.378367768	-0.099725623	0.118094791	-0.84445	0.398415739	0.468989649	grey	-0.0827987	0.302566304		AT4G04630.1		Protein of unknown function, DUF584	senescence regulator
Sapur.016G174500.2	0.151345997	0.6509656	0.771326663	0.843956	0.398694113	0.46930063	grey	-0.056323353	0.483523652	GO:0008270	AT1G10200.1	WLIM1	GATA type zinc finger transcription factor family protein	transcription factor LIM1
Sapur.15WG122400.1	16.11657387	-0.113894832	0.1352167	-0.84231	0.399612579	0.470365011	grey	-0.053074606	0.509142065		AT5G45480.1		Protein of unknown function (DUF594)	NA
Sapur.002G071500.1	0.362678398	-0.416480457	0.494859278	-0.84161	0.400004095	0.470792336	grey	-0.152437569	0.056659547	GO:0005975,GO:0004553	AT1G77780.1		Glycosyl hydrolase superfamily protein	NA
Sapur.016G006600.1	16.11290855	-0.098127785	0.116643491	-0.84126	0.400200941	0.471007256	grey	-0.094145166	0.240869669		AT4G16400.1			UPA24, putative
Sapur.018G047800.3	0.273364017	-0.393410722	0.467774348	-0.84103	0.40033297	0.471145879	grey	-0.171495037	0.0317462	GO:0006334,GO:0005634,GO:0003677,GO:0000786	AT1G72740.2		Homeodomain-like/winged-helix DNA-binding family protein	single MYB histone
Sapur.T053000.1	3.263824517	0.120358228	0.143144633	0.840816	0.400451296	0.471268366	grey	0.067315899	0.402212535	GO:0046938,GO:0046872,GO:0016756,GO:0010038	AT5G44070.1	ARA8,ATPCS1,CAD1,PCS1	phytochelatin synthase 1 (PCS1)	phytochelatin synthase
Sapur.010G005400.1	38.79355741	0.065978048	0.078539855	0.840078	0.400864769	0.471738174	grey	0.091781237	0.25293874		AT3G16760.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.002G073800.1	8.398443084	-0.083495295	0.099435109	-0.8397	0.401078679	0.471956318	grey	-0.08166175	0.30927646	GO:0005515	AT1G22050.1	MUB6	membrane-anchored ubiquitin-fold protein 6 precursor	membrane-anchored ubiquitin-fold protein
Sapur.019G092700.4	6.165547547	0.428687252	0.510653248	0.839488	0.401195545	0.47207704	grey	-0.063940573	0.426273067	GO:0043531	AT5G17680.1		disease resistance protein (TIR-NBS-LRR class), putative	TIR-NBS-LRR resistance protein
Sapur.018G001900.1	619.1301013	0.040842489	0.048673647	0.839109	0.40140821	0.472310474	grey	0.06271102	0.43524016		AT2G24390.1		AIG2-like (avirulence induced gene) family protein	AIG2-like protein
Sapur.002G009100.1	0.204537558	0.536158891	0.639021453	0.839031	0.401451842	0.47234501	grey	0.090461734	0.259853966	GO:0005515	AT5G42220.1		Ubiquitin-like superfamily protein	scythe/bat3 protein, putative
Sapur.T092500.1	1.741234509	0.156022346	0.185984006	0.838902	0.40152433	0.472413493	grey	0.061386727	0.445017665					NA
Sapur.010G020600.1	0.713488435	-0.276458512	0.329665954	-0.8386	0.401692716	0.472594796	grey	-0.092796889	0.247702643					NA
Sapur.005G058400.1	791.7165589	0.031907505	0.038060861	0.838329	0.401846232	0.472758592	grey	0.082927967	0.301809497	GO:0005515,GO:0005634,GO:0003677	AT2G22300.2	CAMTA3,SR1	signal responsive 1	calmodulin-binding transcription activator
Sapur.008G112500.2	1.732797759	-0.158498286	0.189150161	-0.83795	0.402059057	0.472992148	grey	-0.054041428	0.501445215		AT1G25220.1	ASB1,TRP4,WEI7	anthranilate synthase beta subunit 1	anthranilate synthase component II
Sapur.012G043100.1	3.087263535	0.223243095	0.266470047	0.837779	0.402154654	0.473087784	grey	0.074643884	0.352833022	GO:0016788	AT1G29660.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.004G080700.1	13.62835106	-0.082343133	0.098300266	-0.83767	0.402216357	0.473143541	grey	-0.076928926	0.338247375	GO:0006468,GO:0004672	AT1G26150.1	ATPERK10,PERK10	proline-rich extensin-like receptor kinase 10	tyrosine kinase domain protein
Sapur.010G136800.1	13.71937877	0.114603578	0.136925964	0.836975	0.402606747	0.473585928	grey	0.072066858	0.369747632					hypothetical protein
Sapur.011G064000.1	0.240643421	0.353694283	0.422732624	0.836686	0.402769337	0.473760333	grey	0.05548612	0.490058775	GO:0055114,GO:0016491,GO:0008270	AT5G63620.2		GroES-like zinc-binding alcohol dehydrogenase family protein	NA
Sapur.007G025800.1	0.810545681	0.235685384	0.281724814	0.83658	0.402828614	0.473813207	grey	0.046152946	0.565981646					NA
Sapur.019G093300.3	0.331413426	-0.380545776	0.454907029	-0.83654	0.402853841	0.473826029	grey	-0.078575381	0.327979144	GO:0005515,GO:0043531	AT5G17680.1		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.005G092800.1	90.09912731	0.15751627	0.18835167	0.836288	0.402992818	0.473972634	grey	0.075243445	0.348968369		AT3G51160.1	GMD2,MUR1,MUR_1	NAD(P)-binding Rossmann-fold superfamily protein	NA
Sapur.010G108700.5	1.080164865	-0.214441307	0.256433494	-0.83625	0.403016913	0.473984118	grey	-0.074913077	0.351094551	GO:0008299	AT2G34630.1	GPPS,GPS1	geranyl diphosphate synthase 1	geranyl diphosphate synthase
Sapur.013G070300.1	0.279049828	-0.40163858	0.480316806	-0.8362	0.40304513	0.474000449	grey	-0.175780681	0.027658198		AT1G08710.2		F-box family protein	F-box protein SKIP24
Sapur.016G271700.1	0.340402417	0.416161968	0.498496988	0.834833	0.403811481	0.474884828	grey	0.011560242	0.885739974		AT4G27290.1		S-locus lectin protein kinase family protein	NA
Sapur.005G095600.1	141.3767514	0.061861647	0.074131516	0.834485	0.40400767	0.475098655	grey	0.069572051	0.386589485		AT5G44230.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.019G058500.1	14.07016063	-0.139855291	0.167622456	-0.83435	0.404085482	0.475173264	grey	-0.053489133	0.505834542		AT5G36100.1			NA
Sapur.005G007400.5	1.681399103	0.165923803	0.198945535	0.834016	0.404271843	0.475372185	grey	0.047920135	0.551187284		AT1G08060.1	MOM,MOM1	ATP-dependent helicase family protein	chromatin remodeling complex subunit
Sapur.016G228300.6	0.176467815	0.503203362	0.603364434	0.833996	0.404283389	0.475372185	grey	-0.024973754	0.756205014	GO:0006396,GO:0003723	AT5G55100.2		SWAP (Suppressor-of-White-APricot)/surp domain-containing protein	suppressor-of-white-apricot-like protein, putative
Sapur.008G006400.1	0.404242824	-0.3558339	0.426838694	-0.83365	0.404478476	0.475584668	grey	-0.087674581	0.274883758	GO:0004857,GO:0042545,GO:0030599,GO:0005618	AT3G10710.1	RHS12	root hair specific 12	pectinesterase/pectinesterase inhibitor, putative
Sapur.006G224300.1	28.33197016	-0.070674553	0.084874293	-0.8327	0.405015742	0.476199454	grey	-0.080528417	0.316061458		AT3G29230.1		Tetratricopeptide repeat (TPR)-like superfamily protein	pentatricopeptide (PPR) repeat protein
Sapur.011G103200.2	19.40022652	-0.069987331	0.084062511	-0.83256	0.40509127	0.476271326	grey	-0.054763807	0.495734455		AT3G20390.1		endoribonuclease L-PSP family protein	perchloric acid soluble translation inhibitor protein
Sapur.002G172600.1	0.121361137	0.628259585	0.754721614	0.832439	0.405161286	0.476336712	grey	0.207216998	0.009214275		AT2G44310.1		Calcium-binding EF-hand family protein	NA
Sapur.006G139500.1	5.393531384	0.142827826	0.171692508	0.831882	0.405475817	0.476672609	grey	0.071683187	0.372307903	GO:0005515,GO:0006468,GO:0004672	AT5G57610.1		Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain	Serine/Threonine kinase domain protein
Sapur.010G044900.1	1084.54181	-0.080123487	0.096407305	-0.83109	0.405920799	0.477178763	grey	-0.079206377	0.324097552		AT2G05620.1	PGR5	proton gradient regulation 5	proton gradient regulation protein
Sapur.017G029400.1	115.4768096	0.038723119	0.046612087	0.830753	0.406113327	0.477388121	grey	0.054439697	0.498292447	GO:0016757,GO:0016020	AT4G15240.1		Protein of unknown function (DUF604)	glycosyltransferase family protein
Sapur.014G080200.1	0.138943654	0.651630134	0.784409369	0.830727	0.406127804	0.477388172	grey	0.234326415	0.003138073	GO:0046872,GO:0000166	AT4G00900.1	ATECA2,ECA2	ER-type Ca2+-ATPase 2	endoplasmic reticulum-type calcium-transporting ATPase
Sapur.001G023800.1	6.257499684	0.230391958	0.277468891	0.830334	0.406349758	0.477632096	grey	0.08163816	0.309416709	GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	Tir-NBS-LRR resistance protein, putative
Sapur.003G071400.1	421.8555211	-0.030151269	0.03633109	-0.8299	0.406593806	0.477884987	grey	-0.085967816	0.284372211		AT5G45275.1		Major facilitator superfamily protein	major facilitator protein
Sapur.15WG096600.3	0.670189607	-0.271640968	0.32740557	-0.82968	0.406721261	0.478017802	grey	-0.071085908	0.376315194	GO:0015937,GO:0005524,GO:0004594	AT4G32180.1	ATPANK2,PANK2	pantothenate kinase 2	pantothenate kinase
Sapur.016G204600.2	0.419795999	-0.30110393	0.362971546	-0.82955	0.406791878	0.47808381	grey	-0.377721879	1.08E-06		AT3G27090.1		DCD (Development and Cell Death) domain protein	Gda-1, putative
Sapur.006G148000.3	0.273416022	0.351769295	0.424137077	0.829376	0.406891433	0.47818382	grey	0.028731575	0.720940196		AT5G57880.1	ATPRD2,MPS1,PRD2	multipolar spindle 1	recombination initiation defect 2 protein, putative
Sapur.007G089900.1	2272.553932	0.038214602	0.046080709	0.829297	0.40693627	0.47821952	grey	0.069463061	0.387335668	GO:0030246,GO:0005975,GO:0004553	AT5G63810.1	BGAL10	beta-galactosidase 10	NA
Sapur.016G250900.1	0.178632954	-0.561282463	0.677777781	-0.82824	0.407532408	0.478903068	grey	-0.231827603	0.003483646		AT1G40390.1		DNAse I-like superfamily protein	NA
Sapur.014G008500.2	1.829489838	0.166005755	0.200480335	0.82804	0.407647796	0.479021644	grey	0.051336299	0.523133293	GO:0009116	AT1G27450.1	APT1,ATAPT1	adenine phosphoribosyl transferase 1	adenine phosphoribosyltransferase
Sapur.T023300.1	0.704814745	-0.225730537	0.272664178	-0.82787	0.407744035	0.479117711	grey	-0.061814071	0.441849028		AT5G67550.1			NA
Sapur.006G002200.1	355.6729109	-0.027619366	0.033364559	-0.82781	0.407780655	0.479143718	grey	-0.096481611	0.229341408	GO:0005515	AT5G47790.1		SMAD/FHA domain-containing protein	nuclear inhibitor of protein phosphatase
Sapur.005G052900.2	0.651727639	0.259756929	0.31392486	0.827449	0.407982406	0.479363747	grey	0.047727397	0.552791635	GO:0006355,GO:0003677	AT1G01720.1	ANAC002,ATAF1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC transcription factor
Sapur.018G110800.1	0.146515478	0.598815676	0.723786142	0.827338	0.408045592	0.479420956	grey	0.179940583	0.024128859		AT1G58190.1	AtRLP9,RLP9	receptor like protein 9	NA
Sapur.002G087900.1	0.106462603	0.646685923	0.782304142	0.826643	0.40843967	0.479866919	grey	0.261294814	0.000948175	GO:0016740	AT5G26780.1	SHM2	serine hydroxymethyltransferase 2	serine hydroxymethyltransferase
Sapur.016G256700.1	320.6597371	-0.038914949	0.047106828	-0.8261	0.40874739	0.480211395	grey	-0.13272984	0.097489057	GO:0055114,GO:0004616,GO:0016491,GO:0006631,GO:0003857	AT3G15290.1		3-hydroxyacyl-CoA dehydrogenase family protein	3-hydroxyacyl-CoA dehydrogenase
Sapur.T054800.1	4.865700838	0.142649313	0.172691322	0.826036	0.408783461	0.480236713	grey	0.079470249	0.322483154		AT3G54750.3			NA
Sapur.008G094900.1	0.299594259	0.308952254	0.374086648	0.825884	0.408869781	0.480321061	grey	-0.101520357	0.205816583	GO:0030163	AT1G68660.1		Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein	ATP-dependent Clp protease adaptor protein ClpS
Sapur.T180300.1	34.38634617	-0.073478977	0.088984259	-0.82575	0.408944488	0.48039176	grey	-0.084356494	0.293529223	GO:0006351,GO:0003899,GO:0003677,GO:0032549	AT3G18090.1	NRPD2B	nuclear RNA polymerase D2B	NA
Sapur.004G131200.1	5.708134469	0.226016521	0.273821056	0.825417	0.409134957	0.480598436	grey	0.080355491	0.317105171	GO:0008270,GO:0003676				NA
Sapur.011G059000.5	3.907530871	0.143990624	0.174536574	0.824988	0.409378258	0.480867156	grey	0.053142649	0.508598384		AT1G56160.1	ATMYB72,MYB72	myb domain protein 72	Myb-like DNA-binding domain protein
Sapur.T092400.1	0.968051766	-0.192771911	0.23368996	-0.8249	0.409425785	0.480905903	grey	-0.115851857	0.148488938					NA
Sapur.016G048900.1	2802.47945	-0.040112456	0.048634161	-0.82478	0.409496814	0.480972251	grey	-0.075640299	0.34642502		AT5G05170.1	ATCESA3.ATH-B.CESA3.CEV	Cellulose synthase family protein	cellulose synthase A, catalytic subunit
Sapur.006G209300.1	0.260245866	-0.388788801	0.471781112	-0.82409	0.409889982	0.481416949	grey	-0.129327862	0.106459976		AT5G27530.1		Pectin lyase-like superfamily protein	NA
Sapur.012G018600.2	0.691352032	0.248161066	0.301224669	0.82384	0.410030222	0.48154746	grey	0.073401217	0.360928007	GO:0016987,GO:0006355,GO:0006352,GO:0003700,GO:0003677	AT5G24120.1	ATSIG5,SIG5,SIGE	sigma factor E	RNA polymerase sigma factor RpoD
Sapur.008G173100.2	2.611586162	-0.143082366	0.173939216	-0.8226	0.410735608	0.482358751	grey	-0.07688069	0.338551252	GO:0005634,GO:0003677	AT5G18830.3	ATSPL7,SPL7	squamosa promoter binding protein-like 7	squamosa promoter-binding-like protein
Sapur.004G027000.6	0.16439879	0.496880976	0.604066012	0.822561	0.410757842	0.482363998	grey	-0.045196277	0.574068564	GO:0003676	AT1G60900.1		U2 snRNP auxilliary factor, large subunit, splicing factor	U2 snRNP auxilliary factor, large subunit
Sapur.005G023300.1	51.03089313	-0.230884148	0.28076322	-0.82234	0.410880739	0.482477794	grey	-0.084589798	0.292191386	GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT5G27550.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.T013600.2	0.651834239	0.318436539	0.387247495	0.822308	0.41090188	0.482480942	grey	0.067630208	0.400013853	GO:0006413,GO:0003743	AT1G71350.1		eukaryotic translation initiation factor SUI1 family protein	NA
Sapur.006G124800.1	952.8574051	-0.026625834	0.032380152	-0.82229	0.410912595	0.482480942	grey	-0.096306242	0.230192958	GO:0045454,GO:0015035,GO:0006662	AT4G29670.1	ACHT2	atypical CYS HIS rich thioredoxin 2	thioredoxin-like protein, putative
Sapur.004G145100.1	0.319916466	-0.377112714	0.458742459	-0.82206	0.411044129	0.482618251	grey	-0.121783217	0.128660183	GO:0030247,GO:0006468,GO:0004672	AT1G21270.1	WAK2	wall-associated kinase 2	tyrosine kinase family protein
Sapur.019G098400.1	0.481365297	0.326111028	0.396721461	0.822015	0.411068308	0.482629507	grey	0.1109972	0.166371508					hypothetical protein
Sapur.004G017200.1	1.673373424	-0.177292852	0.215744158	-0.82177	0.411205765	0.482773756	grey	-0.072337164	0.36795038		AT2G32235.1			hypothetical protein
Sapur.004G141500.1	403.6091812	0.070410579	0.085729976	0.821306	0.411471762	0.483051754	grey	0.05887983	0.463861948		AT5G22620.2		phosphoglycerate/bisphosphoglycerate mutase family protein	2-carboxy-D-arabinitol 1-phosphate (CA1P) phosphatase
Sapur.T100800.1	0.114497484	0.588438327	0.716657828	0.821087	0.411596793	0.48316423	grey	0.230439899	0.003690032					NA
Sapur.005G159900.1	94.23130702	0.05049669	0.061500727	0.821075	0.411603734	0.48316423	grey	0.056199185	0.484489893	GO:0043565,GO:0006355,GO:0003700	AT4G18170.1	ATWRKY28,WRKY28	WRKY DNA-binding protein 28	WRKY transcription factor
Sapur.016G194700.1	280.4354787	0.028259846	0.034418683	0.821061	0.411611397	0.48316423	grey	0.07526397	0.348836542		AT5G43490.1			hypothetical protein
Sapur.013G115600.1	0.335488456	-0.323732989	0.394312165	-0.82101	0.411642367	0.483183435	grey	-0.135099082	0.091602851	GO:0005515	AT3G59690.1	IQD13	IQ-domain 13	IQ-domain protein
Sapur.004G001100.1	0.30820458	0.33926837	0.413544549	0.820391	0.411993046	0.483577047	grey	0.073781837	0.358436407	GO:0046983,GO:0003677	AT5G60440.1	AGL62	AGAMOUS-like 62	SRF-type transcription factor (DNA-binding and dimerization domain) protein
Sapur.004G165300.4	4.733018343	-0.112090338	0.136634388	-0.82037	0.412006942	0.483577047	grey	-0.05148904	0.521896134	GO:0008270,GO:0005515	AT5G22000.2	RHF2A	RING-H2 group F2A	RING zinc finger protein, putative
Sapur.003G075000.8	0.18798041	0.586054954	0.714552239	0.820171	0.412118688	0.483691039	grey	-0.05521555	0.492180755	GO:0005515,GO:0008270	AT4G25230.2	RIN2	RPM1 interacting protein 2	E3 ubiquitin protein ligase RIN3
Sapur.016G036200.1	0.304005337	0.38273687	0.466674009	0.820138	0.412137708	0.483696198	grey	0.072286865	0.368284404		AT2G41380.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	NA
Sapur.016G097800.1	353.5059286	-0.033714862	0.041115276	-0.82001	0.412211448	0.483765575	grey	-0.07911623	0.324650271		AT2G38090.1		Duplicated homeodomain-like superfamily protein	MYB transcription factor
Sapur.007G022800.1	4.892892269	0.153722345	0.187487807	0.819906	0.412269797	0.483816884	grey	0.05168301	0.520327178					NA
Sapur.016G169800.3	64.23774233	0.076725602	0.093583002	0.819867	0.412292014	0.48382579	grey	0.0558116	0.487512626		AT4G33670.1		NAD(P)-linked oxidoreductase superfamily protein	L-galactose dehydrogenase
Sapur.012G096300.1	21.00343218	-0.070165803	0.085600472	-0.81969	0.412393174	0.483927332	grey	0.339492404	1.36E-05		AT5G05010.1		clathrin adaptor complexes medium subunit family protein	NA
Sapur.003G040800.1	1.070475666	0.228234772	0.27849615	0.819526	0.412486506	0.48401968	grey	0.075204858	0.349216287	GO:0016788	AT5G40990.1	GLIP1	GDSL lipase 1	GDSL esterase/lipase
Sapur.004G115600.1	6.82385667	-0.116827512	0.142571588	-0.81943	0.412540823	0.484066243	grey	-0.080470608	0.316410124	GO:0005975,GO:0004553	AT4G34480.1		O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase
Sapur.016G009700.1	0.784622199	0.253709661	0.309808119	0.818925	0.412829119	0.484387337	grey	0.080059414	0.318897362		AT2G44880.1		Pentatricopeptide repeat (PPR-like) superfamily protein	PPR containing protein
Sapur.013G088600.1	33.28884081	-0.062958858	0.076891027	-0.81881	0.412896932	0.484449719	grey	-0.066776309	0.406003826					NA
Sapur.010G130600.1	0.361493834	-0.33091721	0.40436328	-0.81837	0.41314816	0.484710094	grey	-0.099921162	0.213086805					NA
Sapur.006G200500.1	7.31906484	-0.141892281	0.173416875	-0.81821	0.413234457	0.484794141	grey	-0.07348225	0.360396652		AT5G25630.2		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.016G142200.3	0.226474117	-0.46203542	0.56494677	-0.81784	0.413449208	0.485028877	grey	-0.136913155	0.087289997	GO:0005515,GO:0035556,GO:0007165,GO:0006629,GO:0004435	AT2G40116.1		Phosphoinositide-specific phospholipase C family protein	phosphoinositide-specific phospholipase C
Sapur.005G162200.1	1.421860376	0.192372903	0.235233705	0.817795	0.413474362	0.485041181	grey	0.07559086	0.346740421	GO:0016021	AT4G19645.2		TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	plant/T19E23-12 protein
Sapur.019G069000.1	0.49357143	-0.304859435	0.372869907	-0.8176	0.413584097	0.485152701	grey	-0.125903383	0.116132175					NA
Sapur.003G041700.1	1093.584476	-0.030231454	0.036992367	-0.81723	0.413794183	0.485381927	grey	-0.102443294	0.201702858	GO:0019773,GO:0006511,GO:0004175,GO:0051603,GO:0005839,GO:0004298	AT1G53850.1	ATPAE1,PAE1	20S proteasome alpha subunit E1	proteasome subunit alpha type-5 protein
Sapur.009G070200.1	22.5247288	-0.1000992	0.122514725	-0.81704	0.413906647	0.485496629	grey	-0.072828922	0.36469454	GO:0005515,GO:0009958	AT2G14820.1	NPY2	Phototropic-responsive NPH3 family protein	BTB/POZ domain protein
Sapur.005G128200.2	1.189007742	-0.195999565	0.23990389	-0.81699	0.413932985	0.485510304	grey	-0.097450279	0.224677791	GO:0019904	AT1G26480.1	GF14 IOTA,GRF12	general regulatory factor 12	14-3-3 family protein Lil 1433-3 protein
Sapur.003G039900.3	1.240254479	-0.238367369	0.291772897	-0.81696	0.413950146	0.485513214	grey	-0.059827211	0.456689274		AT3G14160.1		2-oxoglutarate-dependent dioxygenase family protein	2OG-Fe(II) oxygenase family oxidoreductase
Sapur.001G121500.1	3.823900006	0.115802796	0.141822446	0.816534	0.414195	0.485765946	grey	0.028298884	0.724972536		AT1G32410.4		Vacuolar protein sorting 55 (VPS55) family protein	vacuolar protein sorting-associated-like protein
Sapur.016G052900.1	6.025166143	-0.440952828	0.540255239	-0.81619	0.414389459	0.485976774	grey	-0.111176997	0.165681828	GO:0005515	AT1G55000.2		peptidoglycan-binding LysM domain-containing protein	NA

Sapur.003G043400.2	0.84656858	-0.22661279	0.27760203	-0.81608	0.41445248	0.48603348	grey	-0.42741923	2.36E-08	AT4G47640.1	PYE	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH protein, putative
Sapur.0006234500.1	0.10818618	0.70265515	0.86133074	0.815693	0.41467522	0.48620646	grey	0.29142984	0.00021953	AT5G11040.1	AtTRS120,TRS120	TRS120	NA
Sapur.0002033300.5	0.59631564	0.28868242	0.93250488	0.815564	0.41473526	0.48610105	grey	0.06164991	0.44123407	GD:0046881,GO:0003677		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	helix loop helix DNA-binding domain protein
Sapur.0004263600.2	1.12847555	0.20031051	0.2455546	-0.81524	0.41487829	0.48447191	grey	-0.14310586	0.07304048	GO:0046506,GO:0005515		Calcium-dependent lipid-binding (CaLB domain) family protein	Arf GTPase activator, putative
Sapur.0102808300.1	0.13853834	0.12969357	0.10049867	0.815204	0.41495512	0.48615968	grey	0.07317884	0.36243472				NA
Sapur.0108105600.1	0.2784235	0.35375983	0.43397086	0.815112	0.41508035	0.48656188	grey	0.04733763	0.55042784	GO:0046483,GO:0006722		Protein kinase superfamily protein	NA
Sapur.0010611300.1	57.88898887	0.42267573	0.52806128	0.814963	0.41539347	0.48667323	grey	0.1659516	0.04278764			Alcohol dehydrogenase transcription factor Myb/SANT-like family protein	alcohol dehydrogenase transcription factor myb/SANT-like protein, putative
Sapur.0006138800.1	6.365972	0.11642423	0.14285431	0.814903	0.41527769	0.48664086	grey	0.06191266	0.44112749			Cyclopropane-fatty-acyl-phospholipid synthase	cyclopropane-fatty-acyl-phospholipid synthase
Sapur.0010611300.1	30.52940878	0.35702268	0.43813795	0.814886	0.41513735	0.48664086	grey	0.12445497	0.10242509				hypothetical protein
Sapur.0106275100.2	0.02265753	0.35168332	0.71877545	-0.81474	0.41512187	0.48676247	grey	-0.08261686	0.31704337			methyl esterase 12	polyneuridine-aldehyde esterase
Sapur.0110690100.1	0.15193586	0.88070927	1.08120728	0.814693	0.41532662	0.48689662	grey	0.19409382	0.01484047			Late embryogenesis abundant (LEA) protein-related	late embryogenesis abundant-like protein
Sapur.0102594200.1	0.32194427	0.20151106	0.44517802	-0.81388	0.41574145	0.48738845	grey	-0.19001143	0.08251968	GO:0006355,GO:0005634	IAA30	Indole-3-acetic acid inducible 30	auxin-responsive protein IAA32, putative
Sapur.0030470400.1	0.10686291	0.54661982	0.67203589	0.813388	0.41595729	0.48758146	grey	0.17505783	0.02725583	GO:0055114,GO:0020037,GO:0016705,GO:0005506	CYP86A6	cytochrome P450, family 86, subfamily A, polypeptide 6	NA
Sapur.0012630700.6	0.47352509	0.28847127	0.71818466	0.813268	0.41598491	0.48758146	grey	0.16349849	0.18241063			Protein prenylhexaprenase superfamily protein	2-Octad-Gt/Nic transferase-like protein
Sapur.0090430400.1	0.11952372	0.74100355	0.91197735	0.81274	0.41624397	0.48796768	grey	0.25055812	0.00155078				NA
Sapur.0051378500.1	0.15617555	0.31321621	0.19036529	0.81277	0.41680866	0.48820206	grey	-0.05828751	0.48375968	GO:0003677			B3 DNA-binding domain protein
Sapur.0020619300.1	1.18521782	0.23578483	0.29031178	-0.81218	0.41690403	0.48811684	grey	-0.08952601	0.26481707	GO:0055114,GO:0020037,GO:0016705,GO:0005506		cytochrome P450, family 83, subfamily B, polypeptide 1	NA
Sapur.0013338800.2	0.19118496	0.46306723	0.57027189	0.811984	0.41680044	0.48842483	grey	0.08209969	0.30681508	GO:0006355,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AGAMOUS-like 20	AGAMOUS-like 20	MADS-box transcription factor
Sapur.0006215005.1	0.11888337	0.35128228	1.02383823	0.811911	0.41684176	0.48844766	grey	0.24431571	0.00831765				NA
Sapur.0050097700.1	14.62690199	0.17109723	0.21081353	0.811237	0.41729615	0.48889529	grey	0.08770182	0.27468147			AAA-type ATPase family protein	NA
Sapur.0070291200.3	0.78092609	0.17109723	0.2753175	-0.81065	0.41730979	0.48892753	grey	-0.088587	0.27092152	GO:0001735	FCLY	farnesylcysteine lyase 1	prenylcysteine lyase
Sapur.0070272500.1	2.21967035	0.19941039	0.24578301	-0.81028	0.41778128	0.48948941	grey	-0.08910528	0.26835627				NA
Sapur.0106279400.1	0.58529362	0.29071507	0.35916406	0.8101	0.41827923	0.49004653	grey	-0.07867027	0.32732622	GO:0031225,GO:0016048,GO:0010215	COB	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family	phytochelatin synthetase-like protein
Sapur.1595G117800.1	0.96894507	0.34830391	0.43085026	0.809405	0.41857526	0.49004954	grey	0.08374183	0.29701955	GO:0016021		Nodulin MtN3 family protein	bidirectional sugar transporter SWEET14
Sapur.0102680600.1	0.17493766	0.88425344	0.71818466	0.809145	0.41888308	0.49062771	grey	0.17472358	0.06284421	GO:0005515	SALR1	SALR1 interactor, Nucleoporin protein family	NA
Sapur.0102680500.1	1.445.50081	0.07695294	0.09528814	0.807602	0.41954056	0.49098751	grey	0.05326263	0.50761144	GO:0055114,GO:0020037,GO:0016705,GO:0005506	CYP758L1,D501,T77	Cytochrome P450 superfamily protein	flavonoid 3'-hydroxylase
Sapur.7040900.1	4.86199262	0.61566349	0.19988286	-0.80778	0.41921758	0.49104689	grey	-0.04913948	0.54109351				NA
Sapur.0013610800.1	0.17842464	0.45422126	0.61973656	-0.80688	0.41973656	0.49167925	grey	0.22267015	0.05097584		CIP1	COP1-interactive protein 1	endosomic protein E, putative
Sapur.0060274600.1	0.29235389	0.31525416	0.39091384	0.806454	0.41980935	0.49188658	grey	0.03413695	0.67248767				NA
Sapur.0065105900.2	1.09110415	0.31312568	0.40687883	0.806466	0.42004096	0.49241063	grey	-0.03882406	0.55246854				hypothetical protein
Sapur.0051869800.1	5.45379482	0.12335095	0.15191954	-0.80519	0.42070182	0.49287109	grey	-0.01840281	0.81904854				NA
Sapur.0105311700.1	10.92515177	0.09318761	0.11307584	0.805164	0.42075976	0.49273191	grey	0.06823074	0.36789944	GO:0005515	NTMC2T5.2,NTMC2TYPE5.1	Calcium-dependent lipid-binding (CaLB domain) family protein	integral membrane single C2 domain protein
Sapur.0090309200.2	16.06863635	0.07319728	0.09113276	0.80448	0.42119563	0.49335217	grey	0.0588223	0.43822047		NF-YC10	nuclear factor Y, subunit C10	histone-like transcription factor and archaeal histone protein
Sapur.0010611400.2	0.19722815	0.15298666	0.18740741	0.804347	0.42133188	0.49370789	grey	0.1188279	7.20E-05	GO:0003723		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif (RRM)-containing protein musashi-like musashi protein
Sapur.0060863600.1	1.35849724	0.26343553	0.32784707	-0.80351	0.42180511	0.49379555	grey	-0.05799145	0.52752316				DUF4228 domain protein
Sapur.0090309300.1	1.15.54584	0.49208584	0.59813103	0.803	0.42179748	0.49400924	grey	0.04469368	0.57934053	GO:0005662,GO:0003824		N-myc-like negative transcriptional regulator family protein	phosphoglycomann benzoic ether reductase
Sapur.0180245800.1	2.94932461	0.11766802	0.14628104	0.803143	0.42189187	0.49395197	grey	0.03613124	0.68493963				NA
Sapur.0106210800.1	0.56479732	0.35118226	0.32538268	-0.80246	0.42239841	0.49439649	grey	0.12828247	0.19349924	GO:0055115,GO:0005634,GO:0003677		calmodulin-binding transcription regulator	calmodulin-binding transcription activator
Sapur.0162870001.1	0.38989544	0.34271474	0.42287675	0.80212	0.42239355	0.49460829	grey	0.09393304	0.26399134				NA
Sapur.0191100600.2	0.16808706	0.45810158	0.57147684	-0.80199	0.42291148	0.49483506	grey	-0.25735565	0.00118376			Excinuclease ABC, C subunit, N-terminal	Excinuclease ABC, C subunit, N-terminal
Sapur.0070111000.1	0.61352704	0.34138399	0.3614945	0.800888	0.42319169	0.49540452	grey	0.06363035	0.42837768	GO:0016192		Gnt1/SPO-like nucleotide transport protein family	vesicle transport GOT1B, putative
Sapur.0081150000.1	0.17005021	0.55076675	0.68797475	-0.80061	0.42339360	0.49582484	grey	-0.2461675	0.00234424	GO:0006355,GO:0003700	CCA1,LHY	DRN-LHR,DRN6_ESR2,SOB2 DORNROSCHEN-like	AP2/ERF domain transcription factor
Sapur.0005202100.3	4.93688315	0.09318761	0.12809121	0.80053	0.42349422	0.49602	grey	0.05557066	0.49308203		AB12,ABE12,ATABI5	abscisic acid responsive elements-binding factor 2	bZIP transcription factor family protein
Sapur.0106904200.1	0.23061173	-0.43024351	0.53808852	-0.8001	0.42363493	0.49587509	grey	-0.15896513	0.04549592				hypothetical protein
Sapur.0010611400.2	0.39554812	0.31382424	0.39160745	-0.80062	0.42367606	0.49588105	grey	0.07364835	0.32816487	GO:0006355,GO:0003677		Dof protein 2	BLL1-related transcription factor, putative
Sapur.0040521400.1	1.01912855	-0.22723738	0.27846788	-0.79982	0.42381581	0.49602968	grey	-0.03924292	0.62669371	GO:0009285		homeodomain GLABROUS 11	homeobox leucine zipper protein
Sapur.0010611400.3	0.31584641	0.31382424	0.39160745	0.799828	0.42424742	0.49630234	grey	0.10030914	0.23864855	GO:0016491,GO:0008152	PORA	protochlorophyllide oxidoreductase A	NADPH-protochlorophyllide oxidoreductase
Sapur.0170235600.1	5.87809718	0.10716527	0.13421843	0.798439	0.42465509	0.49609133	grey	0.02659041	0.79798417				NA
Sapur.0130284100.1	0.16874985	-0.49878829	0.62461569	-0.79842	0.42462472	0.49605133	grey	-0.25551437	0.01128824	GO:0008270,GO:0003676			NA
Sapur.0050100500.1	137.4165346	0.07070561	0.0664652	0.798134	0.42470154	0.49708238	grey	0.05715399	0.47461356				C2H2-like zinc finger protein
Sapur.0162343400.1	151.5735608	0.02498805	0.03708858	-0.79775	0.42505113	0.49709593	grey	-0.09453855	0.23893403			Sucrose/hexedrulo-like family protein	sucrose-like protein
Sapur.7081200.1	0.36402788	0.09318761	0.12809121	0.79767	0.42509399	0.49737162	grey	-0.13502847	0.05652588	GO:0008270,GO:0008022,GO:0006625,GO:0005779	APM4,ATPX12,PEX12	peroxin-12	NA
Sapur.0170241400.1	2.35867601	0.14991806	0.18740704	0.797451	0.42518892	0.49740024	grey	0.06255487	0.43638788			Plant protein of unknown function (DUF247)	NA
Sapur.0010618200.2	0.87.519204	0.07695294	0.09528814	0.797	0.42524692	0.49754596	grey	0.04765471	0.5093184		cplna-70-1	Chloroplast heat shock protein 70	NA
Sapur.0070202300.1	0.54323924	0.27467964	0.34118364	0.796322	0.42548653	0.49817971	grey	-0.03129123	0.69721063	GO:0006796,GO:0005737,GO:0004427,GO:0000287	AtPPa6,PPa2	pyrophosphorylase 2	soluble inorganic pyrophosphatase
Sapur.0060960200.1	0.35705388	0.49208584	0.59813103	0.796	0.42548663	0.49817831	grey	0.05504784	0.94848549		ATGT11,GDT1D,GDT11	glutathione S-transferase TheTA1	glutathione S-transferase theta
Sapur.0050200400.1	58.40963962	0.14123671	0.17740166	0.796143	0.42549868	0.49827271	grey	0.07457317	0.35289843	GO:0007165,GO:0005515,GO:0043531,GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005875		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.0106218800.3	0.30709927	0.51641162	0.64860257	-0.79829	0.42597974	0.49829851	grey	-0.43945872	1.42E-09		IRA2	Endosulfanase/exonuclease/phosphatase family protein	type I inositol 1%2C4%2C5-trisphosphate 5-phosphatase
Sapur.0040260300.1	2.74018840	0.09318761	0.12809121	0.79236	0.42653290	0.49884856	grey	-0.07243803	0.36743931		DegP7	DegP protease 7	NA
Sapur.0070130800.1	13.07171248	0.36754785	0.13653829	-0.79502	0.42680156	0.49895763	grey	-0.06491938	0.41992878	GO:0055114,GO:0020037,GO:0006979,GO:0004601		Peroxidase superfamily protein	NA
Sapur.0082687000.1	28.80391440	0.09318761	0.12809121	0.79487	0.42679392	0.49927342	grey	0.02448531	0.51093759				hypothetical protein
Sapur.0090285400.1	134.2612316	0.16611408	0.20904178	0.794653	0.42681546	0.49936814	grey	0.06742969	0.40141713	GO:0055114,GO:0020037,GO:0016705,GO:0005506	CYP82C4	cytochrome P450, family 82, subfamily C, polypeptide 4	NA
Sapur.0106193200.1	0.54817679	0.35118226	0.32538268	0.793	0.42708391	0.49947062	grey	0.07703098	0.31668725			Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.0191060900.1	1.99681191	0.16545211	0.20845964	0.793149	0.42753676	0.50000589	grey	0.03813441	0.62847704	GO:0002247,GO:0005544,GO:0006468,GO:0004672		S-locus lectin protein kinase family protein	S-locus lectin protein kinase family
Sapur.0050207500.1	18.9813993	0.05267505	0.06630551	0.793	0.42885524	0.50016561	grey	0.08145675	0.33476809	GO:0055114,GO:0047134		Cysteine/histidine-dependent aminotransferase 1	C1-like domain protein
Sapur.0061905000.2	0.15572228	-0.62569771	0.78926422	-0.7928	0.42732147	0.50017373	grey	-0.24300892	0.02016367		NDL1	N-MYC downregulated-like 1	pollen specific protein SF21, putative
Sapur.0010618300.1	0.29386607	0.09318761	0.12809121	0.79	0.42734198	0.50017373	grey	0.03104697	0.68393841			Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.0072645400.4	7.2858445	-0.09787969	0.12436225	-0.79302	0.42778413	0.50017546	grey	-0.00659875	0.93547077	GO:0008270		DHHC-type zinc finger family protein	zinc finger protein, putative
Sapur.0106281100.1	0.09462694	0.59476553	0.98017928	0.792997	0.42779859	0.50017546	grey	0.2923815	0.00019175	GO:0006281,GO:0003676,GO:0000723		PIF1 helicase	NA
Sapur.0070299400.1	24.09055092	0.09318761	0.12809121	0.79247	0.42795166	0.50029851	grey	0.01835557	0.83921662	GO:0016567,GO:0004842		ARM repeat superfamily protein	phosphoprotein responsive protein
Sapur.0100240100.1	0.17074929	0.65094772	0.82132612	0.792554	0.42803793	0.50036204	grey	0.13568683	0.09023767	GO:0006355,GO:0003700		Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor, putative
Sapur.0090242900.1	1.45735766	-0.16881241	0.21516807	-0.7922	0.42834735	0.50750032	grey	-0.06126404	0.46317945				NA
Sapur.0010217000.1	0.35357561	0.55708827	0.70401742	0.791842	0.42845281	0.50855653	grey	0.16809586	0.03528276	GO:0004843	ATUBP5,PDE12D,UBP5	ubiquitin-specific protease 5	ubiquitin carboxyl-terminal hydrolase
Sapur.0050210100.2	41.12824807	0.04917656	0.06211838	0.79112	0.42863188	0.50917819	grey	-0.0848156	0.43270552		AtHB37,BEP	Bait-expert protein	GDP-dissociation inhibitor
Sapur.0010688800.16	8.96936154	-0.07184395	0.09103367	-0.79114	0.42886129	0.51026657	grey	0.11369373	0.15256795	GO:0055115,GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005875		P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain	kinesin motor, calpain-like and calcium-binding and coiled-coil protein
Sapur.0106264400.3	2.50460654	0.11818663	0.16579176	0.790503	0.42889002	0.51183362	grey	0.07262073	0.35854246			Carbohydrate-binding X8 domain superfamily protein	CCM-NOT transcription complex subunit
Sapur.0162870001.1	46.03474675	-0.07643074	0.0968748	-0.7903	0.42919547	0.51573213	grey	0.16895874	0.03621167	GO:0016787		Pectinacetylesterase family protein	pectinacetylesterase
Sapur.0080235200.4	8.82434415	0.08284888	0.11163225	0.790589	0.42932933	0.51584079	grey	0.06283197	0.43542627	GO:0016192,GO:0030904	ATVPS21,VPS33	Sec1/munc18-like (SM) proteins superfamily	vacuolar protein sorting-associated-like protein
Sapur.0010611000.1	0.17620737	0.62780924	0.54124677	0.790454	0.42932603	0.51618362	grey	0.14469556	0.07084185	GO:0004601,GO:0030410	AtNAK4,NAK4	nicotinamine synthase	nicotinamine synthase
Sapur.0013614000.2	0.31344188	0.31733748	0.40133159	0.790249	0.42932841	0.52178049	grey	0.01169719	0.88449084	GO:0006468,GO:0005524,GO:0004672		Protein kinase family protein	casein kinase, putative
Sapur.0162303300.1	688.0133807	0.06079193	0.07687544	0.789	0.42944919	0.52180884	grey	-0.08665481	0.28557616				transmembrane protein, putative
Sapur.0051869500.1	2607.772928	-0.02871979	0.03634551	-0.79	0.42952787	0.52195112	grey	-0.07021594	0.18222853	GO:0016021,GO:0008250,GO:0006487			dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 2
Sapur.7056600.1	0.57962616	0.22775896	0.28837818	-0.7886	0.42964037	0.52198033	grey	-0.10093465	0.11249868	GO:0006355,GO:0008270,GO:0003700,GO:0005634,GO:0005779	APM4,ATPX12,PEX12	peroxin-12	NA
Sapur.0086172600.1	107.2.4752	-0.05128958	0.06474697	-0.7894	0.42987213	0.52269946	grey	-0.07589933	0.34479309	GO:0048871,GO:0003160	AHP1	histidine-containing phosphotransmitter 1	NA
Sapur.0010611000.1	0.1106667	0.34948761	0.60812854	0.789402	0.42987725	0.52269946	grey	0.15303215	0.05474735				hypothetical protein
Sapur.0192608800.1	0.23482337	0.44605472	0.5427908	-0.78894	0.43014882	0.52351153	grey	-0.18312063	0.02169804		ATMYB115,ATY19,MYB115	myb domain protein 15	Myb-related transcription factor
Sapur.0006201000.1	64.93415139	0.02260014	0.08406836	-0.7884	0.43026531	0.52600037	grey	0.14616874	0.04270408			Carbohydrate-binding X8 domain superfamily protein	glycosyl hydrolase family protein
Sapur.0080169900.1	5.66962022	0.14605655	0.18374655	0.788724	0.43027497	0.52605053	grey	0.04888196	0.53493135				hypothetical protein
Sapur.0130195000.1	1021.30229	0.04776394	0.05679622	-0.78867	0.43030748	0.52680588	grey	-0.10239163	0.20191591	GO:0003735,GO:0009058	ATHMA1MB2196,HMGNA4	histidinol phosphate aminotransferase 1	histidinol-phosphate aminotransferase
Sapur.0010211000.1	130.3127159	0.01656999	0.04014526	0.788662	0.43039048	0.52682665	grey	0.14469556	0.07084185	GO:0005634	LIP2	lipoyltransferase 2	NA
Sapur.0061005900.1	2.82426233	0.12375273	0.16788728	0.787893	0.43075905	0.52358214	grey	0.05101301	0.51275224	GO:0016567,GO:0004842	ATCAND1,CAND1,ETA2,HVE	cullin-associated and NEDD8-dissociated protein 1, putative	cullin-associated NEDD8-dissociated protein, putative
Sapur.0010618800.1	307.7481104	0.07876231	0.09997283	-0.7877	0.43084149	0.52362243	grey	-0.24202294	0.01015567	GO:0016020,GO:0008150,GO:0005215	NIP5;1,NLM6,NLM8	NODULIN-like family protein	aquaporin NIP derivative
Sapur.0105123900.3	0.21375888	-0.46134728	0.58182578	-0.78752	0.43097497	0.53374667	grey	-0.1888546	0.0172871		ATSNAP50,SNAP50	soluble N-ethylmaleimide-sensitive factor adaptor protein 30	synaptosomal-associated protein
Sapur.0140288300.3	1.94601192	0.09372264	0.11902316	-0.7493	0.43103277	0.53423557	grey	-0.03703879	0.67291681	GO:0006418,GO:0005634,GO:0048812,GO:0000166,GO:0006433,GO:0005737,GO:0004824		Class II aaRS and biotin synthetase superfamily protein	tRNA-synthetase
Sapur.0051769900.1	85.11267736	-0.09128153	0.11594776	-0.78726	0.43118806	0.53518121	grey	-0.0646676	0.42102145		CPUDR7	conserved peptide upstream open reading frame 7	conserved peptide upstream open reading frame 7
Sapur.0010677200.2	0.24182069	0.92722284	0.77134671	-0.78723	0.43144341	0.53520049	grey	-0.37604586	1.37E-06			Tryptophan/tyrosine permease family protein	tryptophan/tyrosine permease family protein
Sapur.0170291300.1	0.16079483	0.46028949	0.58487574	0.786987	0.43189223	0.53565655	grey	0.08256127	0.30354763				NA
Sapur.0145674700.1	1.77176656	0.06279152	0.08258162	0.786878	0.43189437	0.53565655	grey	0.03408142	0.68089995	GO:0016758,GO:0008152	GT72B,UGT72B1	UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase
Sapur.0030251800.2	0.37059614	0.31644245	0.42223391	-0.78673	0.43143792	0.53080457	grey	0.13347601	0.09159819		CLPR4	CLP protease R subunit 4	ATP-dependent Clp protease proteolytic subunit
Sapur.0161802000.1	705.7118495	0.02860561	0.03658864	0.786644	0.43149242	0.53852149	grey	0.05054816	0.52959728		ATTIC21,CLV6,PIC1,TIC21	translocon at inner membrane of chloroplasts 21	TIC21
Sapur.0050281000.1	1.46932625	0.14774542	0.18820434	-0.78502	0.43240485	0.5490263	grey	0.13417256	0.09387602	GO:0006468,GO:0004672	AtPEPKR1,PEPK1	proline extensin kinase/ receptor kinase 1	tyrosine kinase domain protein
Sapur.0162050000.1	1.494.93414	0.02104393	0.02795816	0.78428	0.43287635	0.50546811	grey	0.06352566	0.43924172	GO:0055114,GO:0030151,GO:0016491,GO:0042128	AT-SO,AtSO,SOX	sulfite oxidase	sulfite oxidase
Sapur.0130227001.1	495.5154498	0.02104393	0.02795816	0.783161	0.43291924	0.50559564	grey	0.02516926	0.75456776	GO:0005515		peptidoglycan-binding LysM domain-containing protein	peptidoglycan-binding LysM domain protein
Sapur.0010278800.1	193.7886785	0.02661843	0.03097523	0.783581	0.43282636	0.50584218	grey	0.0685181	0.39353189	GO:0005515		PO2/TBTB containing G-protein 1	BTB/POZ domain protein POB1
Sapur.0010211800.1	1.12141.6556	0.36148044	0.47845532	-0.78329	0.43318277	0.50810171	grey	-0.05458128	0.49202051	GO:0055114,GO:0004871,GO:0016702	ATLOX2,LOX2	lipoxygenase 2	lipoxygenase 2
Sapur.0010182900.1	42.69415697	0.12766409	0.16276364	-0.78249	0.43392581	0.50637033	grey	0.05088739	0.33724828			NADP(+)-binding Rossmann-fold superfamily protein	beta-keto acyl carrier reductase
Sapur.0061897200.1	0.26269842	0.24148149	0.32603924	-0.78243	0.43397366	0.50637033	grey	0.06248354	0.43830177			RING/U-box protein with domain of unknown function (DUF 1232)	C3HC4-type RING finger protein
Sapur.1595G093100.1	1.13824286	0.31495279	0.39821289	-0.78224	0.43407584	0.50692403	grey	-0.06297163	0.43141757				NA
Sapur.0170273100.1	445.7818753	0.02600182	0.03440749	-0.7821	0.43415823	0.50674794	grey	-0.07301269	0.36438392	GO:0006073,GO:0004106	ATCM1,CM1	chorismate mutase 1	chorismate mutase
Sapur.0130200900.4	0.26269842	0.24148149	0.32603924	-0.78217	0.43416007	0.50674794	grey	-0.15318148	0.05875422		HCT,CCOM,CCOMAM4	carotenoid cleavage dioxygenase 8	carotenoid cleavage dioxygenase
Sapur.0010619500.6	16.77851189	-0.07338427	0.09160853	-0.78158	0.43461236	0.50700751	grey	0.08327045	0.29987563	GO:0016747		hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase
Sapur.1595G065000.4	0.21110884	0.34948761	0.60812854	0.781	0.43482426	0.50710946	grey	-0.08168208	0.35909942	GO:0006950,GO:0005516		calmodulin-binding protein	calmodulin-binding protein
Sapur.0020293900.2	2.16615864	0.19041527	0.24316528	0.781304	0.43462765	0.50722644	grey	0.06051565	0.45123139		ATMYB14,MYB14,MYB14A7	myb domain protein 14	Myb-related transcription factor
Sapur.0170195600.1	0.30795682	-0.42163789	0.54540897	-0.7804	0.43510418	0.50781351	grey	-0.1857458	0.01658884				hypothetical protein
Sapur.0040203100.2	0.11558184	0.66711957	0.85497005	0.780278	0.43527491	0.50780375	grey	0.26308737	0.00071153	GO:0006355,GO:0003677	ATAC85B0,ATAC0,NAC073,NAC073,ND2	NAC domain containing protein 73	NAC transcription factor O96
Sapur.0010682700.1	64.26641247	0.08284888	0.11163225	0.780487	0.43546428	0.50906885	grey	0.01343025	0.87538077	GO:0005515	ARIF12,RLP12	receptor like protein 12	Ic/9-Avr4-gel1
Sapur.1595G124800.1	0.28760934	0.37007655	0.47670486	-0.77958	0.43566059	0.50834286	grey	-0.1313251	0.10106615			Regulator of chromosome condensation (RCC1) family protein	Protein of unknown function (DUF789)
Sapur.0060703200.1	1.82571939	0.24148149	0.32603924	0.77549555	0.43648884	0.50917596	grey	0.07648531	0.33046857			Phosphoglycerate mutase family protein	BTB/POZ domain protein
Sapur.0096113300.1	0.92716617	-0.24298246	0.32228956	-0.77819	0.43654629	0.50921596	grey	-0.09135184	0.25517847	GO:0046983,GO:0008171		O-methyltransferase family protein	O-methyltransferase family
Sapur.7102500.1	0.27494526	0.44247391	0.58723464	0.778012	0.43656170	0.50924551	grey	0.05377886	0.52799495			RNA-directed DNA polymerase (reverse transcriptase)-related family protein	RNA-directed DNA polymerase
Sapur.0040274700.7	20.94173148	0.07773468	0.09887324	0.07007714	0.77468	0.43688847	0.50988733	0.05889675	0.43936916	GO:0005622,GO:0003779,GO:0030042,GO:0015629	ADF4,ATADF4	actin-depolymerizing factor 4	actin-depolymerizing factor
Sapur.0120110300.2	0.93842053	0.07302469	0.09120567	0.777169	0.43705911	0.50986884	grey	0.08325032	0.39924139	GO:0016491,GO:0008152		NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase TIC 32
Sapur.0180220200.1	0.73965251	0.24298246	0.32228956	0.7469	0.43750273	0.51684024	grey	-0.09189996	0.31105654	GO:0005515	AtPP2-B1,PP2-B1	phloem protein 2-like 1	DUF241 domain protein
Sapur.0096113100.1	0.10864125	0.75153231	0.92116888	0.775567	0.43770587	0.51606053	grey	0.23279628	0.00346177			Arabidopsis protein of unknown function (DUF241)	DUF241 domain protein
Sapur.7039700.1	0.73973072	0.21808205	0.27768705	-0.7567	0.43796938	0.51680426	grey	-0.06254873	0.43910264	GO:0055515,GO:0006468,GO:0005524,GO:0004672		Leucine-rich repeat receptor-like protein kinase family protein	NA
Sapur.0130197800.1	9.40045551	-0.07338278	0.09488071	-0.75506	0.43835729	0.51133326	grey	-0.07494754	0.35088876				hypothetical protein
Sapur.0010611000.2	0.13312773	0.70302469	0.95164168	0.754328	0.43897507	0.51284024	grey	0.18243498	0.03416955				hypothetical protein
Sapur.0170136800.1	144.541	0.14363973	0.18610685	0.773556	0.43919599	0.51278311	grey	-0.06843207	0.40482905			Protein of unknown function (DUF789)	NA
Sapur.0160252100.1	2.92600285	0.37387128	0.22480616	-0.7733	0.43934710	0.51232194	grey	-0.05233197	0.5558785			Leucine-rich repeat (LRR) family protein	NA
Sapur.7090300.1	0.27074416	0.22775896	0.28837818	-0.77323	0.43936637	0.51246051	grey	-0.17455707	0.03836262		CLE25	CLAVATA/ESR-like 25	NA
Sapur.0170237200.1	0.94960988	0.39618792	0.13647585	0.773197	0.43945578	0.51

Sapur.001G145400.4	2.50046409	0.123689041	0.167198149	0.739775	0.459436421	0.533284207	grey	0.096694224	0.228311994	GO:0005515	AT1G80210.1		Mov34/MPN/PAD-1 family protein	Mov34/MPN/PAD-1 family protein
Sapur.004G148300.2	0.65586665	-0.225994808	0.305696594	-0.73928	0.459738124	0.53361309	grey	-0.114572847	0.153052727		AT2G27100.1	SE	C2H2 zinc-finger protein SERRATE (SE)	serrate RNA effector molecule protein
Sapur.013G099700.1	0.250472385	-0.384395127	0.519976202	-0.73926	0.45975203	0.53361309	grey	-0.258663872	0.001071678		AT1G51965.1	ABO5	ABA Overly-Sensitive 5	PPR containing plant protein
Sapur.T090700.1	0.161673349	0.447395373	0.605255662	0.739184	0.459795203	0.533644473	grey	0.153339459	0.055194849	GO:0006950	AT5G14680.1		Adenine nucleotide alpha hydrolases-like superfamily protein	ethylene-responsive-like protein
Sapur.014G038500.1	0.115410882	0.851241852	1.151893189	0.738994	0.459910801	0.533759907	grey	0.200301346	0.011894575		AT5G51160.1		Ankyrin repeat family protein	NA
Sapur.008G140900.1	45.64245771	0.239402756	0.324195505	0.738452	0.460239943	0.534104417	grey	0.103570396	0.196760068					NA
Sapur.T145700.1	2.431939896	-0.118002503	0.159839904	-0.73825	0.460359909	0.534224892	grey	-0.060328884	0.452916222	GO:0007165,GO:0005515	AT3G44480.1	cog1,RPP1	Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.007G036600.1	10.11007099	0.092971825	0.125956827	0.738125	0.460438774	0.534297664	grey	0.029894631	0.710139718	GO:0043531	AT5G66900.1		Disease resistance protein (CC-NBS-LRR class) family	CC-NBS-LRR resistance protein
Sapur.016G048800.1	0.168114551	-0.451901364	0.61234333	-0.73799	0.460522402	0.534375957	grey	-0.270916408	0.000599467	GO:0005975,GO:0004650	AT3G57510.1	ADPG1	Pectin lyase-like superfamily protein	polygalacturonase
Sapur.013G092900.1	2.133428303	0.167709994	0.227290451	0.737866	0.460595618	0.534442165	grey	0.007191704	0.928769703	GO:0008270,GO:0003676	AT1G21280.1			NA
Sapur.004G099900.2	21.75594359	0.068773074	0.093231369	0.73766	0.460720935	0.53456882	grey	0.045017311	0.575587395	GO:0005515	AT1G33420.1		RING/FYVE/PHD zinc finger superfamily protein	PHD finger protein
Sapur.001G064400.1	0.240100649	0.385125898	0.522181012	0.737533	0.460798085	0.53463958	grey	0.005768592	0.94283807	GO:0016021,GO:0012511	AT4G25140.1	OLE1,OLEO1	oleosin 1	oleosin
Sapur.016G243200.1	175.0661546	-0.061794367	0.083943001	-0.73615	0.4616414	0.535599244	grey	-0.072234981	0.368629155	GO:0005515,GO:0043531	AT3G14470.1		NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.010G078500.2	4.214590296	-0.106041186	0.144113975	-0.73581	0.461843454	0.535814872	grey	-0.06537471	0.415950012	GO:0071805,GO:0016020,GO:0015079	AT1G70300.1	KUP6	K+ uptake permease 6	high-affinity potassium transporter protein, putative
Sapur.014G101500.1	0.314456958	-0.324477218	0.441330565	-0.73522	0.46220254	0.536212663	grey	-0.11828251	0.140100549	GO:0015969	AT4G02260.2	AT-RSH1,ATRSH1,RSH1	RELA/SPOT homolog 1	RelA-SpoT-like protein RSH1
Sapur.001G050500.1	82.49374909	-0.072236473	0.098271448	-0.73507	0.462296369	0.536302704	grey	-0.059286416	0.460776079		AT2G33520.1			NA
Sapur.005G180800.1	0.593320617	0.253546504	0.344981741	0.734956	0.462366108	0.536364795	grey	0.060076249	0.454814093	GO:0016787,GO:0005524,GO:0003677	AT2G18760.1	CHR8	chromatin remodeling 8	DNA repair and recombination protein RAD26
Sapur.014G112000.1	5.314301736	0.093614453	0.127428102	0.734645	0.462555558	0.536552455	grey	0.055826175	0.487398776					hypothetical protein
Sapur.010G054200.7	1.528363668	0.161321135	0.219592855	0.734637	0.462560324	0.536552455	grey	0.097435521	0.224748338	GO:0018342,GO:0008318	AT4G24490.2	ATRGTA1,RGTA1	RAB geranylgeranyl transferase alpha subunit 1	Rab geranylgeranyl transferase-like protein, putative
Sapur.006G222400.1	18.11166731	-0.068138898	0.09278292	-0.73439	0.462710757	0.536708128	grey	-0.037955343	0.636963329		AT2G24610.1	ATCNGC14,CNGC14	cyclic nucleotide-gated channel 14	NA
Sapur.014G026000.1	1.241925013	-0.201506702	0.274423255	-0.73429	0.462771012	0.536740464	grey	-0.020475429	0.799083881	GO:0016020,GO:0006810,GO:0005215	AT1G59740.1		Major facilitator superfamily protein	NA
Sapur.T071900.1	3.321153004	-0.210210043	0.286320064	-0.73418	0.462839938	0.53680149	grey	-0.049317249	0.539625957		AT3G18670.1		Ankyrin repeat family protein	NA
Sapur.006G157600.3	18.81102055	0.062678735	0.085409207	0.733864	0.46303168	0.536983785	grey	0.050930379	0.526428363	GO:0046872	AT3G58030.3		RING/U-box superfamily protein	zinc-RING finger protein
Sapur.006G035400.1	0.214211875	-0.422699408	0.576009752	-0.73384	0.463045823	0.536983785	grey	-0.172256313	0.030984648		AT4G20990.1	ACA4,ATACA4	alpha carbonic anhydrase 4	carbonic anhydrase
Sapur.016G150100.1	177.7895971	-0.04003275	0.054568021	-0.73363	0.463174127	0.537113744	grey	-0.043403	0.589371782	GO:0043531	AT3G14460.1		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.019G103600.1	7.180585341	-0.135026627	0.184368614	-0.73237	0.463940828	0.537970305	grey	-0.044258207	0.582050498		AT4G10265.1		Wound-responsive family protein	wound-induced protein, putative
Sapur.016G211400.1	715.521647	0.022058521	0.030119539	0.732366	0.463945304	0.537970305	grey	0.005599764	0.944508298		AT5G50960.1	ATNBP35,NBP35	nucleotide binding protein 35	cytosolic Fe-S cluster assembly factor nbp35
Sapur.002G152700.1	5.988706253	-0.121523712	0.166019787	-0.73198	0.464178759	0.53820327	grey	-0.06349218	0.429530757					NA
Sapur.T033900.1	0.438083824	0.232841305	0.318108616	0.731955	0.464195819	0.538204182	grey	0.051165851	0.524515629		AT4G17900.2		PLATZ transcription factor family protein	NA
Sapur.002G189000.1	107.4358085	-0.055605622	0.075980151	-0.73184	0.464263755	0.538250627	grey	-0.232022743	0.003455473		AT5G48720.2	XRI,XRI1	x-ray induced transcript 1	XRI1
Sapur.001G192600.1	19.07286813	0.067070092	0.091646291	0.731836	0.464268425	0.538250627	grey	-0.058644151	0.465655885		AT1G31720.1		Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.010G059500.1	221.9563356	0.053864442	0.073604955	0.731805	0.464287862	0.538254294	grey	0.046562062	0.562539916	GO:0009055	AT5G26330.1		Cupredoxin superfamily protein	mavicyanin, putative
Sapur.005G006900.1	125.520119	-0.041428838	0.056675517	-0.73098	0.464789557	0.538817028	grey	-0.06786422	0.398381526	GO:0043531	AT3G07040.1	RPM1,RPS3	NB-ARC domain-containing disease resistance protein	NBS-LRR resistance protein
Sapur.005G007100.1	56.21693061	0.061237271	0.08377974	0.730932	0.46482085	0.538834418	grey	0.050052995	0.53358626	GO:0043531	AT3G07040.1	RPM1,RPS3	NB-ARC domain-containing disease resistance protein	NA
Sapur.016G112100.4	6.987333054	-0.100018406	0.136887075	-0.73066	0.46498464	0.538986506	grey	0.078548531	0.32814497	GO:0034755,GO:0016021,GO:0005381	AT5G03570.1	ATIREG2,FPN2,IREG2	iron regulated 2	solute carrier family 40 protein
Sapur.006G220200.5	0.377889723	0.311885583	0.426869024	0.730635	0.465001936	0.538987665	grey	0.095822356	0.232554128	GO:0016758,GO:0009247	AT4G31780.2	MGD1,MGDA	monogalactosyl diacylglycerol synthase 1	monogalactosyldiacylglycerol synthase
Sapur.019G081300.1	1.925545156	0.136488283	0.186844866	0.73049	0.465090799	0.539071774	grey	0.025938787	0.747097313	GO:0006355,GO:0003677	AT1G71930.1	ANAC030,VND7	vascular related NAC-domain protein 7	NAC transcription factor
Sapur.016G053500.1	3.235445875	-0.174109511	0.238498039	-0.73002	0.465374955	0.539363327	grey	-0.042194137	0.599791786	GO:0007165,GO:0005515,GO:0043531	AT1G69550.1		disease resistance protein (TIR-NBS-LRR class)	NA
Sapur.011G069900.1	0.230109252	0.428520828	0.587151609	0.72983	0.465494136	0.539482551	grey	0.039552213	0.62284657		AT1G73160.1		UDP-Glycosyltransferase superfamily protein	glycosyltransferase family 4 protein
Sapur.005G007200.1	67.97234011	-0.212559893	0.291271801	-0.72976	0.465533994	0.53950984	grey	-0.117842261	0.141592497	GO:0043531	AT3G07040.1	RPM1,RPS3	NB-ARC domain-containing disease resistance protein	NBS-LRR resistance protein
Sapur.016G052300.1	1.307902911	0.307284979	0.421091266	0.729735	0.465552264	0.539512109	grey	0.089791138	0.26341764		AT5G16360.1		NC domain-containing protein-related	NA
Sapur.001G156000.1	2.799709714	-0.293892919	0.403105444	-0.72907	0.465957581	0.539962897	grey	0.06263341	0.43580976	GO:0006355,GO:0005634	AT3G15540.1	IAA19,MSG2	indole-3-acetic acid inducible 19	indole-3-acetic acid inducible protein, putative
Sapur.010G067000.3	106.7664681	0.063032369	0.08647793	0.728884	0.4660727	0.540077377	grey	0.046343534	0.564377063	GO:0030955,GO:0006096,GO:0004743,GO:0000287	AT3G22960.1	PKP-ALPHA,PKP1	Pyruvate kinase family protein	pyruvate kinase
Sapur.013G142300.1	0.256236484	0.457626733	0.62795115	0.728762	0.466147458	0.54014508	grey	0.059380463	0.460063914					NA
Sapur.016G162000.2	1.298803455	-0.163195659	0.224041717	-0.72842	0.46635864	0.540370854	grey	-0.042492837	0.597209417		AT4G14590.1	emb2739	embryo defective 2739	integrator complex subunit 3, putative
Sapur.005G066300.1	708.321386	-0.062406986	0.085691103	-0.72828	0.466443136	0.540449826	grey	-0.079219625	0.324016376		AT2G21970.1	43710	stress enhanced protein 2	stress enhanced protein
Sapur.017G019800.1	169.276981	-0.047291149	0.06494399	-0.72818	0.466501194	0.540498161	grey	-0.043452842	0.588943943	GO:0005524,GO:0003676,GO:0046872	AT2G47680.1		zinc finger (CCCH type) helicase family protein	zinc finger CCCH domain protein
Sapur.013G140600.1	271.9992063	-0.246013405	0.338324307	-0.72715	0.46713247	0.541191653	grey	-0.13754141	0.085834758	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT5G05340.1		Peroxidase superfamily protein	peroxidase
Sapur.004G139100.1	0.225994945	-0.461461201	0.634734945	-0.72701	0.467217371	0.541271054	grey	-0.143197357	0.073590359					NA
Sapur.003G144700.1	6.161978218	0.084397057	0.116157944	0.726572	0.467488465	0.541566147	grey	0.048334296	0.547747499					NA
Sapur.001G045200.1	0.203199666	0.403951645	0.556048611	0.726468	0.467551782	0.541620526	grey	0.229772418	0.003793171		AT1G67350.2			RW1-like protein, putative
Sapur.013G010100.2	0.407748755	0.264816081	0.364735275	0.72605	0.467808061	0.541898424	grey	0.065939545	0.411924745	GO:0005515	AT3G05710.2	ATSYP43,SYP43	syntaxin of plants 43	syntaxin
Sapur.011G118000.1	30.57141126	-0.111452664	0.153661426	-0.72531	0.468259895	0.542402822	grey	-0.080942073	0.313573871	GO:0055114,GO:0050660,GO:0016491	AT1G34575.1		FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.006G145500.1	0.11286716	0.660936296	0.911324857	0.725248	0.468300058	0.542430346	grey	0.246694372	0.001841607		AT5G05800.1			Myb/SANT-like DNA-binding domain protein
Sapur.017G084500.1	30.88137774	0.120269716	0.165873583	0.725069	0.468409987	0.542538677	grey	0.072687834	0.365626829	GO:0043531	AT5G17680.1		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.003G165800.3	0.436590112	-0.248588448	0.34301996	-0.72471	0.468632726	0.542777657	grey	-0.097005097	0.226812703	GO:0006367,GO:0005669	AT1G55300.1	TAF7	TBP-associated factor 7	transcription initiation factor TFIID subunit, putative
Sapur.011G064700.1	0.313744162	0.300048466	0.414430665	0.724002	0.469064751	0.543259011	grey	0.058581771	0.466131351		AT1G03670.1		ankyrin repeat family protein	ankyrin repeat protein
Sapur.T141700.1	0.265508794	0.314387931	0.434301367	0.723893	0.469131129	0.543316863	grey	0.088292813	0.271500238					NA
Sapur.014G112400.1	0.601516887	-0.24519666	0.338774285	-0.72378	0.469203333	0.543381457	grey	-0.06178369	0.442073871	GO:0055114,GO:0016491,GO:0016209,GO:0006979,GO:0004602	AT2G48150.1	ATGPX4,GPX4	glutathione peroxidase 4	phospholipid hydroperoxide glutathione peroxidase, putative
Sapur.007G022700.1	4.557614392	0.139094093	0.192254962	0.723488	0.469380332	0.543567406	grey	0.070159385	0.382583383		AT5G02530.1		RNA-binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.004G148100.1	15.57628719	-0.162962052	0.225287328	-0.72335	0.469463619	0.543644821	grey	-0.090221435	0.26112714		AT3G43720.2		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/LTP family protein
Sapur.004G173000.1	736.8701637	0.023499229	0.03249672	0.723126	0.469602382	0.543786471	grey	0.038314333	0.633778134		AT3G08670.1			hypothetical protein
Sapur.013G065400.7	10.72497094	0.068536717	0.094834072	0.722701	0.46986335	0.544050568	grey	0.073679566	0.35910483		AT2G23910.1		NAD(P)-binding Rossmann-fold superfamily protein	dihydroflavonol-4-reductase
Sapur.004G071800.1	1.349310701	0.161988009	0.224183878	0.722568	0.469945575	0.544126727	grey	0.047791618	0.55225681	GO:0016758,GO:0008152	AT3G02100.1		UDP-Glycosyltransferase superfamily protein	NA
Sapur.002G186900.1	0.435748126	0.338334866	0.468758101	0.721769	0.470436773	0.544676393	grey	0.083967351	0.295769737	GO:0009055	AT2G02850.1	ARPN	plantacyanin	basic blue protein
Sapur.012G041100.1	9.761390043	0.095138039	0.131913275	0.721217	0.470776281	0.545047009	grey	-0.096080466	0.231292543	GO:0046872,GO:0000166,GO:0016021,GO:0015914,GO:0005524,GO:0004012,GO:000028	AT1G68710.1		ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	phospholipid-transporting ATPase, putative
Sapur.017G045500.12	0.167790951	0.514917157	0.713978175	0.721195	0.470789834	0.545047009	grey	0.12479914	0.119392722		AT2G32760.1			UV radiation resistance-associated protein, putative
Sapur.016G150000.1	347.5997675	-0.025198973	0.034951458	-0.72097	0.470927616	0.54518744	grey	-0.047117804	0.55788077	GO:0043531	AT3G14460.1		LRR and NB-ARC domains-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.009G084200.1	81.54092549	-0.229427452	0.318267736	-0.72086	0.470993777	0.545244948	grey	-0.091478189	0.254515607	GO:0055114,GO:0016491	AT3G19000.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.008G023900.1	17.3513701	-0.067594448	0.093801073	-0.72061	0.4711465	0.545402658	grey	-0.088862468	0.268407681	GO:0006468,GO:0005524,GO:0004672	AT3G47570.1		Leucine-rich repeat protein kinase family protein	receptor-kinase, putative
Sapur.017G100400.1	0.337938335	0.308432536	0.428273305	0.720177	0.471456093	0.545695641	grey	-0.009071633	0.91021986		AT3G03280.1			DUF4228 domain protein
Sapur.006G213900.1	702.3021673	0.024669805	0.034293719	0.719368	0.471914195	0.54625311	grey	0.041343839	0.607170164		AT5G25265.1			transmembrane protein, putative
Sapur.005G055100.5	1.230138179	-0.170039378	0.236477274	-0.71905	0.472109088	0.546459577	grey	-0.027831481	0.729336861	GO:0006351,GO:0003714	AT4G40050.1		Protein of unknown function (DUF3550/UPF0682)	NA
Sapur.013G028100.1	23.43804609	0.141803834	0.197310688	0.718683	0.47233627	0.546703405	grey	0.069502318	0.387066798	GO:0055085,GO:0022857,GO:0016021	AT1G54730.2		Major facilitator superfamily protein	NA
Sapur.016G101700.1	28.68637303	-0.163568506	0.227639623	-0.71854	0.472423498	0.546785231	grey	-0.05713658	0.477221037					NA
Sapur.010G033100.1	543.4323139	0.026433972	0.036810754	0.718105	0.472692795	0.547058738	grey	0.055220512	0.492141794		AT1G27150.1		Tetratricopeptide repeat (TPR)-like superfamily protein	StaR-like domain protein
Sapur.016G238300.1	4.005801001	0.129905584	0.180949864	0.717909	0.472813232	0.547166267	grey	0.332984351	2.03E-05	GO:0055114,GO:0016491,GO:0008270	AT3G15090.1		GroES-like zinc-binding alcohol dehydrogenase family protein	zinc-binding dehydrogenase, putative
Sapur.007G027700.2	9.311433549	-0.085415431	0.119041634	-0.71753	0.473049791	0.547414323	grey	-0.432995914	1.48E-08	GO:0055085,GO:0016021	AT4G36790.1		Major facilitator superfamily protein	carbohydrate transporter, putative
Sapur.006G184000.1	260.748137	-0.039489181	0.055048618	-0.71735	0.473157547	0.547519862	grey	-0.065871061	0.412411568	GO:0005515,GO:0042393,GO:0006355	AT5G20510.1	AL5	alfin-like 5	PHD finger protein
Sapur.017G114500.1	111.4363419	0.092228216	0.128586757	0.717245	0.473222904	0.547576333	grey	0.061362944	0.445194381	GO:0016157,GO:0005985	AT5G37180.1	ATSUS5,SUS5	sucrose synthase 5	sucrose synthase
Sapur.001G147400.3	0.394445991	-0.319266593	0.445173849	-0.71717	0.473267456	0.547608727	grey	0.050577561	0.529300885	GO:0005525	AT1G17470.2	ATDRG,ATDRG1,DRG1	developmentally regulated G-protein 1	developmentally-regulated GTP-binding protein
Sapur.019G106400.1	3.049379076	-0.124983952	0.17431319	-0.71701	0.473369161	0.547707246	grey	0.071375987	0.374365705	GO:0030247,GO:0048544,GO:0006468,GO:0004672	AT4G03230.1		S-locus lectin protein kinase family protein	NA
Sapur.003G112000.1	0.170758028	0.399973678	0.558010159	0.716786	0.473506364	0.54784683	grey	0.068061557	0.397008116		AT5G07590.1		Transducin/WD40 repeat-like superfamily protein	WD repeat protein WRAP73
Sapur.011G065300.1	0.624314749	0.240369565	0.335365787	0.716738	0.473535477	0.547861349	grey	0.380585375	8.79E-07		AT3G14760.1			transmembrane protein, putative
Sapur.010G138300.1	0.535389489	-0.272030042	0.379651605	-0.71653	0.47366695	0.54797512	grey	-0.091159113	0.256183178					NA
Sapur.15WG120900.1	585.6743265	-0.029523586	0.041208365	-0.71645	0.473715726	0.548012379	grey	-0.073622199	0.359480117	GO:0046983	AT3G26744.2	ATICE1,ICE1,SCRM	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	inducer of CBF expression 1 protein
Sapur.15WG035300.1	11.40284469	-0.095648773	0.133574032	-0.71607	0.473946204	0.548254999	grey	-0.031815035	0.692432729					NA
Sapur.001G137500.2	4.592282231	-0.088640318	0.123790159	-0.71605	0.473958606	0.548254999	grey	0.06116799	0.446644491	GO:0006468,GO:0004672	AT1G52310.1		protein kinase family protein / C-type lectin domain-containing protein	tyrosine kinase domain protein
Sapur.007G105500.1	0.229068995	0.372870875	0.520762308	0.71601	0.473985347	0.548266756	grey	0.073731585	0.358764749		AT1G11480.1		eukaryotic translation initiation factor-related	translation initiation factor-like protein, putative
Sapur.014G114500.1	0.474786932	0.254374675	0.355292709	0.715958	0.474017252	0.54828485	grey	-0.05477356	0.495657586		AT1G12930.1		ARM repeat superfamily protein	transportin-3 protein
Sapur.016G015800.2	0.164808622	0.77193083	1.078994947	0.715417	0.474351696	0.548652142	grey	0.149335025	0.061944725		AT2G32190.2			hypothetical protein
Sapur.002G189300.1	25.55328242	-0.064855485	0.090665627	-0.71533	0.474407593	0.548697606	grey	-0.034534397	0.667643102		AT1G04850.1		ubiquitin-associated (UBA)/TS-N domain-containing protein	ubiquitin-associated UBA/UBX domain protein, putative
Sapur.016G275300.2	1.871467275	-0.141953056	0.198519116	-0.71506	0.474572041	0.548868612	grey	-0.06025193	0.453493857	GO:0046983	AT5G54680.1	bHLH105,ILR3	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	BHLH transcription factor
Sapur.15WG144300.1	2.419325483	-0.115780419	0.161924936	-0.71503	0.474593438	0.548874165	grey	-0.090512672	0.259584629	GO:0006468,GO:0005524,GO:0004672	AT1G12580.1	PEPKR1	phosphoenolpyruvate carboxylase-related kinase 1	calcium-dependent kinase
Sapur.018G097100.1	1819.792975	-0.037570586	0.052551646	-0.71493	0.474654207	0.548925251	grey	-0.068413636	0.394564776	GO:0016787	AT5G34850.1	ATPAP26,PAP26	purple acid phosphatase 26	iron(III)-zinc(II) purple acid phosphatase, putative
Sapur.012G100100.1	23.71229641	-0.200477041	0.280443063	-0.71486	0.47469663	0.548955116	grey	-0.068125465	0.39637637					NA
Sapur.008G003400.1	108.0925738	0.053758773	0.075227003	0.714621	0.474843452	0.54909448	grey	0.036301091	0.6517262	GO:0016020,GO:0008375	AT1G71070.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	secondary cell wall-related glycosyltransferase family 14 protein
Sapur.008G166900.2	1.886759656	0.152417607	0.213354272	0.714387	0.47498765	0.54923405	grey	0.053344217	0.506989558		AT2G39080.1		NAD(P)-binding Rossmann-fold superfamily protein	hypothetical protein
Sapur.011G064600.1	4.943639001	-0.127024883	0.177824047	-0.71433	0.475023731	0.549237949	grey	-0.018120334	0.821783807		AT1G03670.1		ankyrin repeat family protein	NA
Sapur.006G210000.11	3.479235384	0.111530546	0.156133469	0.714328	0.475024235	0.549237949	grey	0.08065511	0.315298211		AT5G25360.1			DUF4050 family protein
Sapur.006G218500.1	0.317161894	0.293780523	0.411409854	0.714082	0.475176247	0.549394505	grey	-0.144363587	0.071250579		AT4G31850.1	PGR3	proton gradient regulation 3	PPR containing plant protein
Sapur.016G082500.1	378.5033458	-0.026910794	0.037699571	-0.71382	0.475337079	0.549561246	grey	-0.117728687	0.141979339		AT5G03080.1		Phosphatidic acid phosphatase (PAP2) family protein	dolichyldiphosphatase
Sapur.008G001700.1	263.9104109	-0.039333068	0.055110416	-0.71371	0.475404129	0.549619553	grey	-0.085172997	0.288864901	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G20260.1		Protein of unknown function (DUF1666)	DUF1666 family protein
Sapur.016G179100.1	0.550420527	-0.279876665	0.392594269	-0.71289	0.475913613	0.55018934	grey	-0.067552481	0.400556911		AT3G19508.1			NA
Sapur.008G017400.7	8.405305247	0.075721879	0.106270889	0.712536	0.476132664	0.550423339	grey	0.068873677	0.391385824	GO:0006468,GO:0004672	AT5G03730.1	AtCTR1,CTR1,SIS1	Protein kinase superfamily protein	Serine/Threonine-kinase CTR1
Sapur.009G019100.3	0.217854236	0.413057108	0.579827953	0.712379	0.476230276	0.550516939	grey	0.16132214	0.043544459	GO:0006468,GO:0005524,GO:0004672	AT1G07870.2		Protein kinase superfamily protein	receptor Serine/Threonine kinase, putative
Sapur.019G043800.1	8.499792985	0.150574233	0.2115103	0.7119	0.476526553	0.550840179	grey	0.067477969	0.401077911		AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.010G127300.2	0.261390646	0.31944235	0.449047222	0.711378	0.476849979	0.551194779	grey	0.078548531	0.32814497		AT1G14020.1		O-fucosyltransferase family protein	GDP-fucose O-fucosyltransferase-like protein
Sapur.15WG091200.1	0.136785367	0.536325793	0.754137747	0.711177	0.476974253	0.55131916	grey	0.164885231	0.039051586	GO:0003682,GO:0006351,GO:0005634,GO:0003677	AT3G48050.1		BAH domain ;TFIIS helical bundle-like domain	BAH and TFIIS domain protein
Sapur.005G179600.1	22.8185477	-0.145370701	0.20442594	-0.71112	0.47701192	0.55134343	grey	-0.056815113	0.479707115		AT1G06190.1		Rho termination factor	NA
Sapur.013G048600.1	0.091963676	0.683517903	0.962060269	0.710473	0.477410831	0.551765938	grey	0.312543767	6.74E-05		AT5G39110.1		RmlC-like cupins superfamily protein	NA
Sapur.010G185800.2	0.148169701	-0.554563189	0.780832674	-0.71022	0.477567556	0.551927785	grey	-0.263751895	0.000844764	GO:0008138,GO:0006470	AT3G52180.1	ATPTPKIS1,ATSEX4,DSP4,SE	dual specificity protein phosphatase (DsPTP1) family protein	tyrosine phosphatase, putative
Sapur.007G019900.1	24.22672868	-0.081074817	0.114221768	-0.7098	0.477827048	0.552189091	grey	-0.119542722	0.135896059		AT3G50900.1			hypothetical protein
Sapur.002G201100.1	2883.300536	0.061790103	0.087080807	0.709572	0.477969583	0.552334509	grey	0.029145495	0.717089965		AT5G44030.1	CESA4,IRX5,NWS2	cellulose synthase A4	cellulose synthase A catalytic subunit 4 [UDP-forming] protein
Sapur.001G011500.1	3.33247967	-0.134453804	0.189548484	-0.70934	0.478115205	0.552483484	grey	-0.033506327	0.676974556	GO:0006468,GO:0005524,GO:0004672	AT5G60900.1	RLK1	receptor-like protein kinase 1	G-type lectin S-receptor-like Serine/Threonine-kinase RLK1, putative
Sapur.15WG018700.1	0.25360228	0.338329742	0.476984624	0.70931	0.478132413	0.552484066	grey	0.043113487	0.591859751	GO:0055085,GO:0042626,GO:0016021,GO:0016810,GO:0005524,GO:0016887	AT3G59140.1	ATMRP14,MRP14	multidrug resistance-associated protein 14	multidrug resistance protein ABC transporter family protein, putative
Sapur.002G180000.6	0.255990145	0.342770744	0.483401801	0.70908	0.478274583	0.552629037	grey	0.029189579	0.716680313	GO:0005634,GO:0005515	AT1G05830.1	ATX2,SDG30	trithorax-like protein 2	histone-lysine N-methyltransferase ATX2
Sapur.T096700.1	2.698248887	0.10210264	0.144020948	0.708943	0.478359862	0.552708265	grey	0.061651204	0.44305513	GO:0043531	AT3G14460.1		LRR and NB-ARC domains-containing disease resistance protein	NA
Sapur.T002800.1	1.072774091	0.193999316	0.2737957	0.708555	0.478600663	0.552967174	grey	0.062840053	0.434294096					NA
Sapur.012G054900.1	9.758431861	-0.091998987	0.130072196	-0.70729	0.479385214	0.553858283	grey	-0.064050397	0.425477351		AT1G04555.1			transmembrane protein, putative
Sapur.019G058300.1	1.688600432	0.149887564	0.212059003	0.70682	0.479678286	0.554154166	grey	0.061085048	0.447262236		AT5G17020.1	ATCRM1,ATXPO1,HIT2,XPO	exportin 1A	NA
Sapur.012G054200.4	0.807738346	0.203316548	0.287661325	0.706791	0.479696125	0.554155419	grey	0.026509322	0.741729082		AT5G13690.1	CYL1,NAGLU	alpha-N-acetylglucosaminidase family / NAGLU family	alpha-N-acetylglucosaminidase
Sapur.019G010300.1	2.449620346	-0.181092514	0.256272105	-0.70664	0.47978927	0.554243662	grey	-0.084693424	0.291598462					NA
Sapur.005G086100.1	20.89907638	0.058331056	0.082588355	0.706287	0.480009868	0.554479127	grey	-0.013629651	0.865464566	GO:0003824,GO:0006470,GO:0004722	AT3G51370.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.011G017400.1	0.46594221	-0.293339512	0.415343294	-0.70626	0.480027726	0.55448039	grey	-0.084605236	0.292103001		AT4G16050.1		Aminotransferase-like, plant mobile domain family protein	NA
Sapur.003G010400.1	0.441082858	-0.289368369	0.40988298	-0.70598	0.480201816	0.55466211	grey	-0.085725039	0.285739505		AT2G25737.1		Sulfite exporter TauE/SafE family protein	NA
Sapur.001G056600.4	4.998017772	-0.101758768	0.144188828	-0.70573	0.480354394	0.554818971	grey	0.051293084	0.52348359		AT5G47890.1		NADH-ubiquinone oxidoreductase B8 subunit, putative	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2
Sapur.007G027100.1	0.111607257	-0.644778917	0.913984086	-0.70546	0.480524218	0.554995739	grey	-0.323362411	3.61E-05	GO:0016758,GO:0008152	AT3G50740.1	UGT72E1	UDP-glucosyl transferase 72E1	NA
Sapur.001G178200.1	0.676402248	-0.28034616	0.39742716	-0.7054	0.480559713	0.555017354	grey	-0.101930543	0.203980908					NA
Sapur.018G061800.2	18.96500491	-0.05984738	0.085006587	-0.70403	0.481412677	0.555963647	grey	-0.031573424	0.694651598	GO:0006468,GO:0005524,GO:0004672,GO:0003824	AT2G20050.1		protein serine/threonine phosphatases;protein kinases;catalytics;cAMP-dependent protein kinase regulators;ATP	protein phosphatase 2C and cyclic nucleotide-binding/kinase domain protein
Sapur.006G225100.1	0.174392963	0.375100912	0.532954509	0.703814	0.481548535	0.55608171	grey	0.079859416	0.320111688		AT4G31410.1		Protein of unknown function (DUF1644)	DUF1644 family protein
Sapur.007G028900.1	8.510657453	-0.097789904	0.138977231	-0.70354	0.481720221	0.556260547	grey	-0.099975999	0.212834505		AT2G18630.1		Protein of unknown function (DUF677)	transmembrane protein, putative
Sapur.010G051500.1	3.978668229	-0.134204202	0.19081222	-0.70333	0.481849324	0.556390202	grey	-0.049549889	0.53771257	GO:0005515	AT1G73080.1	ATPEPR1,PEPR1	PEP1 receptor 1	NA
Sapur.005G205900.2	19.38564038	-0.098383058	0.139911439	-0.70318	0.481942992	0.556478931	grey	-0.052889872	0.510619676		AT2G33585.1			transmembrane protein, putative
Sapur.009G034700.5	0.39531425	-0.278655161	0.396666123	-0.70249	0.482371787	0.556915715	grey	-0.043504581	0.58849997		AT5G58740.1		HSP20-like chaperones superfamily protein	NUDCD2-like protein
Sapur.002G204000.1	1241.731613	-0.030072206	0.04281202	-0.70242	0.482414559	0.556945655	grey	-0.049753034	0.536044529	GO:0005515	AT5G42950.1		GYF domain-containing protein	GYF domain protein
Sapur.004G166300.2	0.176286409	0.543525889	0.774209315	0.70204	0.482654233	0.557202908	grey	0.098224181	0.221000394		AT5G01750.1		Protein of unknown function (DUF567)	tubby C 2 protein
Sapur.011G059900.7	0.274859519	-0.391376101	0.557596007	-0.7019	0.482742128	0.557283454	grey	-0.111161194	0.16574236		AT1G29350.1		Kinase-related protein of unknown function (DUF1296)	plant/F15D2-27 protein, putative
Sapur.014G133300.3	0.11331767	0.670147185	0.9547969	0.701874	0.482757702	0.557283454	grey	0.262719162	0.000886897	GO:0005737,GO:0005094	AT3G07880.1	SCN1	Immunoglobulin E-set superfamily protein	Rho GDP-dissociation inhibitor, putative
Sapur.004G032000.1	319.8755348	-0.052317426	0.074604643	-0.70126	0.483139312	0.55770451	grey	-0.072469591	0.36707185					NA
Sapur.003G021600.1	48.28808642	-0.129877765	0.185248202	-0.7011	0.483239765	0.557800998	grey	-0.081138	0.312400094		AT3G13890.2	ATMYB26,MS35,MYB26	myb domain protein 26	Myb transcription factor
Sapur.011G019400.1	0.477300831	0.272773294	0.389156766	0.700934	0.483344068	0.557901923	grey	0.061723023	0.442523048					NA
Sapur.005G035000.1	69.05985752	0.057277898	0.081728648	0.70083	0.483409043	0.557957448	grey	0.062043387	0.440153995		AT1G12700.1		ATP binding;nucleic acid binding;helicases	PPR containing plant protein, putative
Sapur.013G033500.1	34.0210748	-0.09887629	0.141098262	-0.70076	0.483451601	0.557987097	grey	-0.053809622	0.503285043					hypothetical protein
Sapur.002G177200.1	2.289394499	-0.206321426	0.294483136	-0.70062	0.483538814	0.558068281	grey	-0.076961243	0.338043885		AT4G27870.1		Vacuolar iron transporter (VIT) family protein	NA
Sapur.15WG152200.4	0.186872288	-0.491117057	0.701225504	-0.70037	0.483696488	0.558230778	grey	-0.184112336	0.02098498	GO:0008168,GO:0006139	AT4G09980.1	EMB1691	Methyltransferase MT-A70 family protein	methyltransferase-like protein
Sapur.012G108500.1	9.155818476	-0.096023348	0.137139811	-0.70019	0.483811281	0.558343778	grey	-0.039484804	0.623439765		AT5G52290.1	SHOC1	shortage in chiasmata 1	NA
Sapur.011G063200.1	0.611347816	-0.245668331	0.350904582	-0.7001	0.483864797	0.558386054	grey	-0.106542888	0.184147027	GO:0008270,GO:0005515	AT1G53490.1		RING/U-box superfamily protein	NA
Sapur.001G135600.1	0.551552897	-0.265965559	0.379950188	-0.7	0.483926601	0.558437891	grey	0.341521306	1.20E-05		AT1G17280.2	UBC34	ubiquitin-conjugating enzyme 34	ubiquitin-conjugating enzyme E2, putative
Sapur.002G048700.1	2.617758155	-0.207141149	0.296013234	-0.69977	0.484071027	0.558585058	grey	-0.064692675	0.420841027	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT5G09970.1	CYP78A7	cytochrome P450, family 78, subfamily A, polypeptide 7	cytochrome P450 family 78 protein
Sapur.009G057800.2	14.25907025	-0.059485803	0.085038282	-0.69952	0.484228411	0.558747181	grey	-0.107887659	0.178639744	GO:0055085,GO:0046873,GO:0030001,GO:0016020	AT2G30080.1	ATZIP6,ZIP6	ZIP metal ion transporter family	ZIP zinc/iron transport family protein
Sapur.010G025300.3	0.118240953	0.553626358	0.791476697	0.699485	0.484248762	0.558751171	grey	0.095551196	0.233884693		AT1G10700.1	PRS3	phosphoribosyl pyrophosphate (PRPP) synthase 3	ribose-phosphate pyrophosphokinase
Sapur.010G036000.2	0.278393036	0.300758403	0.430309844	0.698935	0.484592955	0.559120479	grey	0.068757936	0.392184159		AT1G17350.1		NADH:ubiquinone oxidoreductase intermediate-associated protein 30	NADH dehydrogenase 1 alpha subcomplex, assembly factor 1
Sapur.001G125000.1	1083.207812	0.022851138	0.032694972	0.698919	0.484602638	0.559120479	grey	0.071798558	0.371536882	GO:0009073,GO:0003849	AT4G33510.1	DHS2	3-deoxy-d-arabino-heptulosonate 7-phosphate synthase	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase
Sapur.005G188300.3	4.783393385	0.081733823	0.1169531	0.69886	0.484639636	0.55914366	grey	0.081149024	0.312334134					hypothetical protein
Sapur.005G099200.1	0.124882418	0.746542076	1.068938625	0.698396	0.484929802	0.559458918	grey	0.244913322	0.001991787					NA
Sapur.014G011000.1	15.07669801	0.084398449	0.120910001	0.698027	0.485160291	0.559705307	grey	0.062339081	0.437973784	GO:0003723	AT5G56510.1	APUM12,PUM12	pumilio 12	pumilio-family RNA-binding repeatprotein
Sapur.014G081000.4	0.955759767	-0.182592995	0.261626529	-0.69791	0.485230552	0.559766839	grey	0.020932318	0.794698864	GO:0046540,GO:0000398,GO:0000244	AT1G60170.1	emb1220	pre-mRNA processing ribonucleoprotein binding region-containing protein	U4/U6 small nuclear ribonucleoprotein Prp31
Sapur.017G061100.1	0.666532448	0.223513366	0.32038608	0.697638	0.48540388	0.559947261	grey	0.037271939	0.643045307	GO:0008270,GO:0008022,GO:0006625,GO:0005779	AT3G04460.1	APM4,ATPEX12,PEX12	peroxin-12	NA
Sapur.019G024800.1	13.45494375	-0.095258484	0.136564313	-0.69754	0.485467604	0.56000124	grey	-0.022524409	0.779469655	GO:0006629	AT5G43590.1		Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein	NA
Sapur.018G063600.2	11.95523868	-0.083711375	0.120050947	-0.6973	0.48561585	0.560152709	grey	-0.034969293	0.663710799	GO:0055114,GO:0004471,GO:0051287	AT1G79750.1	ATNADP-ME4,NADP-ME4	NADP-malic enzyme 4	malic enzyme NAD(P) binding domain protein
Sapur.005G040800.1	0.60906924	0.300196833	0.430856589	0.696744	0.485962888	0.560533464	grey	0.039909926	0.619702786		AT4G14640.1	CAM8	calmodulin 8	calmodulin
Sapur.15WG077400.1	0.281718084	0.365302128	0.524402363	0.696607	0.486049047	0.560613293	grey	-0.000196527	0.998050929		AT1G33800.1		Protein of unknown function (DUF579)	NA
Sapur.016G023100.2	22.41517045	-0.060706386	0.087156783	-0.69652	0.486103641	0.56065671	grey	-0.484852829	1.24E-10		AT5G05080.1	ATUBC22,UBC22	ubiquitin-conjugating enzyme 22	ubiquitin-conjugating enzyme E2
Sapur.005G086100.5	12.41793037	0.062148207	0.089252208	0.696321	0.486227685	0.560780223	grey	0.047014349	0.558746695	GO:0003824,GO:0006470,GO:0004722	AT3G51370.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.016G306200.1	0.093063572	0.707474009	1.016167571	0.696218	0.486292406	0.560835311	grey	0.300647324	0.000130297	GO:0046872,GO:0030001	AT4G05030.1		Copper transport protein family	NA
Sapur.016G002500.1	182.5911419	0.037477273	0.053853913	0.695906	0.486487563	0.56104082	grey	-0.425023023	2.88E-08	GO:0055085,GO:0016021,GO:0015299,GO:0006812	AT1G79610.1	ATNHX6,NHX6	Na+/H+ antiporter 6	sodium/hydrogen exchanger
Sapur.017G001800.2	0.443572093	-0.285428241	0.410215854	-0.6958	0.486554013	0.561096627	grey	0.375631583	1.25E-06	GO:0006468,GO:0005524,GO:0004672	AT5G48380.1	BIR1	BAK1-interacting receptor-like kinase 1	tyrosine kinase domain protein
Sapur.15ZG058100.1	8.230523931	-0.094957893	0.136477917	-0.69577	0.486569885	0.561096627	grey	-0.072027294	0.370011147					NA
Sapur.019G021300.1	242.9526098	0.044456094	0.06393597	0.695322	0.486853453	0.56140098	grey	0.035198794	0.661639912	GO:0048544,GO:0006468,GO:0005524,GO:0004672	AT5G60900.1	RLK1	receptor-like protein kinase 1	Serine/Threonine kinase domain protein
Sapur.003G012300.6	8.329944042	-0.076449743	0.109952281	-0.6953	0.48686776	0.56140098	grey	-0.003520112	0.965100058	GO:0016758,GO:0008152	AT5G24750.1		UDP-Glycosyltransferase superfamily protein	sterol glucosyltransferase-like protein
Sapur.016G009000.1	0.210822725	0.403083144	0.580196196	0.694736	0.487220806	0.561788487	grey	0.080139807	0.318410088					NA
Sapur.016G255000.1	1048.904706	-0.020712726	0.029827032	-0.69443	0.487413843	0.561991474	grey	-0.072152146	0.369179977	GO:0043248	AT3G15180.1		ARM repeat superfamily protein	26S proteasome non-ATPase regulatory subunit, putative
Sapur.019G001700.1	1020.54929	-0.264361569	0.38103592	-0.6938	0.487809539	0.562404045	grey	-0.079451017	0.322600642		AT5G25610.1	ATRD22,RD22	BURP domain-containing protein	BURP domain protein
Sapur.009G079000.5	0.410207484	0.265462582	0.382742816	0.69358	0.487945935	0.562526538	grey	0.045838021	0.568637789		AT4G34000.3	ABF3,DPBF5	abscisic acid responsive elements-binding factor 3	ABA responsive element-binding factor
Sapur.013G123900.1	11.13314444	-0.09172531	0.132257588	-0.69354	0.487973663	0.562538897	grey	0.165756082	0.038014805		AT4G28260.2			monothiol glutaredoxin-S11 protein, putative
Sapur.006G002500.1	1.390391851	-0.172471006	0.248972526	-0.69273	0.488478332	0.563081429	grey	-0.066918553	0.405002337					NA
Sapur.006G090600.1	0.40002403	-0.336755461	0.486217458	-0.6926	0.488558997	0.563154786	grey	-0.091281463	0.25554286	GO:0003993	AT2G38600.1		HAD superfamily, subfamily IIIB acid phosphatase	acid phosphatase
Sapur.004G166800.2	0.806394853	-0.221514945	0.320130887	-0.69195	0.488967988	0.56358694	grey	-0.070290263	0.381694135	GO:0030170,GO:0008483	AT3G08860.1	PYD4	PYRIMIDINE 4	alanine-glyoxylate aminotransferase, putative
Sapur.011G098700.2	0.164938546	-0.467112692	0.675443195	-0.69156	0.489210716	0.56384706	grey	-0.205317787	0.009891216		AT4G21880.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.006G207400.1	0.543543586	0.234518253	0.339155921	0.691476	0.489266323	0.563891499	grey	0.324792784	3.32E-05		AT4G32440.1		Plant Tudor-like RNA-binding protein	agenet domain protein
Sapur.T121100.1	0.098365723	0.743698034	1.075619219	0.691414	0.489305498	0.563916999	grey	0.297137342	0.000157406		AT5G37055.1	ATSWC6,SEF	HIT-type Zinc finger family protein	NA
Sapur.013G047400.1	2.70329464	0.24827988	0.359149095	0.6913	0.489376839	0.563979566	grey	0.061003738	0.447868295		AT5G39130.1		RmlC-like cupins superfamily protein	rhicadhesin receptor, putative
Sapur.016G053100.1	0.155453546	0.722480849	1.0452267	0.691219	0.489427749	0.564018584	grey	0.10142553	0.20624264					NA
Sapur.016G131600.1	0.539264953	-0.228123384	0.330163382	-0.69094	0.489602683	0.564200521	grey	-0.05489958	0.494664951		AT2G28840.1	XBAT31	XB3 ortholog 1 in Arabidopsis thaliana	E3 ubiquitin-protein ligase
Sapur.005G120200.1	1.811613744	0.123884954	0.179357789	0.690714	0.489745224	0.564345116	grey	0.025500973	0.751225032					NA
Sapur.002G178900.1	10.28273967	-0.069924743	0.101247041	-0.69063	0.489794993	0.564382803	grey	-0.071713446	0.372105587		AT1G05790.1		lipase class 3 family protein	NA
Sapur.005G116700.1	0.080867965	0.707027303	1.023813729	0.690582	0.489828281	0.564401497	grey	0.295534369	0.000171459					NA
Sapur.005G004700.1	1.28206326	0.185358366	0.268467417	0.690432	0.489922861	0.56449081	grey	0.073724061	0.358813925	GO:0016021,GO:0016020,GO:0022857	AT1G09380.1		nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4
Sapur.15WG130000.2	0.410409715	0.249973518	0.36212601	0.690294	0.490009136	0.564570549	grey	0.053624197	0.50475928	GO:0005525	AT5G45130.1	ATRAB-F2A,ATRAB5A,ATRA	RAB homolog 1	Ras-related protein Rab5
Sapur.006G138800.1	0.404445481	0.258430369	0.374621468	0.689844	0.490292301	0.564857446	grey	0.062022397	0.440308995					NA
Sapur.005G123100.1	4.890167691	0.132286192	0.191839057	0.689569	0.490465515	0.56503732	grey	0.034584094	0.667193248					NA
Sapur.005G121500.6	10.94065559	-0.069508294	0.100846489	-0.68925	0.490666885	0.565249619	grey	-0.057153857	0.477087624		AT4G07990.1		Chaperone DnaJ-domain superfamily protein	heat shock protein-binding protein
Sapur.001G026900.4	3.078153121	0.098028975	0.142237077	0.689194	0.490701037	0.565269273	grey	-0.028365773	0.724348685	GO:0004869	AT3G12490.2	ATCYS6,ATCYSB,CYSB	cystatin B	NA
Sapur.001G186900.1	2.142530327	-0.199022633	0.289011326	-0.68863	0.491054472	0.565637015	grey	-0.085129646	0.289111298					NA
Sapur.001G140800.1	11.08974538	-0.078140934	0.113480633	-0.68858	0.491085171	0.565652676	grey	-0.028247698	0.725450049	GO:0030983,GO:0006298,GO:0005524	AT4G17380.1	ATMSH4,MSH4	MUTS-like protein 4	DNA mismatch repair protein MutS
Sapur.016G149200.2	5.128904593	0.094995459	0.138078467	0.687982	0.491464302	0.566069662	grey	0.091456335	0.254629584		AT5G13800.2	CRN1,PPH	pheophytinase	alpha/beta fold hydrolase
Sapur.001G116300.1	1019.835895	0.030884926	0.044897674	0.687896	0.491518336	0.566112183	grey	0.016171015	0.840685907	GO:0055114,GO:0016491,GO:0008270	AT5G61510.1		GroES-like zinc-binding alcohol dehydrogenase family protein	quinone oxidoreductase
Sapur.016G110200.1	22.55868014	-0.19336107	0.281221898	-0.68757	0.491720627	0.566323348	grey	-0.069329295	0.388252662		AT2G34450.2		HMG-box (high mobility group) DNA-binding family protein	NA
Sapur.016G026900.1	0.150262212	-0.546237306	0.794468696	-0.68755	0.491735923	0.566323348	grey	-0.23378654	0.003209999	GO:0008270,GO:0005515	AT2G40830.1	RHC1A	RING-H2 finger C1A	thioredoxin-like protein, putative
Sapur.011G108600.3	0.21883366	-0.455775121	0.663056502	-0.68739	0.491840121	0.566423628	grey	-0.111398823	0.164833869	GO:0016746,GO:0008152,GO:0006644	AT1G78690.1		Phospholipid/glycerol acyltransferase family protein	phospholipid/glycerol acyltransferase family protein
Sapur.018G085600.1	1.607854127	-0.15359437	0.223579951	-0.68698	0.492096982	0.566660246	grey	-0.007372139	0.926987467	GO:0005975,GO:0004553	AT4G19810.1		Glycosyl hydrolase family protein with chitinase insertion domain	NA
Sapur.15WG059700.1	0.096349994	0.624630239	0.909490122	0.686792	0.492214021	0.566775285	grey	0.283237669	0.000325026					NA
Sapur.019G071100.1	1.69294471	0.169989521	0.247537084	0.686723	0.492257016	0.56680506	grey	0.037983816	0.636710461	GO:0006355,GO:0003700	AT1G22810.1		Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.006G134800.1	224.8683041	-0.038057261	0.055499648	-0.68572	0.492889203	0.567486091	grey	-0.042908563	0.593623675	GO:0016773,GO:0005975,GO:0005524,GO:0046835,GO:0005536,GO:0004396,GO:000167	AT4G29130.1	ATHXK1,GIN2,HXK1	hexokinase 1	hexokinase
Sapur.002G103700.1	263.4275747	0.03113364	0.045403923	0.685704	0.49289995	0.567486091	grey	0.061331387	0.445428928	GO:0055114,GO:0016616,GO:0006694,GO:0003854	AT4G33360.1	FLDH	NAD(P)-binding Rossmann-fold superfamily protein	dihydroflavonol-4-reductase
Sapur.013G013400.1	513.8342434	-0.046926125	0.068461177	-0.68544	0.493065426	0.567656847	grey	-0.121714269	0.128878344		AT1G02816.1		Protein of unknown function, DUF538	DUF538 family protein
Sapur.007G077100.1	1.033255029	-0.169565844	0.247593881	-0.68485	0.493435587	0.568060748	grey	-0.101939205	0.203942268		AT5G64940.1	ATATH13,ATH13,ATOSA1,O:	ABC2 homolog 13	ABC transporter-like protein
Sapur.014G041300.2	0.491978828	0.251780974	0.3676542	0.684831	0.493450604	0.568060748	grey	-0.021045355	0.793614975		AT4G13970.1		zinc ion binding	zinc ion-binding protein
Sapur.005G171900.1	10.0576366	0.077038328	0.112575823	0.684324	0.49377065	0.5684094	grey	0.022341312	0.781216935					hypothetical protein
Sapur.15WG048700.1	0.65697633	-0.256339531	0.374828674	-0.68388	0.494048084	0.568691165	grey	-0.098529715	0.219560398	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT3G47570.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.016G105000.1	33.69614483	0.130955672	0.191488751	0.683882	0.494049805	0.568691165	grey	0.082948874	0.301687216	GO:0005515	AT1G45616.1	AtRLP6,RLP6	receptor like protein 6	verticillium wilt disease resistance protein
Sapur.014G034000.1	0.172767843	0.491284105	0.718824462	0.683455	0.494319435	0.568961928	grey	0.129848045	0.10504776		AT1G25370.1		Protein of unknown function (DUF1639)	NA
Sapur.003G075000.6	0.771740028	-0.192571648	0.281983523	-0.68292	0.494658606	0.569312688	grey	0.123592916	0.123035096	GO:0005515,GO:0008270	AT4G25230.2	RIN2	RPM1 interacting protein 2	E3 ubiquitin protein ligase RIN3
Sapur.007G109700.1	121.3312914	0.067383645	0.098751512	0.682356	0.495014139	0.56968223	grey	0.021370549	0.790498945		AT1G01380.1	ETC1	Homeodomain-like superfamily protein	MYB transcription factor
Sapur.016G125800.1	0.805943801	0.213928937	0.313659221	0.682043	0.495212043	0.569890157	grey	0.031486707	0.695448605		AT1G05577.1		Domain of unknown function (DUF966)	DUF966 domain protein
Sapur.004G158600.1	0.232747906	-0.453674172	0.665450673	-0.68175	0.495394027	0.570079749	grey	-0.187127963	0.018938532		AT5G03170.1	ATFLA11,FLA11	FASCICLIN-like arabinogalactan-protein 11	fasciclin-like AGP protein
Sapur.019G081500.2	0.440884667	0.243622708	0.357447745	0.681562	0.495516112	0.5702004	grey	0.045695525	0.569841564	GO:0005515	AT5G56150.1	UBC30	ubiquitin-conjugating enzyme 30	ubiquitin-conjugating enzyme E2, putative
Sapur.013G056100.3	4.618911208	0.088200396	0.129516437	0.680998	0.495872943	0.570591161	grey	0.099022976	0.217249737	GO:0006491	AT5G56360.1	PSL4	calmodulin-binding protein	glucosidase II beta subunit, putative
Sapur.008G072700.1	289.5794892	0.059435805	0.087311716	0.680731	0.496041618	0.570765393	grey	0.028950545	0.718902486		AT2G03350.1		Protein of unknown function, DUF538	DUF538 family protein
Sapur.002G189600.1	0.20713448	-0.369192567	0.54250134	-0.68054	0.496164114	0.570866621	grey	-0.182633986	0.02205608					NA
Sapur.014G050500.1	23.35315671	-0.077886756	0.114474888	-0.68038	0.496262046	0.570956168	grey	-0.057661688	0.47317516		AT5G62280.1		Protein of unknown function (DUF1442)	DUF1442 family protein
Sapur.018G079100.1	1.047031902	-0.219920888	0.323241887	-0.68036	0.496276469	0.570956168	grey	-0.088402928	0.270900568	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT2G24130.1		Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.009G094700.1	226.2197651	-0.182423727	0.268257	-0.68003	0.496483295	0.571174249	grey	-0.125973992	0.115926065		AT4G34588.1	CPuORF2	conserved peptide upstream open reading frame 2	BZIP transcription factor ATB2
Sapur.001G170500.1	1.611983594	-0.177024195	0.260342405	-0.67997	0.496525476	0.571202907	grey	-0.048171083	0.5491018	GO:0046983,GO:0003677	AT3G42170.1		BED zinc finger ;hAT family dimerisation domain	hAT-like transposase
Sapur.001G163600.3	0.864813412	-0.23659775	0.348098781	-0.67969	0.496703517	0.571370839	grey	-0.077137704	0.336934116		AT1G69750.1	ATCOX19-2,COX19-2	cytochrome c oxidase 19-2	cytochrome C oxidase assembly protein COX19
Sapur.003G038900.1	1213.271964	0.021624969	0.031816317	0.679682	0.496706003	0.571370839	grey	0.008284825	0.917978229	GO:0016021	AT1G72480.1		Lung seven transmembrane receptor family protein	lung seven transmembrane receptor
Sapur.019G043700.1	0.133286182	0.556977259	0.820297966	0.678994	0.49714177	0.571832333	grey	0.214419042	0.007004479					NA
Sapur.001G052200.2	6.649212222	-0.077198847	0.113738486	-0.67874	0.497302687	0.571997533	grey	-0.042902026	0.593679985		AT2G33550.1		Homeodomain-like superfamily protein	myb/SANT-like DNA-binding domain protein
Sapur.006G029700.1	44.60111449	-0.066289264	0.09777965	-0.67795	0.497806309	0.572556888	grey	-0.125986756	0.115888837	GO:0006468,GO:0005524,GO:0004672	AT2G41140.1	ATCBK3,ATCRK1,CRK1	CDPK-related kinase 1	CDPK-related kinase
Sapur.014G115000.1	12.17074233	-0.063492668	0.093659538	-0.67791	0.497829234	0.572563344	grey	-0.044210226	0.582460135	GO:0016787	AT2G42810.2	PAPP5,PP5,PP5.2	protein phosphatase 5.2	serine/threonine-protein phosphatase
Sapur.005G191900.1	22.9632597	0.134884402	0.198983924	0.677866	0.497856771	0.572575104	grey	0.046123836	0.566226921		AT1G75750.2	GASA1	GAST1 protein homolog 1	cold-regulated LTCOR12 protein
Sapur.007G103300.1	0.93983267	-0.197065998	0.290825771	-0.67761	0.498019992	0.572730545	grey	-0.023478963	0.770378455	GO:0009733	AT1G29500.1		SAUR-like auxin-responsive protein family	NA
Sapur.013G052300.1	111.4144485	-0.049930145	0.073686964	-0.6776	0.498026561	0.572730545	grey	-0.063759967	0.427583499		AT3G13540.1	ATMYB5,MYB5	myb domain protein 5	MYB transcription factor
Sapur.008G129500.1	1988.000384	0.034487678	0.050929207	0.677169	0.49829876	0.573023649	grey	0.025823351	0.748184953	GO:0030955,GO:0006096,GO:0004743,GO:0000287	AT3G22960.1	PKP-ALPHA,PKP1	Pyruvate kinase family protein	pyruvate kinase
Sapur.016G240800.2	1.19317442	0.167729791	0.24796149	0.676435	0.498764603	0.573539409	grey	0.063796031	0.427321639		AT1G73140.1	TBL31	Plant protein of unknown function (DUF828)	Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.016G173600.1	0.114242772	-0.688229124	1.017609501	-0.67632	0.49883783	0.573603671	grey	-0.26269716	0.000887815	GO:0006629	AT5G14930.2	SAG101	senescence-associated gene 101	lipase

Sapur.001G107500.1	0.18099579	-0.45307752	0.670115285	-0.67611	0.468869709	0.573735369	grey	-0.169820077	0.033477875	GO:0051743	AT4G00910.1	Aluminum activated malate transporter family protein	aluminum activated malate transporter
Sapur.001G122500.1	0.168661574	0.388134667	0.574782112	0.675273	0.499505236	0.574308091	grey	-0.131242324	0.101335084	GO:0043189,GO:0006355,GO:0005634	AT1G26470.1	chromatin modification-related protein Eaf7	chromatin modification-related protein Eaf7
Sapur.006G221400.1	0.1717851	0.562734072	0.836201665	-0.6769	0.499937072	0.574787733	grey	-0.118073517	0.012587132		AT2G28680.1	Protein of unknown function (DUF1631)	UPA23, putative
Sapur.006G195100.1	1.542955859	0.547121628	0.218204891	-0.67424	0.505100792	0.57502496	grey	-0.051164841	0.52612831		AT5G10030.1	amino acid permease 8	amino acid permease
Sapur.006G189100.1	7.815617668	0.104005727	0.154275871	-0.67415	0.500021281	0.57505198	grey	-0.029395151	0.7147038	GO:0005975,GO:0004553	AT2G01630.1	O-Glycosyl hydrolases family 17 protein	glucan endo-1\3\2-beta-glucosidase, putative
Sapur.008G063400.1	14.40476882	0.081996028	0.121629696	0.674145	0.500192033	0.57505198	grey	-0.046342249	0.56437958		AT5G05620.1	AS2	asymmetric leaves protein, putative
Sapur.011G104300.1	7599.170994	0.02463927	0.036402172	0.674118	0.500236123	0.57505198	grey	-0.011208754	0.889191481	GO:0005515	AT5G57310.1	AT5G57310.1,GSTB,GSTU19	glutathione S-transferase TAU 19
Sapur.003G095700.1	474.3686697	-0.030113638	0.044668982	-0.67392	0.500309151	0.57571015	grey	-0.074423263	0.354202824	GO:0004428,GO:0005634,GO:0004672	AT4F09.1,MAP44	MAP kinase 4	MAP kinase
Sapur.T026000.1	0.00774342	0.588039984	0.862188607	0.673681	0.500514217	0.57531291	grey	-0.242282894	0.002224328		AT5G38380.1		NA
Sapur.011G120900.1	12.13133312	0.079792982	0.11404088	-0.673	0.500715707	0.57568871	grey	-0.073051484	0.223268257		AT5G60511.1	Expressed protein	hypothetical protein
Sapur.010G207000.1	48.34659392	0.094698724	0.138826376	0.672978	0.50806131	0.57705518	grey	0.070212653	0.182231305		AT4G26800.1	DRB4	double-stranded-RNA-binding protein 4	NA
Sapur.002T144500.1	90.34486604	0.061860004	0.112626267	0.672667	0.501193301	0.57207212	grey	0.049743027	0.513727614		AT2G46880.1		plant/VHH17-10 protein, putative
Sapur.014G128500.1	20.19012967	0.074543567	0.110820097	0.672625	0.501185897	0.57388324	grey	-0.054034539	0.501499839		AT1G26470.1		NA
Sapur.003G204400.2	2.660795851	0.458842412	0.681264016	0.672618	0.501806306	0.57568631	grey	-0.029203304	0.717498947	GO:0016773,GO:0016020,GO:0005524	AT4F09.1,MPK1	mitogen-activated protein kinase 1	MAP kinase
Sapur.004G065800.1	3.350198604	0.191006595	0.284606562	0.670988	0.502220253	0.57707516	grey	-0.072037783	0.369701523		AT3G60160.1	AT3HDA5,HDA5,HDA5	histone deacetylase 5	class I histone deacetylase family protein
Sapur.013G076500.1	0.352870505	0.175031763	0.134002169	0.670071	0.502339256	0.57397516	grey	-0.100234602	0.21124069		AT2G44880.1	Helicase/SWI2/SNF2-related, DNA binding protein	NA
Sapur.017G033300.1	0.42370227	-0.284500706	0.42431883	-0.67049	0.503546719	0.57406732	grey	-0.069164802	0.389382085		AT1G77950.1	ATMYB52,BWS2,MYB52	myb domain protein 52	NA
Sapur.010G078800.5	0.26477187	0.332588802	0.49617525	0.670263	0.503800119	0.57551429	grey	0.012789547	0.87368541		AT2G29310.1		Protein of unknown function (DUF616)	NA
Sapur.T030000.2	0.160929216	0.303001312	0.450639093	0.669809	0.503929042	0.57841963	grey	0.102797742	0.201388984		AT5G27190.1	NA	NA
Sapur.008G010000.2	0.841981118	0.224841975	0.335885315	0.669411	0.503323341	0.57805222	grey	0.077632599	0.333834113	GO:0005198,GO:0031072	AT1G12120	DNA/ nucleosome 2	chaperone protein Dnaj
Sapur.007G021200.2	1.175605592	0.09792312	0.146075727	0.669257	0.503429794	0.57812491	grey	-0.055878526	0.488393522	GO:0007264,GO:0005525	AT2G18190.1	ARL2,ATARLC1,HAL,TTN5	ADP-ribosylation factor family protein	ADP-ribosylation factor(Arf)/Arf-like (Arl) small GTPase family protein
Sapur.T029200.1	15.4203966	-0.061777549	0.092420586	-0.66929	0.503324272	0.57825884	grey	-0.034924247	0.623928843				NA
Sapur.T018120.1	0.558725245	0.203474621	0.304239497	0.66882	0.503632027	0.57844304	grey	0.013920231	0.802422054		AT2G38455.1	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.008G169200.2	5.325837843	-0.083372403	0.123272366	-0.66821	0.503966572	0.57897462	grey	-0.073708833	0.371655278	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT5G61680.1	Ribosomal protein L34e superfamily protein	60S ribosomal protein L34, putative
Sapur.006G200800.2	0.140623752	0.458804412	0.68604469	0.667969	0.504179149	0.58169751	grey	-0.119162276	0.171353361	GO:0003674	AT5G61810.1	DUF1191 domain-containing protein	nucleic acid-binding protein
Sapur.005G065500.1	17.91914769	-0.070008788	0.104910211	-0.66732	0.504567103	0.57946383	grey	-0.065889774	0.412288466		AT4G14540.1	NF-YB3	nuclear factor Y, subunit B3	nuclear transcription factor Y subunit B-3
Sapur.006G154400.1	1.280894241	0.369936785	0.254681046	0.667253	0.504610308	0.57949588	grey	-0.060363307	0.454911435		AT3G22240.1			NA
Sapur.V049G025980.1	1.607862741	0.139436613	0.207498782	0.667163	0.504684037	0.57954201	grey	-0.078548531	0.31834487		AT1G64685.3	ATBPC2,BBR/BPC2,BPC2	basic pentacysteine 2	GAGA-binding transcriptional activator
Sapur.013G144600.1	0.406039952	0.310337983	0.465667147	0.666437	0.505131591	0.58004102	grey	-0.121609976	0.129288882		AT4G36510.1	EMB2777	Sec31/Lst1 ribonucleoprotein (trp) family protein	hypothetical protein
Sapur.010G132300.1	0.153320954	0.13101082	0.197434898	0.666622	0.505290931	0.58102951	grey	-0.077923414	0.332020686		AT3G18955.1	RING/U-box superfamily protein	RING/U-box superfamily protein	hypothetical protein
Sapur.006G196900.1	5.162812063	-0.105402797	0.158236204	-0.66615	0.505315568	0.58202775	grey	-0.047635992	0.513513288		AT5G35840.1	Protein of unknown function (DUF3677)	Protein of unknown function (DUF3677)	hypothetical protein
Sapur.003G105200.1	451.8908164	0.055424229	0.083236941	-0.66606	0.505327592	0.58204772	grey	-0.129578769	0.102302729		AT1G13120.1	CTL1,GL2,CSLG3	cellulose synthase like G3	cellulose synthase-like protein
Sapur.010G305400.1	0.117051268	0.61380716	0.95207362	0.66521	0.505461175	0.58303625	grey	0.250917761	0.005136199	GO:0055114,GO:0050660,GO:0016491	AT2G18620.1	FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.004G025400.1	2.284621344	0.301305934	0.453000484	-0.66369	0.506683211	0.58480807	grey	-0.125462511	0.117425548		AT4G27660.1	NDY1	Eukaryotic aspartyl protease family protein	digestive organs expansion factor-like protein
Sapur.004G002300.3	2.87478017	0.104824008	0.157554489	0.665319	0.505846427	0.58703963	grey	0.059278444	0.460834077	GO:0005524	AT5G61840.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	AAA family ATPase
Sapur.006G018300.1	0.920513944	0.186110344	0.279815546	0.665002	0.506005192	0.58708951	grey	-0.077729256	0.313848851	GO:0005667	AT5G60580.2	DWBP synthase RBB-like alpha/beta domain	RNA-threonylcarbamoyl adenosine modification protein, Sua5/YrdC/YrdC/YwlC family protein	NA
Sapur.009G025400.1	0.45866279	0.266393493	0.400572131	0.665032	0.506039705	0.58904114	grey	-0.023063886	0.7745279	GO:0005507,GO:0055114,GO:0016491	AT1A1C,LAC2	laccase 2	laccase	laccase
Sapur.I59G097000.1	0.198874216	-0.48205261	0.725534559	-0.66441	0.506427807	0.58134875	grey	-0.166885282	0.036705052		AT4G18730.1	ATMYB98,MYB98	myb domain protein 98	NA
Sapur.001G069900.3	0.280402775	0.158276857	0.420329464	0.6609	0.506754548	0.58169756	grey	0.027569688	0.7310652	GO:0005515	AT5G42010.1	Transducin/WD40 repeat-like superfamily protein	WD40 domain protein	NA
Sapur.008G163600.1	0.15242542	0.424780754	0.640411335	0.661284	0.507429152	0.58220904	grey	0.114820708	0.152160149		AT4G00960.1	AT4TH,ATH9	ABC2 homolog 8	ABC transporter-like protein
Sapur.013G081100.1	0.972127117	0.136568862	0.102180484	-0.66215	0.507874754	0.58240795	grey	-0.077344804	0.331204661	GO:0006260,GO:0005634	AT5G08015.1	POLD4	polymerase delta 4	NA
Sapur.004G149400.1	0.165473882	-0.486338189	0.73562788	-0.66112	0.508135546	0.58383763	grey	-0.25029952	0.010043923	GO:0008234,GO:0006508	AT5G22860.1	Serine carboxypeptidase S28 family protein	NA	NA
Sapur.010G203100.1	45.12108882	0.071011403	0.108450847	0.660617	0.508164017	0.58387481	grey	-0.067092269	0.48039122				NA	NA
Sapur.005G121100.1	0.102862786	0.623116227	0.955434139	0.660916	0.508660944	0.58738117	grey	0.250949933	0.00513926				NA	NA
Sapur.008G008900.1	4.43497023	0.137959504	0.208767867	-0.66083	0.508720078	0.58793313	grey	-0.048616058	0.543431919				NA	NA
Sapur.007G074900.1	4.96461234	0.108488372	0.164190122	-0.66075	0.508773632	0.5883107	grey	-0.042718454	0.595262202	GO:0019089				aphid transmission protein
Sapur.005G047700.2	32.28110716	-0.010888869	0.019096517	-0.66059	0.508875605	0.58380122	grey	-0.053180304	0.506679996	GO:0007165,GO:0005515,GO:0043531	AT5G17680.1	disease resistance protein (TIR-NBS-LRR class), putative		NA
Sapur.009G100300.1	0.176026978	0.554092286	0.726049388	-0.65899	0.509259172	0.58444824	grey	-0.226180909	0.003846657		AT4G38830.1	CRK26	cysteine-rich RLK (RECEPTOR-like protein kinase) 26	NA
Sapur.006G230600.1	0.164932175	0.375769087	0.569887582	0.659374	0.509635894	0.58742048	grey	0.090482213	0.241381754					NA
Sapur.014G095000.1	0.145543884	0.259022104	0.392196404	0.659165	0.509770044	0.58482441	grey	0.108588941	0.175816319	GO:0006457,GO:0003755	AT5G66554.1	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	cyclophilin-like peptidyl-prolyl cis-trans isomerase, putative	AvrRPC1F-rapidly elicited protein, putative
Sapur.001G162600.1	188.3401641	0.045820612	0.069578331	0.659122	0.50898174	0.58856483	grey	-0.046605017	0.563859892		AT5G21480.1			Translation initiation factor SUI1 family protein
Sapur.001G099500.2	0.277316882	0.17111684	0.261214864	0.658107	0.510163124	0.58180287	grey	-0.043660499	0.587149963	GO:0006413,GO:0003743	AT5G24290.1	Translation initiation factor SUI1 family protein	translation initiation factor SUI1, eukaryotic protein	
Sapur.006G127300.1	439.4911569	0.091580162	0.047062132	0.658439	0.510255767	0.58530874	grey	0.065399116	0.415775612	GO:0005634	AT2G15150.1	XCT	XAPS family protein	XAPS circadian timekeeper
Sapur.008G189600.1	0.736977272	0.138466369	0.211287377	0.658275	0.510495208	0.58584287	grey	0.041116287	0.697133408		AT4G25260.1		Ribosomal L29 family protein	60S/50S inner gene protein
Sapur.016G283900.1	79.35160155	0.037341	0.057132531	0.658043	0.510510061	0.58560184	grey	-0.009483171	0.996161168	GO:0005515	AT3G09830.1	AT3GTU19,GSTB,GSTU19	glutathione S-transferase TAU 19	glutathione S-transferase TAU 19
Sapur.005G088800.1	2.550933009	0.098855483	0.150586459	0.658039	0.510533193	0.58557263	grey	0.035357904	0.686093383	GO:0015550	AT4G15550.1	triglyceride hydrolase family protein	triacylglycerol lipase, putative	triacylglycerol lipase, putative
Sapur.002G220800.6	0.34802096	0.235952643	0.358612723	0.657969	0.510564165	0.58580996	grey	0.047639325	0.515315845	GO:0080028,GO:0019762	AT1G19715.2	Mannose-binding lectin superfamily protein	Mannose-binding lectin superfamily protein	NA
Sapur.011G087700.2	0.80407829	0.183768889	0.279400324	0.657726	0.510724266	0.58753284	grey	0.063830105	0.427270284	GO:0016021	AT5G09440.1	peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	peroxisomal membrane protein	peroxisomal membrane protein
Sapur.006G145800.1	0.325606444	0.497480054	0.756492125	-0.65708	0.510807245	0.58584776	grey	-0.168712168	0.054665158	GO:0005506,GO:0004190	AT2G19445.1	Eukaryotic aspartyl protease family protein	eukaryotic aspartyl protease	eukaryotic aspartyl protease
Sapur.007G029400.1	172.3864257	0.058811865	0.089466402	0.657363	0.510947892	0.58594776	grey	-0.049690706	0.538371665	GO:0016757	AT5G07680.1	galactoturonosyltransferase-like 2	CAZy family GT8 glycosyltransferase	CAZy family GT8 glycosyltransferase
Sapur.018G244400.1	1.551994671	0.101966211	0.155184378	0.656926	0.511084673	0.58704779	grey	-0.054875734	0.591262202	GO:0019089	AT5G18370.1	chromamo mutase	chorismate mutase	chorismate mutase
Sapur.018G077900.2	0.380223449	-0.264102337	0.404888798	-0.65722	0.511037107	0.58802232	grey	-0.052329294	0.476505331	GO:0005515	AT3G08360.1	AGH63,SDG4	SET domain group 4	SET domain protein
Sapur.006G150200.1	5.496863824	0.075426316	0.114218195	0.656709	0.511113876	0.58808679	grey	-0.047936936	0.435802606		AT5G15170.1		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.003G017000.1	181.1693908	-0.034013329	0.052450894	-0.65687	0.511265617	0.58222881	grey	-0.078119398	0.33802655		AT5G15630.1	RDD1	phosphatidic acid-phosphatase-related / PAP2-related	PAP2 family protein
Sapur.005G044400.4	0.103022084	0.364582422	0.563775049	-0.65681	0.511268167	0.58223883	grey	-0.110830848	0.048182621	GO:0006950,GO:0005516	AT5G18480.1	Calmodulin-binding family protein	calmodulin-binding protein	NA
Sapur.014G080000.1	231.9065499	0.062362218	0.094987261	0.656564	0.511481289	0.58404582	grey	0.021292757	0.791240057		AT4G46600.1	Calcium-binding EF-hand family protein	Calmodulin-like protein	NA
Sapur.008G162300.1	8.460231355	0.066423401	0.101767843	0.656377	0.511581588	0.58624197	grey	0.054823184	0.498192329	GO:0005515	AT2T3.10	PLX1	plant LRR domain-containing protein 1	NA
Sapur.003G030800.3	0.143446809	0.521645495	0.794090661	-0.65623	0.511676589	0.58610467	grey	-0.165474643	0.038347539		AT1G07180.1		Leucine-rich repeat family protein	cyclin-like F-box protein
Sapur.013G037200.1	295.3030728	-0.020888170	0.031840842	-0.65602	0.511812275	0.58676978	grey	-0.059195584	0.461502388	GO:0008152,GO:0003824	AT1G78240.1	CYP77A6P	cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene	mucorate cyclohexanone, putative
Sapur.001G060600.2	0.972355097	0.136170226	0.171721445	0.655709	0.511911309	0.58691887	grey	0.050934767	0.511760811	GO:0010021,GO:0006886,GO:0005319	AT5G07630.1	lipid transfer protein	Proteinase inhibitor, propeptide	nuclear division rf1-like protein
Sapur.001G145500.1	517.6869738	0.211795671	0.336080998	0.655652	0.512080035	0.58695721	grey	0.109509868	0.172162461		AT5G71950.1	Proteinase inhibitor, propeptide		NA
Sapur.011G081400.1	0.225680903	0.177860056	0.28174024	0.655547	0.512117252	0.58761219	grey	-0.159670546	0.04769484		AT4G05050.1	Ubiquitin family protein		NA
Sapur.001G129400.1	0.142122007	0.783949783	1.197017142	0.654919	0.512519162	0.58765787	grey	0.212328846	0.0079355	GO:0006281,GO:0003678,GO:0000723	AT5G41330.1	AEMRP,RID10,ATMYRB0,MS188	myb domain protein 103	Myb103 transcription factor, putative
Sapur.011G078100.1	0.107891937	0.70369269	1.088226847	0.654467	0.512813127	0.58770871	grey	-0.205481275	0.058872364		AT5G61130.1		Leucine-rich repeat receptor-like protein kinase family protein	receptor kinase-like protein
Sapur.002G053000.4	1.341311176	0.219189447	0.335007029	0.654267	0.512939713	0.58789743	grey	-0.201513614	0.011383015	GO:0055515,GO:0006488,GO:0005524,GO:0004672	AT4G08850.1	Leucine-rich repeat receptor-like protein kinase family protein	receptor kinase-like protein	
Sapur.005G151000.1	5.005769874	0.110188959	0.168427688	-0.65362	0.513160575	0.58852895	grey	-0.064187606	0.629575381		AT5G55150.1	BPS1	Protein of unknown function (DUF231)	BPS1
Sapur.007G106100.1	3.995710064	-0.257908025	0.394413231	-0.6539	0.513374251	0.58852885	grey	-0.005354549	0.529651614					NA
Sapur.006G032300.1	0.187085256	0.460267549	0.704768398	0.653047	0.513725973	0.58715973	grey	0.103777146	0.280229523					hypothetical protein
Sapur.001G126100.3	3.16677759	-0.045427874	0.067805973	-0.65299	0.513819329	0.58715973	grey	-0.044846406	0.581161519		AT4G25680.1	PPPDE putative thiol peptidase family protein	PPPDE peptidase domain protein	PPPDE peptidase domain protein
Sapur.016G272500.1	0.414027867	0.336657647	0.516443683	0.651953	0.514957045	0.58947493	grey	0.033401679	0.677927196		AT5G54062.1			NA
Sapur.001G136300.2	0.103476628	0.696230797	1.068279542	0.651789	0.515047388	0.58956525	grey	0.223624081	0.032232286		AT2G29150.1	NADP(H)-binding Rossmann-fold superfamily protein		3-ketoacyl-(acyl-carrier)-reductase
Sapur.006G135800.1	0.203691794	0.357360226	0.548327576	0.651691	0.515460436	0.58996938	grey	-0.235075381	0.003404699		AT3G02148.1			NA
Sapur.016G050300.1	0.141768232	0.511700893	0.785617787	-0.6129	0.516439789	0.58982076	grey	-0.293383939	0.000102152	GO:0006355,GO:0003700,GO:0007275	AT5G47522.1	Integrase-type DNA-binding superfamily protein		AP2-like ethylene-responsive transcription factor
Sapur.008G068800.1	0.69404593	0.209703893	0.322127402	0.650887	0.515132874	0.59202729	grey	0.015851189	0.842776731					hypothetical protein
Sapur.003G174200.1	0.141278837	0.667476873	0.72205551	0.650601	0.515349329	0.59201272	grey	0.085192924	0.28878384		AT5G17530.2	Protein of unknown function (DUF567)	Protein of unknown function (DUF567)	bubby C 2 protein
Sapur.003G158200.6	1.81900881	0.122305102	0.188019106	0.650524	0.515353748	0.59201781	grey	0.061614503	0.443237174	GO:0055114,GO:0016491,GO:0006631,GO:0003857,GO:0000152,GO:0003824	ATMRP2,MRP2	multifunctional protein 2	glycosyomal fatty acid beta-oxidation MFP-A protein	glycosyomal fatty acid beta-oxidation MFP-A protein
Sapur.005G085500.1	0.079503776	0.664188394	1.022183603	0.649744	0.515875157	0.59804171	grey	-0.389584676	0.003204491					NA
Sapur.013G111700.1	136.8543152	0.348091784	0.535908301	0.649536	0.515916925	0.59104786	grey	0.06468029	0.229697169	GO:0008168,GO:0008171	AT1MT1,DMT1	O-methyltransferase 1	O-methyltransferase 1	NA
Sapur.013G135100.1	5.664396116	0.369575117	0.415230402	0.64907	0.516292848	0.59372721	grey	0.07639864	0.3415976		ATFLA11,FLA11	FASCICLIN-like arabinogalactan-protein 11	fasciclin-like AGP protein	fasciclin-like AGP protein
Sapur.016G161000.1	10.45712158	0.055364487	0.085193934	-0.64896	0.516346616	0.59143831	grey	-0.076508018	0.345452051					DUF4228 domain protein
Sapur.016G245900.2	24.88595435	0.042188115	0.065047709	0.648527	0.516614979	0.59170031	grey	0.030868724	0.70118061					structural maintenance of chromosomes domain protein
Sapur.016G207100.1	0.300687931	0.270048872	0.417422759	0.647781	0.517132621	0.59230824	grey	0.026341005	0.743262537		AT5G01530.1	Plant protein of unknown function (DUF247)	Plant protein of unknown function (DUF247)	NA
Sapur.018G072500.1	4.976687168	0.093666191	0.144600403	0.647741	0.517125528	0.59274757	grey	0.05722369	0.476585274		AT5G21280.1			NA
Sapur.V049G085900.1	6.69926057	0.024101352	0.1152545	-0.64753	0.517180904	0.59240037	grey	-0.070980806	0.337932384	GO:0008270	AT1H7T2,T2	zinc ion binding	zinc finger protein, putative	zinc finger protein, putative
Sapur.010G095900.1	0.279701265	0.27031691	0.417505085	0.647506	0.517304726	0.59240837	grey	0.080409706	0.316777711		AT5G22740.1	glycine-rich protein	glycine-rich protein	NA
Sapur.008G244700.1	158.1608069	0.049111844	0.075059648	-0.64655	0.517620269	0.59284491	grey	-0.06820267	0.393616117	GO:0005515	AT1G07750.1	Tetratricopeptide repeat (TPR)-like superfamily protein	male sterility MS5 family protein	male sterility MS5 family protein
Sapur.006G208200.2	5.914892091	0.077395614	0.120047025	0.644751	0.519134612	0.59449523	grey	0.030515159	0.70468205		AT5G11280.1			transmembrane protein, putative
Sapur.016G266800.1	0.148027866	0.470088488	0.730170064	0.644489	0.519238388	0.59482874	grey	0.124423038	0.135195329	GO:0016757	AT2G18960.1	Glycosyltransferase family 61 protein		NA
Sapur.009G005800.1	29.56238377	0.073897299	0.114604422	0.644183	0.519456569	0.59476854	grey	0.026887879	0.738915473		AT4G08080.1	ACA2,ATACA7	alpha carbonic anhydrase 7	carbonic anhydrase alpha
Sapur.005G176100.7	0.508318853	0.245696902	0.381984574	0.644157	0.519473872	0.59478541	grey	-0.011182679	0.885197513	GO:0046872	AT3G05480.1	DRIP2	DRIP/ZA-interacting protein 2	E3 ubiquitin protein ligase DRIP2, putative
Sapur.013G251300.2	1.819074935	-0.118595817	0.203458841	-0.64366	0.519796406	0.59585523	grey	-0.052431095	0.491152532		AT5G09080.1	RING/U-box superfamily protein	RING/U-box superfamily protein	RING finger protein
Sapur.T082100.1	0.407923701	0.222258709	0.341089609	0.643646	0.519804704	0.59585523	grey	0.022994943	0.774984456		AT2G38455.1	CLE25	CLAVATA/ESR-RELATED 25	CLAVATA/ESR-RELATED 25
Sapur.018G072400.1	302.8251812	0.031147104	0.047884753	0.643452	0.520053029	0.58289997	grey	-0.058163688	0.457127556		AT4G16510.1	ATOSM34,OSM34	osmotin 34	thaumatin-like protein
Sapur.002G135500.1	570.1576098	0.024565589	0.038196263	-0.64301	0.520127449	0.59316188	grey	-0.023834847	0.673987248	GO:0016567,GO:0006402,GO:0006488,GO:0005524,GO:0004672	AT4G35930.1			receptor tyrosine kinase
Sapur.001G160600.1	0.390020016	0.240886248	0.374966411	-0.64249	0.520349211	0.59382023	grey	-0.108874566	0.190765717	GO:0005515	AT5G46170.1	F-box family protein	F-box-like protein	F-box-like protein
Sapur.018G117400.1	9.780575884	0.147497927	0.230065497	0.643305	0.520527524	0.59399654	grey	0.065024765	0.418453376	GO:0006488,GO:0005524,GO:0004672	AT5G60730.1			NA
Sapur.007G132900.1	57.44126063	0.031438389	0.051146658	0.642407	0.520873723	0.59615069	grey	0.047324216	0.515904369	GO:0005506,GO:0004232,GO:0007586,GO:0008233	AT5T2.4,ST2.4	Peptidase family M48 family protein	CAAX prenyl protease	CAAX prenyl protease
Sapur.001G130400.1	0.126568039	0.320080397	0.498835	0.641687	0.521276193	0.5961729	grey	-0.046434364	0.543611119	GO:0055114,GO:0016491	AT5G60560.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	prolyl 4-hydroxylase alpha subunit, putative
Sapur.011G149900.1	0.155843005	-0.496356935	0.696360695	-0.64122	0.521380485	0.59674928	grey	0.002319663	0.978983804	GO:0016787	AT2T2880.2	Survival protein SurE-like phosphatase/nucleotidase	Survival protein SurE-like phosphatase/nucleotidase	acid phosphatase, putative
Sapur.003G084300.2	0.486865478	0.293059557	0.441368168	0.641141	0.521667047	0.59678202	grey	0.037552991	0.649988885	GO:0005515	AT5G60390.1	Chaperonin Cpn60/TCP-1 family protein	chaperonin protein Dnaj	chaperonin protein Dnaj
Sapur.003G078100.1	1.857152312	-0.020457458	0.031916667	-0.64096	0.521455587	0.59892583	grey	-0.086029231	0.284082212	GO:0019904	AT1G47760.2	GF14 OMICRON,GRF11,RHS	general regulatory factor 11	14-3-3 family protein 11 1433-3 protein
Sapur.013G041300.1	0.364960763	0.649017651	0.47409697	-0.64063	0.521671212	0.59695627	grey	0.040500506	0.617404662	GO:0003676	AT5G01140.1	AT5W0.8,ATSRP30,1-8TSR1	SERINE/ARGININE-RICH 30	RNA-recognition motif 3-containing protein serine/arginine-rich splicing factor
Sapur.I59G069000.1	0.174297719	0.506859884	0.791595126	-0.64057	0.521769832	0.59721559	grey	0.021317804	0.007347747	GO:0009055	AT5G26330.1	Cupredoxin superfamily protein		plastocyanin-like domain protein
Sapur.013G052000.1	388.8645217	0.169329413	0.264415724	0.640127	0.521938524	0.59726732	grey	0.078864636	0.321187121		AT5G26040.1	Ubiquitin-like superfamily protein		NA
Sapur.016G145500.1	0.18642879	-0.436211889	0.681466613	-0.64025	0.522007093	0.59731743	grey	-0.150605858	0.059721959		AT2G27230.3	SPT2 chromatin protein	SPT2 chromatin protein	NA
Sapur.017G022000.1	0.365661447	0.640765	1.000147	0.639667	0.522452128	0.59695627	grey	0.040500506	0.617404662	GO:0003676	AT5G01140.1	AT5W0.8,ATSRP30,1-8TSR1	SERINE/ARGININE-RICH 30	RNA-recognition motif 3-containing protein serine/arginine-rich splicing factor
Sapur.I59G056400.1	0.353023606	0.205145497	0.321539392	-0.63978	0.523313631	0.59762683	grey	-0.123067008	0.112775418		AT4G26680.1	CICI3	CTC-interacting domain 3	plastid division1
Sapur.016G070000.9	0.462866223	0.283798668	0.375146616	0.639667	0.523379798	0.59767383	grey	0.045478305	0.517638884	GO:0006468,GO:0005524,GO:0004672	AT4G21390.1	SPA1	SPA (suppressor of phyA-105) protein family	NA
Sapur.T180100.1	0.934730514	-0.1676746	0.262185262	-0.63953	0.523480004	0.59775192	grey	-0.012142657	0.88005573		AT2G47260.2	AETIHO2,TIHO2	TIHO2	TIHO2
Sapur.018G128800.1	142.0799728	-0.098502629	0.154802017	-0.63948	0.523578911	0.59796719	grey	-0.078854296	0.336259718					phosphoglycan O
Sapur.003G091100.1	1.792172867	0.074595488	0.022839609	-0.63932	0.523659197	0.59860984	grey	-0.066334917	0.489099966	GO:0006468,GO:0004672	AT5K41.5,K41	shaggy-like protein kinase 41	shaggy-related kinase	shaggy-related kinase
Sapur.018G021400.1	1391.274662	-0.030515261	0.047361655	-0.63891	0.523838336	0.59833859	grey	-0.07167193	0.372181185		AT5G15560.1	catalytics	catalytics	ppp-dh domain protein
Sapur.011G058000.1	252.4921663	0.027500197	0.043125231	-0.63888	0.523844117	0.59867754	grey	-0.040030212	0.638469818	GO:0055992,GO:0003824	AT1T9S,TP5B	trehalose-phosphatase/synthase 9	trehalose-6-phosphate synthase	trehalose-6-phosphate synthase
Sapur.008G027300.1	0.151446603	0.467406595	0.731875063	-0.63877	0.523975527	0.59897931	grey	-0.197518688	0.011035285	GO:0009733	AT3G70330.1	SAUR-like auxin-responsive protein family	SAUR-like auxin-responsive protein family	auxin-

Sapur.T142900.1	0.08941619	0.15116044	0.91243735	0.603984	0.5458478	0.62147918	grey	0.20622791	0.09356157	AT4G15130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3	NA
Sapur.T031700.1	15.28256663	0.07798779	0.12020471	0.603696	0.54604587	0.62184028	grey	0.05269032	0.51381818	AT3G59560.1	RmlC-like cupins superfamily protein	germin family protein	NA
Sapur.T081000.1	0.19967366	0.36134548	0.42920208	-0.60366	0.54604753	0.62186744	grey	-0.19601818	0.01387936			NA	NA
Sapur.tr70246700.1	1.38685017	0.14962538	0.24700149	-0.60357	0.54623947	0.62176381	grey	-0.03958706	0.62243758			NA	NA
Sapur.tr56025489.1	0.82884777	0.10320413	0.17162038	0.60328	0.54623126	0.62193104	grey	-0.03539467	0.6543305	AT3G21900.1	DNA/ssn-like superfamily protein	type I inositol-1,4,5-trisphosphate 5-phosphatase	NA
Sapur.tr70128500.1	8.36875495	0.11053956	0.18322717	0.603257	0.54638043	0.62193184	grey	0.04984564	0.13525821	AT4G43870.1	Pectin lyase-like superfamily protein	endo-polygalacturonase	NA
Sapur.tr70287800.1	0.93269395	0.17106743	0.28382436	0.603133	0.54642035	0.62200332	grey	0.05833874	0.46799607			NA	NA
Sapur.tr60288200.1	0.25597889	-0.27937862	0.46325648	-0.60294	0.54650815	0.62210624	grey	-0.11503458	0.18667046	AT2G38550.1	Transmembrane proteins 14C	transmembrane protein 14C	NA
Sapur.tr50268900.4	18.23904182	0.06677016	0.07759926	0.602727	0.54669037	0.62226649	grey	0.00972488	0.93278703	GO:0007264,GO:0005525	Ras-related small GTP-binding family protein	Ras-related small GTP-binding family protein	NA
Sapur.tr50264440.1	3.60600533	0.16027562	0.54071394	0.602602	0.54671394	0.62251261	grey	0.06760600	0.89361153	GO:0007165,GO:0005515,GO:0043531	Disease resistance protein (TIR-NBS-LRR class) family	TIR-NBS-LRR disease resistance-like protein	NA
Sapur.tr30614480.1	2.53802146	-0.13924185	0.23107589	-0.60258	0.54679394	0.62314086	grey	-0.32178065	3.96E-05	GO:0006508,GO:0004252	Subtilisin-like serine endopeptidase family protein	subtilisin-like protease	NA
Sapur.tr70128400.1	0.14227204	0.28570471	0.89311584	0.602461	0.54697622	0.62350255	grey	-0.07133681	0.37965023	GO:0005525,GO:0016020,GO:0008821,GO:0005247	Voltage-dependent anion channel family protein	NA	NA
Sapur.tr30614620.1	0.20764551	-0.31068728	0.51657368	-0.60201	0.54716921	0.62372379	grey	-0.12859173	0.10846362	GO:0005975,GO:0004650	Pectin lyase-like superfamily protein	polygalacturonase	NA
Sapur.tr30624900.1	0.14766860	0.32264667	0.52192029	0.601991	0.54716980	0.62372379	grey	-0.13758692	0.07360117			RING/FYVE/PHD zinc finger protein, putative	RING/FYVE/PHD zinc finger protein
Sapur.T049900.1	369.23924	-0.03026689	-0.09204399	-0.60189	0.54717542	0.62372379	grey	-0.05467035	0.50037845	AT5G51610.1	AT5UMS02.SUMO SUMO 2/5	small ubiquitin-like modifier 2	small ubiquitin-related modifier
Sapur.tr30628300.1	0.34966863	0.24275937	-0.41170791	0.601819	0.54730951	0.62382421	grey	0.05782045	0.47356422	AT5G54210.1	APG12,ATG12,ATG12A	Ubiquitin-like superfamily protein	ubiquitin-like protein ATG12
Sapur.tr59G144900.1	1.75757051	-0.12476167	0.20735003	-0.6016	0.54744055	0.62292583	grey	-0.01849514	0.81860192			NA	NA
Sapur.tr01G090700.1	27.05135116	-0.06517255	0.05112448	-0.60123	0.54783496	0.62362377	grey	-0.06276782	0.43497816	GO:0005985	UDP-N-acetylglucosamine (UAP) transporter family	UDP-N-acetylglucosamine pyrophosphorylase family protein	adenosine 3'-phospho 5'-phosphosulfate transporter 2
Sapur.tr01G270500.1	0.81809849	-0.01655165	0.29384035	-0.60114	0.54771181	0.62373177	grey	-0.11503426	0.18667046	GO:0005245,GO:0009029,GO:0005524	Tetratricopeptide (TPR)-like superfamily protein	tetracycloheximide-sensitive 1	tetracycloheximide-sensitive
Sapur.T001600.1	1.68295629	0.12369826	0.20582374	0.600985	0.54789947	0.62387463	grey	0.08260765	0.30368367			NA	NA
Sapur.tr01G192300.1	0.11291344	0.46409829	0.74277593	-0.60049	0.54819236	0.62416093	grey	-0.25353926	0.02165111	AT2G22640.1	ATMYB3,MYB3	myb domain protein 3	MYB transcription factor R2R3-like protein
Sapur.tr50G091500.1	19.64531676	-0.09968436	0.16020932	-0.60031	0.54829526	0.62737286	grey	-0.04368744	0.58932471	GO:0004064,GO:0016762,GO:0000703,GO:0005618,GO:0005975,GO:0004553	AT4G36870.1	ATH32	xyloglucan endotransglucosylase/hydrolase, putative	xyloglucan endotransglucosylase/hydrolase, putative
Sapur.tr50264300.1	0.23339601	0.34524731	0.57556888	-0.60031	0.54829759	0.62836031	grey	-0.14560759	0.04911703			NA	NA
Sapur.tr14G039300.1	0.13115453	0.52179857	0.86994851	0.599799	0.54863935	0.62457406	grey	0.15645038	0.05038416	GO:0005509	Calcium-binding EF-hand family protein	NA	NA
Sapur.tr70G231100.1	5.68182314	0.04420010	0.07368416	0.599645	0.54868658	0.62478887	grey	-0.04809456	0.55463117	GO:0005515,GO:0030598,GO:0005618	Pectin lyase-like superfamily protein	pectinesterase	NA
Sapur.tr61G177700.1	0.91433264	-0.15737229	0.26252812	-0.59945	0.54878428	0.62495964	grey	-0.07364227	0.35985599			transmembrane protein, putative	transmembrane protein, putative
Sapur.tr61G288800.1	219.3194161	0.05776063	0.09637058	-0.59936	0.54893077	0.62496867	grey	-0.08219188	0.38505992	GO:0006355,GO:0003677	AtNAC3/ANAC083,NST1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC transcription factor
Sapur.tr01G113600.1	5.48381458	0.09210452	0.15361828	0.59693	0.54897392	0.62517088	grey	0.02677088	0.73977726		Hydroxyproline-rich glycoprotein family protein	NA	NA
Sapur.tr61G190600.1	163.535068	0.08481012	0.10709613	0.596265	0.54896417	0.62531295	grey	0.02852718	0.72251908	GO:0016567,GO:0004842,GO:0005515	AT2G42340.1	PU1E15	E3 ubiquitin ligase PUB14, putative
Sapur.tr05G079200.1	42.73975928	0.04849276	0.05841261	0.596167	0.54965461	0.62436547	grey	0.03269377	0.68408748	AT5G58470.1,SERAT2;2	serine acetyltransferase 2;2	serine acetyltransferase	serine acetyltransferase
Sapur.tr01G260500.1	2.26987768	0.12484098	0.20838704	0.596079	0.54972052	0.62441795	grey	0.00789885	0.9217857	CML38	AT3G56510.1	calmodulin-like 38	polcalcin jun protein O, putative
Sapur.tr01G201100.4	0.10653522	0.44455274	0.91924616	-0.5889	0.54979128	0.62464683	grey	0.14211745	0.07581001		AT3G10860.1		cytochrome C oxidase assembly protein
Sapur.tr01G053300.1	0.09255288	0.54903039	0.91688704	0.588771	0.54982541	0.62400819	grey	0.19884835	0.01257853	GO:0015931	AT5G17830.1	ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1
Sapur.tr01G250100.3	4.30541041	0.07122148	0.12066499	0.588179	0.5497208	0.62479187	grey	0.03763276	0.64532582	GO:0016887,GO:0005524	AT4G04910.1	ATNAP14,NAP14	non-intrinsic ABC protein 14	ABC transport family protein
Sapur.tr01G164900.1	0.31514255	0.24775256	0.41623682	0.588096	0.54977164	0.62507263	grey	0.05100427	0.52587712			NA	NA
Sapur.tr01G164300.1	136.7819243	0.07338561	0.12377886	0.585888	0.54987482	0.62537786	grey	0.03682229	0.67585817		AT5G23340.1	Mitochondrial substrate carrier family protein	oxoglutarate/fumarate transporter
Sapur.tr01G016800.1	1.06648522	0.12182623	0.20479667	0.587924	0.54980682	0.62515788	grey	0.04881186	0.54513056			NA	NA
Sapur.tr01G192100.1	0.16835266	0.38170988	0.63848749	0.587804	0.54985514	0.62524114	grey	0.10934975	0.17276825		AT5G45310.1		plant/KX6.15-9 protein, putative
Sapur.tr01G082600.1	0.15595453	0.47580576	0.79937409	0.587624	0.55003953	0.62542276	grey	0.06823019	0.3926115	GO:0019205,GO:0006139,GO:0005524	AT5G66673.3	PYR6	P-loop containing nucleoside triphosphate hydrolases superfamily protein	adenylate kinase
Sapur.T116400.1	33.53113345	0.09702368	0.32981123	-0.59728	0.55025102	0.62502823	grey	-0.10269263	0.20079273			NA	NA
Sapur.tr04G070400.1	42.18883024	0.06535119	0.05757785	0.597181	0.55038450	0.62525236	grey	0.3727887?	1.53E-06	GO:0100190	AKIN10,KIN10,SNRK1.1	SNF1 kinase homolog 10	SNF1-related kinase catalytic subunit alpha KIN10
Sapur.tr08G035900.1	250.5294605	-0.03035458	0.05004034	-0.5967	0.55070697	0.62595602	grey	-0.05180259	0.51934769	GO:0016810,GO:0006807	AT4G08790.1	N-trityltase/cyanide hydratase and apolipoprotein N-acyltransferase family protein	nitrilase
Sapur.tr01G113600.1	0.16368691	0.26208385	0.44267081	0.596173	0.55063102	0.62601874	grey	0.14812679	0.06411313	GO:0008270,GO:0005515	AT4G29100.1	RING/zinc ion binding protein	NA
Sapur.tr01G143700.1	0.45042879	0.26589549	0.4457448	-0.59608	0.55110182	0.62638495	grey	-0.08812846	0.27239658		AT5G58280.1	alpha/beta-hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.tr01G183800.1	0.93748337	0.14181744	0.24176088	0.595828	0.55110371	0.62681447	grey	0.06260249	0.21882667		AT4G27060.1	PLATZ transcription factor family protein	NA
Sapur.tr17G101700.3	22.0761307	0.04058729	0.06890946	0.595119	0.55139317	0.62707127	grey	0.05402242	0.49071606			NA	NA
Sapur.tr01G201400.1	549.2129721	0.08158492	0.13867302	0.593889	0.55139317	0.62708082	grey	-0.0213464	0.78509664	BZR1	AT1G75080.1	Brassinosteroid signalling positive regulator (BZR1) family protein	brassinazole-resistant protein
Sapur.tr18G004100.1	24.47472347	0.09962312	0.16759218	0.59442	0.55231403	0.62758273	grey	0.03759107	0.64372168		AT1G10330.1	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.tr05G089900.1	0.96889683	-0.17089325	0.28767344	-0.59405	0.55247881	0.62797988	grey	-0.02315864	0.7316687		AT4G34950.1	Major facilitator superfamily protein	nodulin family protein
Sapur.tr06G073800.1	2.02773836	0.47580326	0.79996764	0.593396	0.55263479	0.62841868	grey	-0.0268381	0.40765047	GO:0030246	AT2G42420.1	Concanavalin A-like lectin protein kinase family protein	legume lectin beta domain protein
Sapur.T138900.1	1.99162185	0.16304055	0.27698815	-0.5938	0.55261423	0.62916756	grey	-0.08393124	0.30765212			NA	NA
Sapur.tr07G080300.1	0.30793171	0.10320728	0.3879876	0.593176	0.55263532	0.62765552	grey	0.11274148	0.15605864	GO:0005515	AT1G22125.1	CSI1	cellulose synthase-interactive protein
Sapur.tr07G091200.1	74.19319171	-0.04341627	0.07318026	-0.59357	0.55278897	0.62807527	grey	-0.02269664	0.78265787	GO:0016853,GO:0005975	AT5G37330.1	Galactose mutarotase-like superfamily protein	NA
Sapur.tr06G241800.1	35.14693923	0.02817184	0.04749247	0.592727	0.55278897	0.62815874	grey	0.06774044	0.39282047		AT3G11250.1	PPDK regulatory proteins	NA
Sapur.tr01G080000.2	1.64325383	0.13461083	0.22658877	-0.59324	0.55302093	0.62839749	grey	-0.07924093	0.34461443	GO:0004648,GO:0005524,GO:0004672	AT3G15220.1	Protein kinase superfamily protein	MAP 4 kinase alpha1
Sapur.tr06G184100.1	769.0127638	0.03173648	0.05345119	0.592664	0.55302553	0.62843193	grey	-0.06288312	0.43015503		AT5G47560.1	hydroxyproline-rich glycoprotein family protein	hypothetical protein
Sapur.tr07G104300.1	1.22417504	-0.17285288	0.29143086	-0.59312	0.55330646	0.62835165	grey	-0.04308751	0.59241373		AT4G38040.1	Exostosin family protein	NA
Sapur.tr18G078200.1	0.20918804	0.36226751	0.61005686	-0.59286	0.55327401	0.62851066	grey	-0.15391767	0.05472335	GO:0005461,GO:0005886,GO:0005622,GO:0003735	AT2G24090.1	Ribosomal protein L35	50S ribosomal protein L35
Sapur.tr01G183500.1	1.97559211	0.26266316	0.44319186	0.593056	0.55350002	0.62906206	grey	0.04393648	0.58769416	GO:0009113,GO:0006207	AT5G08630.1	Glutamate dehydrogenase (GAB) synthetase	phosphoribosylformylglycinamidine ligase
Sapur.tr01G122200.1	39.7648806	-0.05285445	0.08927724	-0.59204	0.55380597	0.62900206	grey	-0.04812667	0.54946712			NA	transmembrane protein, putative
Sapur.tr07G134800.1	0.18027543	0.32264887	0.60051811	0.592033	0.55380435	0.62942507	grey	-0.18047207	0.02376619	GO:0006355	AT3G07580.1	Far-red impaired responsive (FAR1) family protein	Pm5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.tr18G041400.1	0.15310297	-0.41010974	0.83347877	-0.59153	0.55416859	0.62940872	grey	-0.0213464	0.78509664		AT5G20590.1	TRICHOME BIREFRINGENCE-LIKE 5	Pm5/Cas1p GDSL/SGNH-like acyl-esterase family protein
Sapur.tr01G164200.4	1.56808704	0.12182623	0.21318884	0.592714	0.55416859	0.62941317	grey	0.03967710	0.62493221	GO:0003677,GO:0006289,GO:0005634,GO:0003684	AT4G02620.1	DNA repair protein UVH3/XPG/RAD2 of P-C cells protein	DNA repair protein UVH3/XPG/RAD2 of P-C cells protein
Sapur.T169600.1	0.22886017	0.25197926	0.42763635	0.58964	0.55542206	0.63076549	grey	-0.02432075	0.76237485		AT5G40380.1	DNA/ssn-like superfamily protein	NA
Sapur.tr01G111200.1	75.41320006	0.04858695	0.08269257	0.589	0.55552622	0.63086882	grey	-0.03887631	0.63831221	GO:0043531	AT1G44570.1	NB-ARC domain-containing disease resistance protein	R-NBS-LRR resistance protein
Sapur.tr08G169100.1	24.99221149	0.09183147	0.08790361	-0.58916	0.55575351	0.63107007	grey	-0.07606879	0.37954808		AT3G67920.1		hypothetical protein
Sapur.tr08G101300.1	0.23357083	0.41223737	0.70138856	0.589186	0.55613879	0.63122965	grey	-0.0368363?	1.84E-06		AT5G46910.1	Transcription factor jumonji (jmj) family protein / zinc finger (CSHC2 type) family protein	transcription factor jumonji family protein
Sapur.tr01G204900.1	1401.26294	-0.03545836	0.0602501	-0.58852	0.55633567	0.63155207	grey	-0.04291748	0.59354805	GO:2001070,GO:0016310,GO:0016301,GO:0005524	AT5G35570.1	ATGWD3,OK1,PWD	catalytic;carbohydrate kinase;phosphoglucan, water dikinases	phosphoglucan, water dikinase
Sapur.T117700.1	55.34007905	-0.07307261	0.12538515	-0.58786	0.55629129	0.63204548	grey	-0.04507058	0.57513197		AT2G26301.1	MYA/PDR2	phosphate deficiency response 2	phosphate deficiency response 2
Sapur.tr13G116600.9	3.64656118	0.08286168	0.14116425	-0.58701	0.55797881	0.63263861	grey	0.03703128	0.82348888		AT4G04550.1	EMB2777	Sec61/U1 ribonucleoprotein (Lsm) family protein	hypothetical protein
Sapur.tr17G128900.3	5.93282696	0.08245271	0.14078888	0.586638	0.55744705	0.63289397	grey	-0.06221526	0.43888561	GO:0016787		NA	sn/thr protein phosphatase family protein
Sapur.tr12G082700.7	4.00473891	0.11408948	0.19459148	0.585341	0.55767223	0.63313705	grey	0.03881211	0.69366434			NA	succinate dehydrogenase assembly factor
Sapur.tr02G176600.1	2.06288275	0.14960843	0.25540782	0.585758	0.55808038	0.63327274	grey	0.01006839	0.90615619		AT4G12460.1	ATMLATVR9D1,MR9D01	myb domain protein 101	LA-related protein 2 LA RNA-binding domain protein
Sapur.tr01G165400.1	295.4508767	0.02538312	0.04336101	0.585343	0.55816969	0.63328181	grey	-0.18178439	0.07229002		AT1G07820.1	winged-helix DNA-binding transcription factor family protein	NA
Sapur.T093300.1	3.47444021	-0.08141287	0.13919922	-0.58519	0.55847552	0.63380352	grey	-0.06497974	0.83758787			NA	plant broad-spectrum mildew resistance protein RPW8
Sapur.tr07G028200.1	0.10600365	0.61180074	1.1	0.585278	0.55882026	0.63410122	grey	0.21602208	0.06440604		AT5G04570.1	HR3,MLA10	homolog of RPW8 3	
Sapur.tr04G125200.1	228.6899483	0.05558749	0.09513736	0.584284	0.55929061	0.63454364	grey	0.01987819	0.80386684		AT4G22740.1			hypothetical protein
Sapur.tr05G037500.1	19.6542087	0.07501983	0.18479134	0.584111	0.55934139	0.63463849	grey	0.05452904	0.49758623			NA	chorismate synthase, putative / 5-enolpiruvylshikimate-3-phosphate phosphollyase, putative	chorismate synthase
Sapur.tr08G084800.2	2.77024999	-0.14270873	0.24432121	-0.5841	0.55953146	0.63502634	grey	-0.15475409	0.05266764	GO:0009073,GO:0004107	AT4G39510.1	ATMYB32,FDX12	perosin-12	perosin-12
Sapur.T162900.1	0.20195231	0.28683753	0.49134157	-0.58407	0.55957080	0.63463932	grey	-0.12134763	0.13017944	GO:0008702,GO:0008323,GO:0006325,GO:0005779	AT5G04660.1	APM4,ATPDX12,PDX12	perosin-12	NA
Sapur.tr02G043600.1	0.12369492	0.50123279	0.85836326	0.583925	0.55970524	0.63470399	grey	0.11857025	0.13914022	GO:0051114,GO:0006540,GO:0016614	AT1G67260.1	Glucose-methanol-choline (GMC) oxidoreductase family protein	NA
Sapur.tr07G022900.1	0.11720159	0.51663296	0.91059378	0.58388	0.55990188	0.63474342	grey	0.15492349	0.05269811		AT5G19250.1	ATRL1,RL1,RSM2	RAD-like 1	MFB transcription factor
Sapur.tr05G056200.1	0.15353884	0.44577951	0.79400576	0.583	0.55992934	0.63500389	grey	-0.20489968	0.03060408		AT2G37170.2		PHS-like protein	NA
Sapur.tr02G201000.1	3259.04511	-0.03844286	0.06591185	-0.58325	0.55972169	0.63516477	grey	-0.05890078	0.47977092			NA	NA
Sapur.tr01G153700.1	1.42089514	0.20797642	0.36803868	0.582638	0.55985145	0.63538088	grey	-0.07796[illegible]	0.33120735	GO:0006468,GO:0005634,GO:0004672	AT5G11050.1	Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.tr05G161100.1	437.7042525	-0.01993594	0.03419153	-0.58302	0.55987918	0.63589289	grey	-0.05779074	0.47218805	GO:0008080	AT3G03150.1	Acyl-CoA N-acyltransferases (NAT) superfamily protein	amino-terminal acetyltransferase B complex catalytic subunit
Sapur.tr01G180800.1	0.18974664	0.10616800	0.18406421	0.110005153	0.58248	0.63605273	grey	0.02675548	0.7425658	GO:0006468,GO:0004672	AT4G24400.1	Protein kinase superfamily protein	NA
Sapur.tr05G052300.1	1.02367306	-0.15821179	0.27121126	-0.58144	0.56094244	0.63657488	grey	-0.05397627	0.51938546		AT5G09220.1	AAP2	amino acid permease	amino acid permease
Sapur.T003600.4	0.18289936	0.36695124	0.63148849	0.581108	0.56116784	0.63687982	grey	0.10732257	0.18116668	GO:0006281,GO:0005694,GO:0009507,GO:0003677,GO:0003918	AT5G53300.1	MSG5,TOP1,TOP1ALPHA	DNA topoisomerase I alpha	DNA topoisomerase I
Sapur.tr01G042200.1	251.3638044	0.03394357	0.05294406	0.580765	0.56138862	0.63687245	grey	0.06428049	0.43788084	GO:0006468,GO:0005524,GO:0004672	AT2G06010.1	Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.tr07G091000.3	0.23501581	0.28516517	0.49143241	-0.5806	0.56151326	0.63703087	grey	-0.08845092	0.28501659		AT5G25730.1	Plant protein of unknown function (DUF889)	filament-like plant protein, putative
Sapur.tr01G180300.1	0.36125304	0.07457942	0.12869763	0.580368	0.56166435	0.63738788	grey	0.01158461	0.89756889			NA	NA
Sapur.tr17G081000.1	46.54870209	0.05839942	0.10064907	0.580211	0.56177467	0.63771754	grey	0.05251002	0.51651688		AT5G04920.1	EAF30/Vps30 family protein	EAF30/Vps30 family protein
Sapur.tr06G218100.2	3.31266109	0.10245544	0.17658924	0.58	0.56177467	0.63771754	grey	0.05970312	0.4762522	GO:0006618,GO:0048513,GO:0004871	AT3G13120.1	ENP,MA64,NPY1	Phototropic-responsive NPH3 family protein	BTB/POZ domain protein
Sapur.tr10G041800.2	1.3027637	0.13865884	0.23962645	-0.5793	0.56235899	0.63793758	grey	-0.02200537	0.77284199		AT4G24700.2	AETH02,THO2	THO2	NA
Sapur.tr06G238200.1	2.21004267	0.07668294	0.12460849	0.57892	0.56242223	0.63807763	grey	-0.33680653	1.61E-05	GO:0005515,GO:0035556,GO:0007165,GO:0006629,GO:0004435	AT3G02130.2	AFH2,2-PLC2	phosphoinositide-specific phospholipase C	phosphoinositide-specific phospholipase C
Sapur.tr08G049900.1	9.90587567	0.08475804	0.14634127	0.578818	0.56271138	0.63863703	grey	-0.03721584	0.64349387		AT3G39650.1	Protein of unknown function (DUF506)	plant-specific domain TIGR01615 family protein, putative	plant-specific domain TIGR01615 family protein, putative
Sapur.tr06G088500.1	0.16398023	0.45484219	0.78602122	0.57869	0.56298525	0.63884007	grey	0.13748525	0.08360402			NA	NA	NA
Sapur.tr10G011300.1	18.08318986	-0.17514386	0.30367871	-0.57862	0.56298625	0.63872122	grey	-0.07947067	0.32076148	GO:0051114,GO:0020037,GO:0016705,GO:0005506	AT4G27370.1	CYP81D8	cytochrome P450 family protein	cytochrome P450 family protein
Sapur.tr10G025200.1	0.48330638	0.20046146	0.34653627	0.578371	0.56383917	0.68560645	grey	0.02291932	0.77576593			NA	NA	NA
Sapur.tr04G100700.1	241.9838344	0.02256518	0.03969168	-0.57832	0.56387211	0.68560268	grey	-0.43819219	9.62E-09	GO:0016020,GO:0008375	AT5G15050.1	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	glycosyltransferase family 14 protein
Sapur.T182200.1	1.43432885	0.16261729	0.24663701	0.578283	0.56387279	0.68563621	grey	0.05064079	0.52875087		AT3G22340.1			hypothetical protein
Sapur.tr05G047400.1	186.1105354	0.07948889	0.08331025	0.576989	0.56394111	0.63867064	grey	0.06841914	0.41897507	GO:0016887,GO:0005524	AT4G27140.1	ATMAP13,EMB2751	ABC transport family protein	NA
Sapur.T187800.1	4.17594817	0.08826578	0.15268137	0.578086	0.56320577	0.63867064	grey	0.02221183	0.78232002		AT3G08610.1	ATNEK5,NEK5	NIMA-related kinase 5	NA
Sapur.tr05G090700.2	2.50422068	0.07788263	0.13244329	-0.57794	0.56330005	0.63875763	grey	-0.03894955	0.66949501		AT4G26090.3		oxidoreductase, 2OG-Fe(II) oxygenase family protein	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein
Sapur.tr02G172200.1	21.05664562	0.15908137	0.23775372	0.577925	0.56330204	0.63882675	grey	0.08493547	0.81817151			NA	hypothetical protein
Sapur.tr08G023100.1	0.34653863	0.20425235	0.4656084	-0.5773	0.56365835	0.63907106	grey	0.06217915	0.35838361			NA	transmembrane protein, putative
Sapur.tr03G052500.1	0.24568715	0.28568797	0.49489714	0.577259	0.56376549	0.63921616	grey	0.06115762[illegible]	0.44672129	GO:0006468,GO:0005524,GO:0004672	AT4G33950.1	ATOST1/OST1,PK4,SNRK2-6.	Protein kinase superfamily protein	Serine/Threonine kinase SAPK3, putative
Sapur.tr05G096800.3	0.40844825	0.21845086	0.37868938	0.576871	0.56428684	0.63940116	grey	0.01547389	0.84747378		AT4G01370.1	DRN	dwRNA binding protein 5	double-stranded RNA-binding protein
Sapur.tr01G084500.1	66.73819667	0.06487451	0.11523688	0.576547	0.56429799	0.63950486	grey	-0.04259136	0.57392984	GO:0004857	AT1G71910.1	ATCVF01,CVF01	cell wall / vacuolar inhibitor of fructosidase 1	pectinesterase inhibitor
Sapur.tr05G073300.2	0.28779361	0.26320834	0.45958184	-0.57668	0.56435954	0.63958027	grey	-0.10957204	0.17939463		AT2G31410.1	CLPP2,NCLPP7	nuclear-encoded CLP protease P7	ATP-dependent Clp protease proteolytic subunit
Sapur.tr01G162900.1	825.8018237	0.07229332	0.12405617	0.576479	0.56439169	0.63960292	grey	0.02204888	0.65171386	GO:0051114,GO:0016491	AT2G26400.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2OG Fe(II) oxygenase family protein	oxidoreductase, 2OG-Fe(II) oxygenase family protein
Sapur.tr10G201500.1	112.3792881	0.05948393	0.10188455	0.576471	0.56260933	0.63976292	grey	0.07348187	0.73479502	GO:0008270,GO:0005622	AT3G21150.1	BBX32	B-box 32	B-box zinc finger protein
Sapur.tr02G087600.2	0.65028734	0.17268258	0.31800464	-0.57642	0.56433745	0.63970847	grey	0.05622439	0.50388268			NA	NA	hypothetical protein
Sapur.tr10G115500.1	454.5249964	0.13281769	0.23074091	0.575616	0.56487769	0.64029819	grey	0.0492242	0.5452448		AT3G55580.1	Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator RCC1 repeat protein	NA
Sapur.tr01G174600.1	1.12832373	0.16866261	0.29129705	0.57654	0.56488283	0.64032606	grey	0.02766652	0.36609752			NA	NA	NA
Sapur.tr17G037000.1	152.1114916	0.06845838	0.11905284	0.574964	0.56533955	0.64075994	grey	0.04154197	0.57651877	GO:0051114,GO:0016491	AT3G36690.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase family protein	NA
Sapur.tr01G172500.1	21.01612319	0.09207222	0.16016033	0.574735	0.56540557	0.64093977	grey	0.06221062	0.48839955		AT5G44390.1	F-box family protein	F-box protein SKIP31
Sapur.tr17G051200.1	2.14895016	-0.15186189	0.26438332	-0.57445	0.56560032	0.64102372	grey	-0.06030218	0.43078909		AT2G35580.1	Plant protein of unknown function (DUF247)	NA
Sapur.T123800.1	0.16639857	0.32165652	0.59863514	0.57436	0.56572261	0.6411947	grey	-0.17288475	0.02161203		AT3G28455.1	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.tr02G029700.2	7.00797984	0.08509766	0.10285651	0.571882	0.56588509	0.64185829	grey	0.06817634	0.39621199		AT4G34185.3			histone acetyltransferase subunit NuA4
Sapur.tr06G281800.1	78.04595886	0.03357418	0.05858268	0.573307	0.56663572	0.64184168	grey	-0.05185868	0.84377026	GO:0005515	AT5G78380.1	ATGSTU19,GSTB,GSTU19	glutathione S-transferase TAU 19	NA
Sapur.tr13G283000.6	0.85727928	0.14000000	0.24455046	-0.57327	0.56669759	0.64187288	grey	-0.03889396	0.82698897		AT5G42190.1		Outer arm dynein light chain 1, putative	outer arm dynein light chain 1, putative
Sapur.tr01G134000.1	178.4605979	0.08976721	0.08040382	0.572847	0.56748254	0.64281361	grey	0.04334576	0.48747378		AT3G45320.1	ATGRAS2,GRAS2,SCL34	SCARECROW-like 14	GRAS family transcription factor
Sapur.tr01G180500.1	10.42446444	0.14546766	0.24740112	0.57213	0.56720294	0.64290046	grey	-0.02189704	0.81844667	GO:0008270,GO:0005515	AT5G61160.1	Transducin/WD40 repeat-like superfamily

Sapur.15WG111700.1	0.4868627749	-0.17937823	0.328491958	-0.54607	0.585221122	0.659789559	gmy	-0.09515456	0.254325967	AtSG34482.2	Protein of unknown function (DUF167)
Sapur.15WG051900.1	0.117805977	-0.660498894	1.210238326	-0.54576	0.585213136	0.659881656	gmy	-0.24848915	0.001700762	GO:0000160	response regulator 24
Sapur.15WG230800.1	0.227379236	-0.328386806	0.519693276	-0.54525	0.585189124	0.66037612	gmy	-0.13682224	0.09794837		Protein of Unknown Function (DUF239)
Sapur.01GG064400.1	4.158545612	0.231942391	0.425465109	0.545152	0.585468099	0.66007265	gmy	0.05475193	0.495830725		Zinc knuckle (CCHC-type) family protein
Sapur.7J13500.1	3.854271584	-0.127405212	0.233805803	-0.54491	0.585837138	0.66037468	gmy	-0.04327514	0.585468479		PLATZ transcription factor family protein
Sapur.01GG078900.1	45.85721556	0.046759352	0.085891915	0.544398	0.586167896	0.66094768	gmy	0.00371786	0.962181203		HVA22 homologue D
Sapur.09GG131800.1	8.831157353	0.152782858	0.277050637	0.544243	0.586274294	0.66106533	gmy	0.07824708	0.33008781	GO:0003152;GO:0003824	ATP-dependent caseinolytic (Clp) protease/cristonase family protein
Sapur.01GG125200.1	0.145515717	0.365480323	0.671573629	0.544189	0.586313178	0.66106549	gmy	-0.07123466	0.237823014	GO:0009073;GO:0004106	chorismate mutase 3
Sapur.01GG001000.1	0.1408679	-0.493255986	0.790826269	-0.54403	0.586418381	0.66117412	gmy	-0.2934962	0.01058351		Vacuolar iron transporter (VIT) family protein
Sapur.01GG092600.1	2.935758815	0.066496595	0.179211546	0.543914	0.586491253	0.66116891	gmy	0.18491715	0.020193102	GO:0003824;GO:0006470;GO:0004722	protein phosphatase 2C
Sapur.01GG028300.1	44.15961719	0.034169413	0.062818882	0.543935	0.586659192	0.66116895	gmy	0.14743328	0.065305597	GO:0006351	SPOC domain / Transcription elongation factor S-II protein
Sapur.01GG012500.1	11.62703034	0.046468985	0.08360456	0.543861	0.586501081	0.66110076	gmy	0.02370271	0.675185883	GO:0005216	TATA binding protein 2
Sapur.09GG042400.2	0.44654724	0.210468394	0.387204072	0.543559	0.586744737	0.66195182	gmy	-0.25887323	0.00116442		Protein of unknown function (DUF630 and DUF632)
Sapur.01GG082800.2	0.36604999	0.219487706	0.403863218	0.543451	0.586756412	0.66195412	gmy	-0.42687328	0.53435945		Cytosol aminopeptidase family protein
Sapur.01GG054400.2	3.798856783	0.078347948	0.144278831	0.543031	0.587038124	0.66175673	gmy	0.05839126	0.527170553	GO:0055114;GO:0016491	sidehydrate dehydrogenase
Sapur.09GG029100.2	0.117321152	0.154587183	1.195229509	0.542698	0.587338398	0.66276234	gmy	-0.19593426	0.015907587	GO:0005622;GO:0004657	Methylenetetrahydrofolate reductase family protein
Sapur.01BG007700.1	0.277243853	0.231756174	0.426968533	0.542795	0.587721296	0.66386478	gmy	-0.00399239	0.982626353		
Sapur.09GG138200.2	2.913729609	0.085635852	0.157949464	0.542286	0.587821232	0.66267713	gmy	0.08489176	0.290425575	GO:0005515	SWIB complex BAF60b domain-containing protein
Sapur.01GG135200.1	11.75102152	0.067962509	0.125388724	0.542205	0.588798546	0.66279928	gmy	-0.04052121	0.8		NA
Sapur.15WG106300.4	10.37011966	0.06781306	0.125288855	0.541254	0.588325189	0.66304261	gmy	0.02617948	0.797187409		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.09GG095600.2	0.335908021	0.662067436	1.224966251	0.54099	0.589145414	0.66356155	gmy	-0.11468065	0.192355	GO:0006355;GO:0005634;GO:0003677;GO:0009725	auxin response factor 1
Sapur.01GG187300.1	0.111541596	-0.446831829	0.822467387	0.540668	0.5887658	0.66336916	gmy	0.16185982	0.042806053		cullin-associated NEDD8-dissociated protein
Sapur.01BG070300.1	0.320908218	0.27102427	0.502343464	0.5405	0.588847734	0.66349155	gmy	-0.05222249	0.533782742	GO:0005085;GO:0016020;GO:0008811;GO:0005216	cyclic nucleotide-gated ion channel protein, putative
Sapur.01GG062700.1	0.20667934	0.301362598	0.557480587	0.5404	0.588801099	0.66359211	gmy	-0.07379338	0.375581762	GO:0005515;GO:0008270	ubiquitin-associated (UBA)/TS-N domain-containing protein / ostcisoxaxetide/Phea/Bemis1 (PB1) domain-contair zinc ion binding protein, putative
Sapur.01GG212400.1	1.837436257	-0.357352765	0.661000429	0.539853	0.589152729	0.5402424	gmy	-0.04709256	0.534829545		Protein of Unknown Function (DUF239)
Sapur.01GG064000.2	0.132088863	-0.425029307	0.787006455	-0.54002	0.589182273	0.66379014	gmy	-0.2053804	0.0084	GO:0005515	Myc-like anthocyanin regulatory protein
Sapur.09GG177000.1	3.343953151	-0.09223623	0.170816174	-0.53997	0.5891481	0.66274683	gmy	-0.05777244	0.47232423	GO:0016021;GO:0016020;GO:0022857	nodulin MtN21 /EamA-like transporter family protein
Sapur.01BG138800.1	2.027715998	0.066045551	0.124207206	0.539842	0.589349961	0.66380088	gmy	0.06384809	0.43695019		nodulin MtN21 /EamA-like transporter family protein
Sapur.01GG037700.3	0.346419802	-0.21888029	0.405768829	-0.5342	0.589636391	0.6413429	gmy	0.09293867	0.246971194	GO:0016746;GO:0008152	lysophosphatidyl acyltransferase 4
Sapur.09GG188500.1	46.50709327	0.034169413	0.062818882	0.534177	0.5896454	0.66437279	gmy	-0.04341252	0.589282353	GO:0007165;GO:0005515	Disease-resistance protein (TIR-NBS-LRR class) family
Sapur.09GG164300.1	605.6894604	-0.017550887	0.03293473	-0.53895	0.589923162	0.66467113	gmy	-0.02831757	0.7248281	GO:0005515	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain
Sapur.09GG139200.1	1.846831034	0.104121656	0.193136239	0.538552	0.590150378	0.66479646	gmy	-0.04941701	0.815031616	GO:0005524;GO:0003676	RNAHelicase-like 1
Sapur.01GG059000.6	0.470661787	-0.193331407	0.358987858	0.53855	0.590196442	0.66479646	gmy	-0.09727234	0.224306687		Kinase-related protein of unknown function (DUF1296)
Sapur.01GG032800.1	5.457619447	-0.115788001	0.215365518	-0.53768	0.590297256	0.66520941	gmy	-0.02972756	0.715487706		
Sapur.09GG089500.1	0.163171779	-0.425810018	0.792919427	-0.53702	0.591269312	0.66545988	gmy	-0.18953287	0.017431193	GO:0003677	AP2/B3-like transcriptional factor family protein
Sapur.01GG131400.2	0.188803844	-0.095239455	0.177344859	-0.53694	0.591284138	0.66549398	gmy	-0.13132311	0.124386791	GO:0055114;GO:0050660;GO:0016491	Protein of unknown function (DUF630) / DNA6/2_/ RNA5/TLD (DM)
Sapur.01BG055400.1	1.9884 481887	-0.052241493	0.097161499	-0.53668	0.591486847	0.66605582	gmy	-0.04520659	0.573955924		Leucine-rich repeat (LRR) family protein
Sapur.01BG189000.4	0.232948025	0.362279587	0.68885802	0.536524	0.5913671	0.66536015	gmy	0.02878188	0.730471892	GO:0016787	alpha/beta-Hydrolases family protein
Sapur.09GG093900.1	0.47566471	0.18804468	0.346805514	0.536459	0.591641592	0.66538872	gmy	-0.17427176	0.026037881	GO:0005515;GO:0003684	DNA-directed DNA polymerase
Sapur.01GG079700.1	57.68726178	-0.033342488	0.062175383	-0.53627	0.591775346	0.66316393	gmy	-0.32043918	4.26E-05	GO:0005515	Sterile alpha motif (SAM) domain-containing protein
Sapur.09GG139300.1	2.931288444	0.067390565	0.124507603	0.536258	0.592347249	0.66684178	gmy	-0.01737621	0.937227704	GO:0006950	Adenine nucleotide alpha hydrolases-like superfamily
Sapur.01GG207000.1	0.991595324	0.147245686	0.275418283	0.534641	0.592888091	0.6751239	gmy	0.07481848	0.351783354	GO:0008270;GO:0005515	RING/U-box superfamily protein
Sapur.09GG177000.1	518.3148884	0.007497497	0.013816518	-0.53457	0.592900611	0.67548624	gmy	-0.04947651	0.91025616		Coiled-coil domain-containing protein 55 (DUF2040)
Sapur.01GG070800.1	2.031172557	0.109155522	0.204346237	0.534174	0.593231391	0.67360969	gmy	-0.08180294	0.30827563		RING/U-box superfamily protein
Sapur.09GG205900.1	0.488611394	0.267007024	0.49967622	-0.53401	0.593267318	0.67362022	gmy	-0.06319234	0.446285021		Yip/Ras-GAP domain family protein
Sapur.01TG031000.2	1.36282688	-0.113515605	0.212622092	-0.53388	0.593421558	0.66809952	gmy	-0.06025617	0.4534526		Phototropic-responsive NPH3 family protein
Sapur.01GG082700.1	18.78817127	-0.098324229	0.183944339	-0.53386	0.593441629	0.66809952	gmy	0.07261835	0.336296156		armadillo repeat only-6 protein
Sapur.09GG102100.1	22.38538819	-0.079229873	0.148406669	-0.53374	0.593524263	0.66880913	gmy	-0.04153181	0.605523697	GO:0005975;GO:0004553	Glycosyl hydrolase superfamily family 17 protein
Sapur.09GG074100.1	46.11125556	0.096571502	0.181216418	0.532907	0.594097945	0.68370065	gmy	-0.00263841	0.97381801		Plant basic secretory protein (BSP) family protein
Sapur.09TG031500.1	0.102929788	0.570607461	1.070607495	0.532266	0.594549188	0.68491806	gmy	0.20891548	0.08364665		
Sapur.01GG198000.1	1252.537247	0.02375271	0.044685365	0.531555	0.595034538	0.69366949	gmy	0.05645193	0.482514385	GO:0004681;GO:0006278;GO:0005524	calcium dependent protein kinase 1
Sapur.09GG230300.1	0.56022536	0.145351768	0.66601966	0.53145	0.595237214	0.69370164	gmy	-0.11651828	0.146192606		
Sapur.09GG194900.2	1.157725631	0.163704947	0.308270225	-0.53104	0.595388528	0.66996555	gmy	-0.03957702	0.622604735		
Sapur.01GG128700.1	3.362466617	0.103984551	0.196066155	-0.53101	0.595404944	0.66996555	gmy	-0.03134819	0.684909971	GO:0016021;GO:0016020	Nodulin MtN21 /EamA-like transporter family protein
Sapur.15WG074100.1	0.09409921	-0.027352174	0.051609915	-0.53089	0.595459343	0.67009624	gmy	-0.03814827	1.49E-05	GO:0043531	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.01GG083800.1	0.132630394	-0.740038391	1.394077738	-0.53084	0.5955231	0.67090033	gmy	-0.15482584	0.052389656	GO:0016491;GO:0046983	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.01GG035000.1	0.254917733	0.241175058	0.454495849	0.530643	0.595866165	0.67201858	gmy	-0.13973807	0.080824606	GO:0016021	Tetraspanin family protein
Sapur.01BG092000.5	0.115448815	0.486426055	0.912783951	0.530511	0.595757587	0.67202948	gmy	-0.12424371	0.12035807		Metallo-beta-lactamase/oxidoreductase superfamily protein
Sapur.01GG011000.1	1.079448834	-0.117924677	0.2224605	-0.53024	0.595948628	0.67425614	gmy	-0.05291837	0.514923336		
Sapur.09GG058800.1	20.1201348	-0.06018806	0.113515213	-0.53023	0.595959192	0.67425623	gmy	-0.04731273	0.556248964	GO:0016758;GO:0008152	UDP-Glycosyltransferase superfamily protein
Sapur.01GG119200.1	0.113767616	0.208487396	0.394066183	0.529656	0.596230571	0.67682674	gmy	0.07261835	0.336296156		Polyketide/chalcone, stilbene, dihydroxybenzene 4-like superfamily protein
Sapur.01GG056200.1	0.32224857	0.298831606	0.564284771	0.529284	0.596010118	0.67208757	gmy	-0.12438305	0.126637323	GO:0009915;GO:0006996;GO:0004743;GO:0000287	Pyruvate kinase family protein
Sapur.01GG139900.1	1.691007968	0.07183398	0.208261755	-0.53065	0.596367661	0.67211227	gmy	-0.06227754	0.840235661		G2484-1 protein
Sapur.09GG042000.1	10.24021876	-0.055929031	0.112142342	-0.52905	0.596779394	0.67211227	gmy	-0.05503608	0.493669598	GO:0006355;GO:0003700	Integrase-type DNA-binding superfamily protein
Sapur.09TG031500.1	0.102929788	0.570607461	1.070607495	0.528867	0.596829429	0.67125422	gmy	0.20891548	0.08364665		
Sapur.01BG082500.1	1.643320019	0.111495507	0.210594022	-0.52863	0.597131407	0.67156946	gmy	0.05645193	0.482514385	GO:0004681;GO:0006278	calcium dependent protein kinase 1
Sapur.09GG060300.1	0.09613313	0.175087429	0.330296	-0.52836	0.597349039	0.67170706	gmy	-0.11651828	0.146192606		
Sapur.09GG121700.1	140.6746	-0.027341314	0.05175499	0.528263	0.597336557	0.67170682	gmy	-0.03957702	0.622604735		
Sapur.15WG148900.1	0.246375565	-0.24885573	0.469552498	-0.5279	0.597537984	0.67207882	gmy	-0.11122011	0.185555039	GO:0003983;GO:0006298;GO:0005524	Nodulin MtN21 /EamA-like transporter family protein
Sapur.09GG189000.1	27.41425365	0.034169413	0.062818882	-0.52679	0.597731806	0.67219585	gmy	0.02994166	0.70995484		MYB/SANT/LHP1 domain-containing protein
Sapur.15WG145500.3	2.392109128	0.095823984	0.181627559	0.527585	0.597787375	0.67270383	gmy	0.02116602	0.79197244	GO:0007186;GO:0005834;GO:0004871	Wound-responsive family protein
Sapur.01GG129900.2	0.447016654	0.103264505	0.195988563	0.527388	0.597944411	0.67278754	gmy	0.00182416	0.981909946	GO:0004872;GO:0030001	G-protein gamma subunit 2
Sapur.15WG085700.1	833.2821796	-0.035362439	0.067546027	-0.52702	0.598180393	0.67264711	gmy	-0.03564615	0.658506692	GO:0016459;GO:0016579	Zinc finger C-x8-C-x5-C-x3-H type family protein
Sapur.09GG070200.1	17.48831615	-0.048329391	0.09151127	-0.52661	0.598461744	0.67287165	gmy	0.13131168	0.155141428	GO:0005681	Ubiquitin carboxyl-terminal hydrolase-related protein
Sapur.01GG085700.1	0.146317998	-0.345505681	0.646788249	-0.52646	0.598575845	0.67293364	gmy	-0.21838643	0.006030481	GO:0005515	U2 snRNP auxiliary factor, large subunit
Sapur.01GG085800.1	0.118899949	-0.152562507	0.9628136	-0.52644	0.598581775	0.67293367	gmy	-0.21973570	0.050283311	GO:0004981;GO:0003677	F-box/RNI-like superfamily protein
Sapur.01BG025700.1	0.772623236	-0.169849979	0.32180093	-0.52637	0.598633322	0.67296125	gmy	-0.0623896	0.437601473		AGAMOUS-like 80
Sapur.7J29700.1	0.083026804	0.572001587	1.087080171	0.526269	0.598743875	0.67361718	gmy	0.29485615	0.00018555		
Sapur.01BG047600.1	0.116657943	0.416626496	0.8206653	0.526117	0.598807235	0.67111188	gmy	0.21966647	0.088760327	GO:0008270;GO:0003676	
Sapur.01BG110200.1	459.9374998	-0.020358663	0.039080573	-0.52606	0.598849588	0.67334772	gmy	-0.02812047	0.726687253	GO:0000160	response regulator 2
Sapur.09GG138800.4	0.784425764	0.158352128	0.29139157	-0.52588	0.598980331	0.67160049	gmy	-0.02282412	0.683303887	GO:0008270;GO:0006270	Protein kinase superfamily protein
Sapur.01TG079300.2	12.76512994	0.046395692	0.088231497	0.52596	0.598985621	0.67165049	gmy	-0.08045653	0.275046199	GO:0016887;GO:0005524;GO:0005085;GO:0004262;GO:0016021;GO:0006810	ABC transporter family protein, putative
Sapur.01GG042700.6	1.371829216	-0.07062319	0.145011001	0.525845	0.598995587	0.67231362	gmy	0.01735266	0.837132074	ATHAD5,AD43	histone deacetylase family protein
Sapur.09GG100900.3	0.126054418	0.436186112	0.83092561	0.525424	0.599288664	0.67317989	gmy	0.17717258	0.112468686		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.09GG139500.1	1.125175338	0.127788818	0.471962371	0.5252	0.599469178	0.67382711	gmy	-0.06567873	0.417278339	GO:0006412;GO:0005840;GO:0005622;GO:0003735	
Sapur.09GG083400.2	1.417659133	-0.120583325	0.248714652	-0.52503	0.599604046	0.67397575	gmy	-0.04987542	0.535398861	GO:0004680;GO:0006472	with no lysine (K) kinase 1
Sapur.01BG068300.1	1.586260604	0.077595897	0.15235884	0.524551	0.599933367	0.67455684	gmy	0.00614604	0.939093383		HIT-type Zinc finger family protein
Sapur.09GG063000.1	11.26871508	0.048717873	0.091939014	0.52418	0.600132178	0.67459055	gmy	-0.04170327	0.42460939		
Sapur.09GG154100.1	0.800442247	0.189203071	0.361268227	-0.52372	0.600472023	0.67470782	gmy	-0.04561568	0.570521773		Mitochondrome maintenance (MCM2/3/5) family protein
Sapur.01GG123000.1	0.119183542	-0.067551292	0.129275192	0.523355	-0.52349	0.600600429	0.6751225	-0.21468606	0.035454175		Exostosin family protein
Sapur.01GG089600.1	25.9714661	0.034444263	0.065810389	0.522227	0.600816017	0.67532573	gmy	0.04369141	0.597232701	GO:0016592;GO:0006357;GO:0001104	MEDIATOR OF RNA POLYMERASE II TRANSCRIPTION SUBUNIT
Sapur.01GG082600.1	105.1629577	0.025090181	0.050426942	0.521215	0.600874974	0.67532574	gmy	-0.0041232	0.959136275		
Sapur.7J12000.1	53.06453008	0.132263219	0.252802225	0.521189	0.600843077	0.67532573	gmy	-0.07463884	0.352686		
Sapur.15WG072100.1	12.53134657	0.051838337	0.098371717	0.521182	0.600843054	0.67532122	gmy	-0.21298446	0.057573079	GO:0008887;GO:0000145	exocyst subunit exo70 family protein E2
Sapur.01GG118100.1	0.463504606	0.191083631	0.36603589	-0.52204	0.601645768	0.67581594	gmy	-0.03805526	0.636100404	GO:0006486;GO:0006378;GO:0006486	Galactosyltransferase family protein
Sapur.01GG112100.2	0.172792603	-0.134264448	0.6403915	-0.52188	0.601884844	0.67387165	gmy	-0.18183138	0.02237474		SAP domain-containing protein
Sapur.15WG057100.1	0.121126637	0.450130299	0.863824049	0.52109	0.602338396	0.67651266	gmy	0.15682173	0.049834752		
Sapur.09GG147700.2	4.613656544	-0.066827346	0.128264617	0.521011	0.602338262	0.67652139	gmy	0.02327992	0.737265559	GO:0016192;GO:0006904	vacuolar protein sorting 45
Sapur.01GG089500.1	9.74447523	0.056886825	0.109455242	0.520649	0.602611642	0.6768126	gmy	0.02378107	0.7479573		Plasma-membrane choline transporter-like protein
Sapur.09GG161200.1	0.791833532	0.168551502	0.32388017	0.520542	0.602860847	0.67687008	gmy	-0.18441761	0.03076971	GO:0006367;GO:0005634	TBP-associated factor 11
Sapur.01GG028700.1	1.727451134	-0.139357766	0.267177908	-0.5051	0.602958018	0.67687008	gmy	-0.07080219	0.345915715		
Sapur.01TG127300.4	0.102896638	0.631367179	1.213222449	0.520405	0.602781230	0.67691134	gmy	0.15052112	0.059871533	GO:0005085;GO:0016021;GO:0016020;GO:0006810;GO:0005215	Major facilitator superfamily protein
Sapur.01GG192500.1	0.238361224	0.133242932	0.256751799	0.520125	0.603297518	0.67788474	gmy	-0.17456419	0.028409543		
Sapur.01BG018800.2	0.131218643	-0.39313784	0.75258561	-0.51998	0.603800553	0.67719279	gmy	-0.09786205	0.122715064		Phototropic-responsive NPH3 family protein
Sapur.09GG020600.1	1.179683007	0.127682015	0.245616629	0.518813	0.603319363	0.67735117	gmy	0.10758806	0.178052127	GO:0006412;GO:0005840;GO:0003735	60S ribosomal protein L4
Sapur.01GG134200.1	12.82658859	0.08314956	0.160005075	0.51668	0.603924836	0.67350902	gmy	0.04257541	0.597517759	GO:0004372;GRAS2;SCL14	GRAS family transcription factor
Sapur.01GG164900.2	0.110773874	0.204643212	0.691730763	0.516667	0.603935726	0.67350902	gmy	0.08464584	0.28158352	GO:0005515;GO:0004657;GO:0007027	Protein of unknown function (DUF707)
Sapur.09GG019500.1	2.045813634	0.144584002	0.27835423	0.519424	0.603464761	0.67517686	gmy	0.0060935	0.904922487	GO:0005114;GO:0016491;GO:0050664;GO:0004601;GO:0016174	NADH:ubiquinone oxidoreductase family protein
Sapur.01GG075400.1	0.10967791	0.501789215	0.966353485	0.519261	0.603579079	0.6762383	gmy	0.16612945	0.035737454		S/T-AMP-activated protein kinase beta-2 subunit protein
Sapur.01TG078200.1	411.7557551	0.027383516	0.052766545	0.518877	0.603783666	0.67780931	gmy	-0.03139966	0.694956904	GO:0005515;GO:0004680;GO:0006278	receptor-like protein kinase 2
Sapur.09GG123700.2	0.263693552	0.229325553	0.44153199	-0.5189	0.603836323	0.67860348	gmy	-0.02485479	0.761584554	GO:0008270;GO:0006355	FARS-related sequence 3
Sapur.09GG017700.1	0.158637044	0.268405451	0.518447371	0.518851	0.603864643	0.67863689	gmy	-0.17261403	0.031471929		SCARECROW-like 11
Sapur.09GG047000.2	16.94036839	0.059091224	0.07694633	0.518752	0.603931652	0.67906045	gmy	-0.01045891	0.899648095	GO:0005515;GO:0043562;GO:0009744	S/T-AMP-activated protein kinase beta-2 subunit protein
Sapur.09GG047500.1	47.52574464	0.025473068	0.045498183	0.518595	0.604044387	0.67909693	gmy	0.08068545	0.31545012		electron transfer flavoprotein alpha
Sapur.01GG184800.1	579.8608806	-0.018329469	0.03135647	-0.51842	0.604163	0.67921159	gmy	-0.06915814	0.18842589		transmembrane protein, putative
Sapur.01TG025900.1	2.773181631	-0.067486748	0.12689624	-0.51823	0.604269768	0.67921159	gmy	-0.05403606	0.49642278		DNA/RNA-like superfamily protein
Sapur.7J09500.1	0.097559175	0.583701481	1.127037027	0.517913	0.604619261	0.67841276	gmy	0.26243592	0.003988807	GO:0005515;GO:0006488;GO:0005524;GO:0004672	Leucine-rich repeat protein kinase family protein
Sapur.7J13300.1	1.6314122	-0.147749695	0.2816734	0.517195	0.604661188	0.67865383	gmy	-0.01243417	0.880337527		PLATZ transcription factor family protein
Sapur.7J59900.1	0.07885614	0.559250575	1.080070973	0.517767	0.604620866	0.6785926	gmy	-0.24422746	0.010880089		gamma-irradiation and mitomycin c induced 1
Sapur.15GS251200.1	1.565725865	-0.095359461	0.184207554	-0.51751	0.604803775	0.67880022	gmy	-0.03724297	0.442303406		ENTH/VHS family protein
Sapur.09GG189200.5	1.660720126	0.108451557	0.20960051	0.517343	0.605169061	0.67882455	gmy	-0.03765144	0.639267601	GO:0006511	ubiquitin fusion degradation protein
Sapur.01BG130700.1	112.3486556	-0.318926179	0.61653474	-0.51729	0.604589947	0.67882049	gmy	-0.13142087	0.101078171		Plant protein of unknown function (DUF247)
Sapur.09TG047000.1	37.33075625	0.034169413	0.062818882	-0.51726	0.605455129	0.67915594	gmy	0.28732281	0.000102015	GO:0005114;GO:0016491	glutathione reductase
Sapur.01GG092000.1	0.116988327	-0.15609841	1.07070217	-0.5163	0.605643334	0.67958381	gmy	-0.24919718	0.001848812		Late embryogenesis abundant (LEA) protein-related
Sapur.09GG139400.1	66.14414469	0.040288672	0.07820566	0.515315	0.606331108	0.68029092	gmy	0.05978623	0.458202618		ubiquitin-conjugase 9
Sapur.01BG301100.1	15.73654117	-0.05207798	0.10105229	-0.51509	0.606409229	0.68045764	gmy	-0.03708706	0.657046192	GO:0005975;GO:0004650	Pectin lyase-like superfamily protein
Sapur.01GG088300.1	1.362711688	0.072022488	0.139767192	0.513487	0.606682628	0.68221682	gmy	-0.22904701	0.513259944	GO:0005085;GO:0016021;GO:0008324;GO:0006812	Cation efflux family protein
Sapur.09GG117300.1	2.07044709	0.100080057	0.194406525	-0.5148	0.606694301	0.68035234	gmy	-0.01664875	0.894695279		
Sapur.09TG033400.1	29.6628893	0.061660869	0.119768813	-0.51474	0.606734425	0.68057159	gmy	-0.07239641	0.367589109		Sec14p-like phosphatidylinositol transfer family protein
Sapur.09GG125000.1	0.183910846	-0.363301041	0.705747785	-0.51449	0.606909486	0.68087571	gmy	-0.24662101	0.016475584		K-box region and MADS-box transcription factor family protein
Sapur.09GG058000.1	0.185458666	-0.345126289	0.670846332	-0.51446	0.606927499	0.68087571	gmy	-0.17008078	0.033201938	GO:0005515;GO:0003700	Plant invertase/pectin methylesterase inhibitor superfamily protein
Sapur.01BG080500.1	0.126854444	0.159894953	1.010122177	0.514326	0.607029159	0.68091313	gmy	-0.16240432	0.010408207		
Sapur.09GG089600.1	1947.985266	0.010157473	0.019752525	0.514237	0.607086536	0.68095977	gmy	0.0123931	0.877571106		3-dehydroquinate synthase, putative
Sapur.01GG090200.1	0.115824024	-0.147884274	0.287502627	-0.51315	0.607159059	0.68140112	gmy	-0.24662101	0.016475584	GO:0046983;GO:0003677;GO:0006355;GO:0005634;GO:0003700	K-box region and MADS-box transcription factor family protein
Sapur.01GG104400.1	0.104684036	-0.490565813	0.951120463	0.513502	0.607605045	0.68160112	gmy	0.19089996	0.016154054		
Sapur.01BG080600.1	0.126854444	0.159894953	1.010122177	0.513318	0.607622248	0.68171658	gmy	-0.14472888	0.070545018	GO:0003674;GO:0004144;GO:0005622;GO:0003746	elongation factor Ts family protein
Sapur.01GG115100.2	0.273615625	-0.281027163	0.548397904	-0.51253	0.608273853	0.68180384	gmy	-0.03179938	0.692761151		transmembrane protein, putative
Sapur.01GG084000.1	0.703413433	-0.452284774	0.878463	-0.51188	0.608606	0.68340888	gmy	-0.11437562	0.120604887	GO:0020170;GO:0009058	1-aminocyclopropane-1-carboxylate synthase B
Sapur.01TG022900.5	0.137657727	-0.352130967	0.685563833	-0.5114	0.608676582	0.68284241	gmy	-0.13740754	0.086149149	GO:0005515;GO:0006355;GO:0003700;GO:0046983;GO:0003677	K-box region and MADS-box transcription factor family protein
Sapur.09GG083200.2	1.275143388	0.06103644	0.119887512	0.511391	0.609077227	0.68284241	gmy	0.02193031	0.875751106		Transport protein particle (TRAPP) component
Sapur.01GG075000.6	1.691017277	-0.114941556	0.22477989	-0.51136	0.609159	0.68290112	gmy	-0.02522405	0.891002006		O-fucosyltransferase family protein
Sapur.09GG138400.1	2.021002953	0.120083572	0.23497594	0.511046	0.609319675	0.68362398	gmy	0.02489299	0.756928029		NAD+ ADP-ribosyltransferases;NAD+ ADP-ribosyltransferases
Sapur.01GG026400.1	1.256424814	0.154769942	0.303607079	-0.51093	0.609409853	0.68123134	gmy	-0.05997251	0.459971044	GO:0045454;GO:0015035;GO:0009055	thioredoxin family protein
Sapur.01GG130300.1	1.1387394 5	0.160894807	0.315110178	0.510899	0.609419192	0.68231788	gmy	0.03617664	0.649787382	GO:0008270	RING/FYVE/PHD zinc finger superfamily protein
Sapur.09GG139100.1	73.32943824	0.034169413	0.062818882	0.510847	0.609478889	0.68231857	gmy	0.04217688	0.584532013		
Sapur.01TG063300.1	2.779809895	0.098765242	0.193664873	0.510113	0.609658424	0.6837869	gmy	-0.07380892	0.357854985	GO:0004681;GO:0005524;GO:0004672	suppressor of rps5-1 constitutive 4
Sapur.01GG090600.1	0.181616148	0.301881885	0.59144112	0.509929	0.610192261	0.68364425	gmy	-0.14873928	0.068308871	GO:0004664;GO:0004677	HC51
Sapur.15WG053100.1	0.1113825	0.446869

Sapur.002G0284000.6	8.35894394	-0.05483005	0.11446595	-0.48886	0.62494238	0.69791395	grey	-0.03779797	0.6383544	GO:0043565,GO:0006355,GO:0003700,GO:0006351													
Sapur.002G0944900.1	2.36855292	0.11824189	0.24193098	-0.48874	0.62502166	0.69797917	grey	-0.17214810	0.03109194														
Sapur.006G1179000.3	0.60991854	0.18749755	0.18390758	-0.48845	0.62526482	0.69822584	grey	-0.17130562	0.03190601	GO:0006468,GO:0005634,GO:0004672													
Sapur.002G0280000.4	0.07510605	0.5967484	1.3231342	-0.48788	0.62562657	0.69880166	grey	0.26320773	0.00078749	GO:0006468,GO:0005634,GO:0004674,GO:0004672													
Sapur.006G0920500.1	757.2871327	0.07230783	0.07628783	-0.48783	0.62568157	0.69885619	grey	0.03844089	0.65745335														
Sapur.014G0251600.1	464.9814184	-0.01763362	0.0282495	-0.48721	0.62611146	0.69905174	grey	-0.06879296	0.19201981														
Sapur.011G1394000.1	335.5374017	0.01607184	0.03465585	-0.48688	0.62637347	0.69926948	grey	0.00393021	0.98086093														
Sapur.006G0191200.1	0.06979127	0.97122493	1.22863051	-0.48607	0.62692429	0.69987761	grey	0.26703034	0.00071723														
Sapur.019G1142000.1	414.6864076	-0.02976159	0.06142094	-0.48476	0.62784111	0.70082069	grey	-0.03760175	0.64107285														
Sapur.005G047200.3	4.16387445	0.05225665	0.12579275	-0.48404	0.62832805	0.70097662	grey	0.03434365	0.70097662														
Sapur.013G027000.2	1.24875692	0.17106791	0.35318479	-0.48387	0.62844149	0.70111375	grey	0.03641247	0.62406092														
Sapur.005G0618000.1	0.07060103	0.95869881	1.07916151	-0.48367	0.62859197	0.70118932	grey	0.23188809	0.00187147	GO:0016020,GO:0015171,GO:0003333													
Sapur.017G0437300.1	35.11668077	0.03629294	0.07698948	-0.48405	0.62834505	0.70129584	grey	0.06884179	0.19271005														
Sapur.017G0822100.1	2.30405487	0.12773488	0.27134284	-0.48374	0.62857641	0.70129584	grey	-0.05008054	0.49317951														
Sapur.013G0058000.1	3.80418049	-0.12776285	0.26394287	-0.48392	0.62844859	0.70132547	grey	-0.01735943	0.82923814														
Sapur.002G0845200.1	0.69329315	0.05223511	0.3362597	-0.48356	0.62869769	0.70154327	grey	-0.02024665	0.85269937	GO:0009055													
Sapur.011G0257600.2	13.38768	0.07402363	0.15094504	-0.48342	0.62879631	0.70167048	grey	0.0271238	0.73608343	GO:0016021,GO:0008963													
Sapur.018G0941600.1	0.9964012	0.12036265	0.24906822	-0.48249	0.62948934	0.70178564	grey	0.05993788	0.45842856														
Sapur.006G0880800.1	101.6151438	0.02665833	0.2069829	-0.48117	0.62897594	0.70181617	grey	0.03088377	0.38109561														
Sapur.006G0349300.3	0.12007794	0.36271044	0.75124283	-0.48284	0.62927669	0.70280684	grey	0.11041556	0.18861729	GO:0008270,GO:0003677													
Sapur.011G0310100.1	25.52122507	0.03208055	0.09180557	-0.48263	0.62942238	0.70282397	grey	0.20201005	0.01172303														
Sapur.007G0648000.1	1.36270466	0.11036016	0.22868392	-0.48217	0.62972262	0.70285557	grey	0.07148246	0.37351882														
Sapur.005G0000100.1	0.08442456	0.58860554	1.22102283	-0.48069	0.62959761	0.70287746	grey	0.21652048	0.00645181														
Sapur.016G0942900.1	0.35249953	0.20736084	0.43026904	-0.48193	0.62985309	0.70288284	grey	0.00491562	0.95128264														
Sapur.017G0544300.1	0.06071816	0.52773488	1.09470187	-0.48047	0.62988707	0.70288707	grey	0.20966853	0.00180471														
Sapur.012G0188000.1	183.7726647	0.03717434	0.07146431	-0.48187	0.62989561	0.70288787	grey	0.00872507	0.91363829	GO:0055114,GO:0016491,GO:0010181													
Sapur.019G0395900.1	2.67691205	0.08203981	0.2249339	-0.48116	0.63060569	0.70322442	grey	-0.06512235	0.41747018	GO:0055085,GO:0016021													
Sapur.006G1881000.1	2521.128104	0.03362815	0.06852818	-0.48624	0.63078445	0.70326796	grey	0.00309664	0.98273311	GO:0006629													
Sapur.001G0160600.2	0.37691414	0.19706451	0.41007614	-0.48053	0.63085873	0.70367812	grey	0.01261263	0.87592202	GO:0008270,GO:0005515													
Sapur.010G0601500.1	78.61926824	0.04133794	0.08586428	-0.47942	0.63141159	0.70427097	grey	0.22791752	0.00409345														
Sapur.014G1028000.5	10.56728819	0.05469154	0.11387935	-0.47927	0.63149782	0.70436688	grey	0.06069143	0.45014742	GO:0055085,GO:0016021													
Sapur.006G1566000.1	1.62446792	0.10320012	0.21523831	-0.47947	0.63158324	0.70446559	grey	-0.05618008	0.48974567														
Sapur.003G0585800.6	0.10627456	0.37665144	0.78610563	-0.47809	0.63187427	0.70470583	grey	0.14889482	0.06277157	GO:0008168													
Sapur.002G0284800.4	0.22192299	0.32607853	0.68726849	-0.47904	0.63187328	0.70470583	grey	0.07317916	0.37475047	GO:0016788													
Sapur.005G1813000.1	1534.523713	0.01281784	0.02676367	-0.47904	0.63193336	0.70471735	grey	0.00019748	0.99861042	GO:0019773,GO:0006511,GO:0004175,GO:0051603,GO:0005839,GO:0004298													
Sapur.005G0450600.1	0.54988034	0.05205003	0.1087497	-0.47887	0.63208617	0.70525887	grey	-0.06263	0.30234778	GO:0003674,GO:0005739,GO:0000398													
Sapur.017G1131000.1	109.7507888	-0.07511949	0.15712295	-0.47809	0.63258085	0.70537274	grey	0.07327665	0.16176425	GO:0005515,GO:0043531													
Sapur.018G1171000.1	0.10995778	0.45731551	0.95650866	-0.47904	0.63271692	0.70549677	grey	0.10479246	0.19164315														
Sapur.016G1919001.1	0.54153369	0.17744302	0.37008416	-0.47799	0.63329257	0.70550556	grey	-0.06261644	0.9461466	GO:0006355,GO:0003700													
Sapur.016G0612000.10	13.68168072	-0.05007732	0.10562635	-0.47751	0.63300144	0.70576769	grey	0.12017156	0.13491187	GO:0016887,GO:0005524,GO:0016020													
Sapur.007G0949400.4	2.08231334	0.09125248	0.1861542	-0.47694	0.63384743	0.70681872	grey	0.02230281	0.78197761														
Sapur.015W0145800.1	93.35512297	0.02819588	0.05920164	-0.47626	0.63385563	0.70681872	grey	0.03765262	0.63962067	GO:0055114,GO:0020037,GO:0016705,GO:0005506													
Sapur.004G0448000.1	1074.953033	0.01625238	0.03411875	-0.47604	0.63405008	0.70681942	grey	0.05797908	0.47203377	GO:0015773,GO:0016020,GO:0005524													
Sapur.017G0461000.3	0.17316794	-0.40644238	0.85498839	-0.47538	0.63451296	0.70728562	grey	-0.02565144	0.74978557	GO:0000049,GO:0006418,GO:0005524,GO:0004812,GO:0000166													
Sapur.004G0421500.1	471.6406513	0.01938977	0.04083639	-0.47526	0.63477642	0.70752575	grey	-0.17715642	0.02446979	GO:0005912,GO:0008218													
Sapur.003G0753000.1	0.96109207	0.13215924	0.27822795	-0.475	0.63479664	0.70754133	grey	-0.04330275	0.58978845	GO:0071805,GO:0016020,GO:0015279													
Sapur.003G0597000.1	1.88023863	0.11515088	0.24251658	-0.47485	0.63481367	0.70756857	grey	0.03873425	0.8183789														
Sapur.009G0412000.1	14.58225599	0.06232954	0.13134303	-0.47458	0.63520945	0.70776765	grey	0.0463527	0.56429948														
Sapur.006G1129000.1	108.3542821	-0.03775684	0.07962937	-0.47451	0.63536181	0.70815142	grey	-0.06292612	0.43366157	GO:0009733													
Sapur.005G0878000.1	1.48023878	-0.14787397	0.31154789	-0.47409	0.63541287	0.70816274	grey	0.01152991	0.88108565														
Sapur.T014700.1	0.43107653	0.16438849	0.34674061	-0.47408	0.63547259	0.70816471	grey	0.00442854	0.95612818														
Sapur.001G0160200.1	17.13843931	0.05332445	0.11607615	-0.4728	0.63564264	0.70832812	grey	-0.03302162	0.67307128														
Sapur.018G1155000.1	0.99023889	0.47505718	1.01244095	-0.47365	0.6359529	0.70862208	grey	0.20593523	0.00966443	GO:0005515													
Sapur.005G0572000.2	0.95887663	0.07229108	0.2804102	-0.47312	0.63605086	0.70875824	grey	0.02183834	0.78549424	GO:0005515,GO:0006468,GO:0005524,GO:0004672													
Sapur.010G0255000.1	0.28809865	0.21086178	0.44647523	-0.47341	0.63611283	0.70875821	grey	0.04035126	0.59237604														
Sapur.009G0313000.2	4.78314905	0.07238456	0.15296712	-0.47308	0.63625745	0.70878362	grey	-0.05092517	0.62928863														
Sapur.005G0054000.1	15.09721707	0.04602415	0.07121895	-0.47002	0.63621601	0.70881077	grey	0.05139259	0.52267699	GO:0007264,GO:0005525													
Sapur.15W0107700.1	0.41766739	0.17805767	0.37651132	-0.47291	0.63629172	0.70886691	grey	-0.01813162	0.82675217														
Sapur.018G0160600.1	0.10708509	-0.45783884	1.02780284	-0.4726	0.63697294	0.70969149	grey	-0.24002403	0.02442925														
Sapur.008G0285000.2	1.46362335	0.09735658	0.20600446	-0.47245	0.63688842	0.70991085	grey	0.03191892	0.69136492	GO:0016021,GO:0006486,GO:0005783,GO:0004579													
Sapur.002G0284000.1	1.29494323	0.09225881	0.20047577	-0.47189	0.63750703	0.70984021	grey	0.07204004	0.36643201														
Sapur.017G1189000.2	49.79223506	0.03036286	0.06439128	-0.47496	0.63722862	0.7008745	grey	0.04328258	0.58614688														
Sapur.007G0750.1	1.47612926	0.10028612	0.22508965	-0.47171	0.63755465	0.70150445	grey	-0.03282028	0.81904769	GO:0005515													
Sapur.006G0380800.1	138.7037835	0.03001274	0.06756793	-0.47031	0.63783112	0.70345204	grey	0.08251269	0.72261062														
Sapur.004G0281100.1	0.38502847	0.71138232	1.29645127	-0.47069	0.63884918	0.71318238	grey	0.01572291	0.0053768														
Sapur.017G0743000.2	7.32076236	-0.05479269	0.13279951	-0.46938	0.63879916	0.71440346	grey	-0.07329869	0.63197601														
Sapur.006G0190900.1	1.90710207	0.14488529	0.33866456	-0.46869	0.63896456	0.71508973	grey	-0.02150308	0.78349285	GO:0008270,GO:0016168,GO:0019789,GO:0016925,GO:0016049,GO:0005634													
Sapur.012G0060900.1	16.05129383	-0.05319726	0.11539102	-0.46691	0.63869925	0.71572565	grey	0.00706229	0.93009928	GO:0005515													
Sapur.002G0438800.1	1.66563374	0.06438849	0.17925581	-0.46863	0.63933679	0.71963707	grey	0.07053474	0.38035578	GO:0008375,GO:0008486													
Sapur.010G0880800.1	441.262499	-0.02692682	0.05486819	-0.46847	0.63949819	0.71254096	grey	-0.03187329	0.69228118	GO:0005992,GO:0008324													
Sapur.006G1650000.3	0.10764124	-0.40514294	0.86537783	-0.46851	0.63967884	0.71200117	grey	-0.20562935	0.00980144	GO:0006355,GO:0003700													
Sapur.006G1367000.1	0.0878031	0.54041991	1.24026834	-0.46787	0.63979781	0.71246082	grey	0.14189273	0.07745027	GO:0016021,GO:0005992													
Sapur.15W0091800.1	413.5858131	-0.01245919	0.02677459	-0.46756	0.64010166	0.71272284	grey	-0.07496928	0.22645908														
Sapur.015G0118000.2	2.07592738	0.08839369	0.18921918	-0.46709	0.64042019	0.7130386	grey	0.02720249	0.66102715														
Sapur.010G1181000.1	0.10876756	0.44278017	0.95605154	-0.46686	0.64063878	0.71340075	grey	0.12985825	0.10503752														
Sapur.003G0345000.1	0.09955859	0.53207065	1.14506388	-0.46668	0.64120723	0.71385609	grey	0.14227643	0.06837745														
Sapur.012G0180800.2	0.18003783	0.27924124	0.59925769	-0.46509	0.64123047	0.71385609	grey	0.01158182	0.88530485	GO:0046872,GO:0030001													
Sapur.016G1181000.1	66.02888226	0.05669491	0.12134146	-0.46573	0.64180387	0.71482558	grey	0.06267043	0.45498815														
Sapur.004G0854000.1	0.36161145	-0.25476111	0.54757984	-0.46526	0.64174856	0.71488664	grey	-0.04966016	0.53938665														
Sapur.013G0717000.2	0.58492668	-0.15667065	0.33688854	-0.46512	0.64184798	0.71497405	grey	-0.05399126	0.50182363														
Sapur.004G0830500.1	1.91743915	0.08982168	0.21431664	-0.46466	0.64230578	0.71540273	grey	0.04428434	0.53938709	GO:0005085,GO:0046872,GO:0030001,GO:0016020													
Sapur.009G0200400.1	0.32001749	-0.1811187	0.38966407	-0.46481	0.64309467	0.71457485	grey	-0.10727066	0.18145552	GO:0005525													
Sapur.018G0301300.1	0.09284733	0.46705219	1.07018125	-0.46407	0.64329329	0.71468202	grey	0.20631875	0.03459963														
Sapur.006G0783000.3	3.47279635	-0.06489428	0.13962853	-0.46426	0.64264586	0.71565073	grey	-0.05290639	0.51453462														
Sapur.002G0525000.1	0.17945027	0.51218145	1.10488715	-0.46426	0.64257322	0.71544224	grey	0.02611692	0.76455374	GO:0006355,GO:0003700,GO:0003899													
Sapur.017G1199000.1	126.147805	0.06092909	0.13140409	-0.46323	0.64329146	0.71597653	grey	0.05943031	0.46188664														
Sapur.015G0250000.2	1.20742784	0.08102559	0.17480266	-0.46296	0.64347663	0.71597653	grey	0.04847182	0.53238425														
Sapur.15W0101100.1	209.945955	-0.06158198	0.13304097	-0.46287	0.64356732	0.71602761	grey	0.29322753	0.00019753	GO:0055114,GO:0016491,GO:0008152,GO:0051930,GO:0008807,GO:0016638,GO:000653													
Sapur.019G0819800.1	58.11728703	0.03318572	0.07155537	-0.46287	0.64369098	0.71602762	grey	0.03807478	0.63592041														
Sapur.018G0000600.1	189.7414614	0.1196155	0.25850203	-0.46275	0.64376147	0.71609125	grey	0.04228312	0.59018582														
Sapur.001G0671000.1	0.24825469	0.21743476	0.46930315	-0.46269	0.64384115	0.71609231	grey	0.27152888	0.00043114	GO:0005515													
Sapur.018G0301500.1	1457.135242	-0.09450502	0.08528934	-0.46264	0.64388052	0.71618574	grey	-0.03379027	0.67467404	GO:0005886,GO:0004879,GO:0003001,GO:0016020													
Sapur.001G0410400.1	0.43870089	-0.17463131	0.3775122	-0.46249	0.64372835	0.71626288	grey	-0.08167677	0.30919621														
Sapur.006G0854500.1	0.09751274	-0.52284117	1.13080439	-0.46218	0.64389244	0.71635778	grey	-0.20209974	0.03538857														
Sapur.014G0374000.2	1.05117777	0.11388106	0.24633546	-0.46195	0.64411158	0.71653495	grey	-0.08740975	0.31347924	GO:0005634													
Sapur.003G0421200.3	0.41118829	0.47428756	1.03778136	-0.46116	0.64488725	0.71719189	grey	-0.08408804	0.30908942														
Sapur.T112300.1	3.42860369	0.10337254	0.22428245	-0.4609	0.64487946	0.71730524	grey	-0.09017582	0.30986582														
Sapur.005G0410000.1	0.08329648	0.92223217	1.99033869	-0.46063	0.64506676	0.71730545	grey	0.20349312	0.01012583	GO:0006629													
Sapur.001G153700.1	0.10150527	0.12192592	1.13154468	-0.46047	0.64520573	0.7162947	grey	0.20031307	0.01188961														
Sapur.016G1146000.1	448.0496528	0.01468245	0.03186824	-0.46028	0.64545613	0.71764429	grey	0.01657751	0.83738809														
Sapur.011G1238000.1	0.18765832	0.25468318	0.55157684	-0.45974	0.64566627	0.71800587	grey	-0.18009916	0.03627912														
Sapur.006G0254000.1	0.17485078	-0.22747999	0.50360504	-0.45964	0.64576109	0.71834931	grey	-0.14520128	0.08969725	GO:0003924,GO:0007017,GO:0005874													
Sapur.017G0280900.4	78.22608923	0.03181788	0.06904052	-0.45963	0.64582615	0.71832086	grey	0.10747611	0.18509147														
Sapur.009G1053000.2	0.12490862	0.39485263	0.86201377	-0.45934	0.64621841	0.71860713	grey	0.14873325	0.06301353														
Sapur.018G0948300.10	0.12163974	0.67088144	0.15764799	-0.45863	0.64649125	0.7188576	grey	0.16597176	0.0377883	GO:0006468,GO:0004672													
Sapur.013G1069000.1	0.16392657	0.29076343	0.64706396	-0.45852	0.64655571	0.71889294	grey	-0.04787878	0.55157172														
Sapur.016G2840000.1	0.31104968	0.19245546	0.43051381	-0.45848	0.64668283	0.71891365	grey	0.15538848	0.05230341	GO:0043968,GO:0018024,GO:0008270,GO:0005634,GO:0005515													
Sapur.015G2380000.1	0.07187992	0.56055388	1.22358871	-0.45813	0.64684246	0.71921566	grey	0.25959861	0.00102145														
Sapur.002G0394000.3	0.11706259	0.38116988	0.82970140	-0.45809	0.6487382	0.71921566	grey	-0.05297799	0.94254248														
Sapur.006G0880600.1	0.20681540	0.46425145	1.01585571	-0.45803	0.64688275	0.71934261	grey	-0.0197813	0.85181383	GO:0006468,GO:0004672													
Sapur.004G0542000.1	23.34784228	0.05898795	0.13083828	-0.45798	0.64700747	0.71935127	grey	0.05884036	0.46443841														
Sapur.006G0622000.1	0.07687154	0.28284248	1.30509799	-0.45765	0.6472048	0.71939199	grey	0.24280604	0.00318952														
Sapur.011G0751000.2	1.23584978	0.11023109	0.24118531	-0.45741	0.64737195	0.71956224	grey	-0.01593817	0.88544743														
Sapur.006G0180000.1	0.20081540	0.46425145	1.01585573	-0.45737	0.64748944	0.71960984	grey	-0.01747703	0.83803337	GO:0005525													
Sapur.007G1939200.1	0.07007955	0.52280308	1.14506847	-0.45708	0.64759186	0.71975569	grey	0.23211673	0.00341556	GO:0055114,GO:0020037,GO:0006979,GO:0004601													
Sapur.001G0671300.1	2.47316151	0.09000004	0.19706486	-0.45697	0.64768431	0.72001007	grey	0.07864831	0.32834867	GO:0005515													
Sapur.004G1469000.4	0.28732347	0.20650424	0.45213434	-0.45651	0.64796925	0.72015592	grey	-0.02305931	0.79312164	GO:0008270,GO:0003676													
Sapur.017G0813000.1	0.75715666	0.16452331	0.36105726	-0.4565	0.64802938	0.72026769	grey	-0.04734956	0.55157627	GO:0005515													
Sapur.005G0178000.1	0.27760259	0.18680379	0.40933871	-0.45645	0.64807456	0.72037358	grey	-0.06134383	0.44519761														
Sapur.012G0808200.2	0.83278127	0.19238542	0.38598616	-0.45599	0.64839898	0.72050473	grey	0.00708452	0.92892047	GO:0004854													
Sapur.002G0867200.1	0.16885514	0.46425145	1.01585571	-0.4556	0.64864007	0.72080147	grey	-0.02883624	0.71396028	GO:0016758,GO:0008152													
Sapur.003G0908000.1	0.08846101	0.64460168	1.41695707	-0.45562	0.64870759	0.72080147	grey	0.13115477	0.10157796	GO:0003677													
Sapur.004G0284000.1	4.99023819	0.05227104	0.11500159	-0.45546	0.64870707	0.72080147	grey	-0.04918748	0.54772329	GO:0005634													
Sapur.015G1589000.1	58.62638861	0.03918299	0.08604163	-0.45543	0.64879914	0.72087373	grey	0.04276376	0.59508004	GO:0003676													
Sapur.014G0955400.1	14.05955464	0.03886979	0.08492051	-0.45527	0.64892037	0.72097211	grey	-0.01392629	0.8192947	GO:0005515,GO:0007078,GO:0005524,GO:0003777,GO:0005871													
Sapur.010G0304000.2	0.07100376	0.59691865	1.31166146	-0.45086	0.64904729	0.72180487	grey	0.25607572	0.00107388														
Sapur.006G0180000.1	1.11562906	0.09000004	0.19706486	-0.45069	0.64916865	0.72186141	grey	0.08734042	0.27931319	GO:0004674,GO:0048544,GO:0006468,GO:0004672													
Sapur.001G140100.1	0.21723268	0.25889661	0.56974245	-0.45646	0.64978266	0.72182536	grey	0.06824858	0.39576109	GO:0006355,GO:0003700													
Sapur.001G179200.2	0.39194208	0.21483784	0.47323592	-0.45397	0.64984096	0.72287726	grey	-0.05958828	0.45863983	GO:0051276,GO:0006996,GO:0005524,GO:0005515													
Sapur.006G1824000.1	0.10411752	0.22389496	0.49225243	-0.45335	0.65029529	0.72287984	grey	-0.07332926	1.3161-10														
Sapur.010G0410900.1	109.3719067	-0.07806955	0.17200448	-0.45328	0.65046798	0.7232389	grey	-0.03647162	0.64921457	GO:0016747,GO:0008152													
Sapur.002G0282200.1	0.40064644	0.21193576	0.46697759	-0.45324	0.65057759	0.72340594	grey	-0.06334605	0.43390655														
Sapur.007G0929000.1	47.07057138	-0.04900759	0.10814798	-0.45311	0.65048122	0.72339289	grey	-0.0508879	0.52677799														
Sapur.006G0511200.2	1.30456103	0.09000004	0.19706486	-0.45287	0.65066135	0.72349134	grey	-0.08733964	0.27091763	GO:0005085,GO:0016020,GO:0006821,GO:0005247													
Sapur.001G058400.1	0.26609029	0.29879143	0.47456718	-0.45254	0.65085138	0.72375017	grey	-0.05368803	0.59567501														
Sapur.007G1992200.1	0.61924079	0.17353144	0.3794566	-0.45224	0.65139156	0.72387702	grey	-0.11972154	0.15119147	GO:0005515,GO:0003676													
Sapur.001G0946600.1	1354.962183	0.03161543	0.06991305	-0.45189	0.65150109	0.72320424	grey	-0.03537635	0.66005885														
Sapur.006G0984000.1	0.29872308	0.23682863	0.50031717	-0.45165	0.65187706	0.72321988	grey	0.06278006	0.41263762	GO:0015743													
Sapur.012G0720800.1	0.26054541	0.28762331	0.63533404	-0.45169	0.65182773	0.72331252	grey	0.08550669	0.3162999														
Sapur.001G195100.1	4888.392157	0.02540426	0.0562519	-0.45165	0.65156633	0.72334743	grey	0.02729108	0.73439329	GO:0055114,GO:0016616,GO:0006694,GO:0003854													
Sapur.012G0280300.1	2.73842263	0.07420331	0.15460449	-0.45176	0.65157622	0.72346014	grey	0.05458268	0.48373773														
Sapur.019G0924000.1	19.78237151	0.03218557	0.73560143	-0.45152	0.65150497	0.72369014	grey	0.07164529	0.37257168														
Sapur.009G0948500.1	8.8347777	0.04161809	0.10892162	-0.45098	0.65184966	0.72369461	grey	-0.18094026	0.03233191	GO:0008270,GO:0005515,GO:0048872													
Sapur.012G0173300.1	0.31792158	0.19876323	0.44070769	-0.45088	0.65207924	0.72376339	grey	-0.09394004	0.25183679	GO:0055085,GO:0016773													
Sapur.009G0188200.1	0.15395654	0.73239432	1.62166429	-0.45061	0.65219637	0.72396212	grey	0.08397627	0.3279042														
Sapur.019G0775000.2	0.82243856	0.04500948	0.10174329	-0.45027	0.65251466	0.72427799	grey	-0.07703707	0.27423711	GO:0005515													
Sapur.006G1869000.1	0.32882098	0.12449193	0.27606459	-0.44982	0.65265019	0.72465174	grey	-0.13612407	0.08144357														
Sapur.003G1079000.4	0.21819596	-0.21862818	0.48645307	-0.4495	0.65307559	0.72476338	grey	-0.11338808	0.15740577														
Sapur.017G0560800.1	0.10032987	0.46425145	1.01585571	-0.44874	0.65363127	0.72539135	grey	-0.08208138	0.35615508														
Sapur.007G1183000.1	1.91665841	0.10492321	0.2266163	-0.44786	0.65425414	0.72603602	grey	0.08556304	0.27547621														
Sapur.002G0461000.3	0.12014376	0.40788552	0.91076924	0.44787	0.65427048	0.72603602	grey	0.06912189	0.21029918	GO:0008152,GO:0003824													
Sapur.015G0273000.1	0.52627313	0.05292312	0.34161626	0.44764	0.6544043	0.7260907	grey	0.02482218	0.76199284														
Sapur.015G1379000.1	0.19318396	0.38238813	0.85470385	0.44767	0.65427017	0.7260907	grey	0.14669506	0.03911058	GO:

Sapur.01G0127900.2	6.01661734	0.04915836	0.11523928	0.426575	0.66968947	0.74041707	grey	0.04061958	0.61348329	AT4G03220.1		DUF410 family protein
Sapur.01G0299800.1	0.12510723	0.33740887	0.79110304	0.426563	0.66969753	0.74041707	grey	0.06234973	0.43789595	GO:0008270;GO:0003677	AT4G22820.2	A20/AN1-like zinc finger family protein
Sapur.01W0020900.1	255.750001	0.8615841	0.02121544	0.426037	0.67080547	0.74076224	grey	0.01185883	0.88283816	GO:0016787;GO:0008152	AT5G54140.1	IAA-leucine-resistant (ILR)-like 3	IAA amino acid hydrolase ILR1, putative
Sapur.005G0147400.1	0.41824951	0.14070336	0.30316191	0.425966	0.67032842	0.74076229	grey	0.01805725	0.82291313			
Sapur.012G0170800.1	230.637313	0.05061396	0.11950708	0.42591	0.67017626	0.74082542	grey	0.02964071	0.71248831	GO:0055114;GO:0009916	AT2G23370.1	alternative oxidase 1A	ubiquinol oxidase
Sapur.016G2125200.2	0.13895711	0.30679494	0.72025783	0.425868	0.67020869	0.74082874	grey	0.07070296	0.37898299	GO:0044030;GO:0043966;GO:0004402	AT5G14980.1	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein	PHD-Finger protein
Sapur.T005300.1	0.65889588	0.12520221	0.29436319	0.425786	0.67030448	0.74091027	grey	0.00022616	0.99775153				NA
Sapur.006G0284800.2	1.76016614	0.08784704	0.26642087	0.425577	0.67061236	0.74101487	grey	0.15171835	0.0692729	GO:0043565;GO:0006355;GO:0003700;GO:0006351	AT5G12150.1	BZIP45,TGA6	TGA6	TGA6 bZIP transcription factor	TGA2 type basic leucine zipper protein TGA2.2
Sapur.003G0268800.1	0.41228823	0.17506542	0.41361004	0.425436	0.67061872	0.74102275	grey	0.05988592	0.94066164	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	AT5G21730.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	kinesin motor domain protein
Sapur.010G0251200.4	0.35865552	0.47362746	0.81563167	-0.423	0.67063267	0.74138856	grey	-0.12348727	0.11508346	GO:0015170;GO:0006868	AT5G05830.4	ADAT2,GGT2	alanine-2-oxoglutarate aminotransferase 2	alanine-2-oxoglutarate aminotransferase
Sapur.007G0494900.1	22.1581676	0.06468627	0.10623951	-0.4252	0.67068581	0.74164143	grey	-0.03119563	0.68031623		AT5G27370.1	Protein of unknown function (DUF1230)	transmembrane protein, putative
Sapur.004G0127300.1	17.6821221	0.06468627	0.08182589	-0.42516	0.67073499	0.74164893	grey	-0.07039499	0.54988203		AT5G18575.1		plant/trehs1-20 protein
Sapur.005G1233000.1	0.31427858	0.16341093	0.38454705	-0.42494	0.67087552	0.74199497	grey	-0.08063397	0.31540073		AT4G37450.1	AGP18,AT4GP18	arabinogalactan protein 18	hypothetical protein
Sapur.002G0248900.1	0.75068673	0.12180783	0.29062683	-0.42479	0.67102677	0.74204021	grey	0.06692125	0.45268456	GO:0055114;GO:0004097;GO:0016491;GO:0008152				polyphenol oxidase
Sapur.004G0147000.1	0.41728383	0.12983266	0.29206426	-0.42443	0.67124288	0.74253663	grey	0.04017157	0.60867487	GO:0009733	AT5G18020.1	SAUR-like auxin-responsive protein family	auxin responsive protein
Sapur.005G0073300.1	0.31387633	0.09408546	0.86283679	-0.42403	0.67145298	0.74267032	grey	-0.23905071	0.05393674		AT5G39170.1		NA
Sapur.013G0667700.1	0.11263539	0.38420584	0.90600049	-0.42382	0.67170576	0.74287251	grey	0.13894983	0.08243038		AT2G26670.1	Domain of unknown function (DUF213)	NA
Sapur.012G0081100.1	0.34754716	0.30568356	0.73679872	-0.42363	0.67183679	0.74295887	grey	-0.15407384	0.05208172	GO:0019898;GO:0015078;GO:0009654;GO:0009523;GO:0005509	AT5G15510.1	Photosystem II reaction center PsbP family protein	thylakoid lumenal 21.5 kDa protein, precursor
Sapur.019G0222800.1	26.9888334	0.07491479	0.10754526	-0.42357	0.67189254	0.74310282	grey	0.11371835	0.0692729	GO:0005634	AT5G45580.1	Nucleotide/sugar transporter family protein	nucleotide-diphosphо-sugar transferase
Sapur.018G0101100.1	1.04693687	0.11951405	0.28258246	-0.42309	0.67222646	0.7426707	grey	-0.06527691	0.41414432	GO:0009055	AT5G20230.1	AT8G13BCE,SAG14	blue-copper-binding protein	NA
Sapur.007G0261500.1	0.46015164	0.08147237	0.19242195	-0.423	0.67239862	0.74271777	grey	-0.2293927	0.03143882					NA
Sapur.016G2410100.1	27.2378769	0.02634296	0.06210152	0.42587	0.67255661	0.74300146	grey	0.02814122	0.76624245		AT5G14580.1	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein	
Sapur.006G1364100.1	309.258002	0.01521065	0.03603821	0.42354	0.67266553	0.74344672	grey	-0.02578625	0.74854821		AT5T20220.1	Mitochondrial substrate carrier family protein	NA	
Sapur.002G0200600.1	226.542888	0.02337279	0.05153149	0.422343	0.67277935	0.74344872	grey	-0.26831728	0.00567824		AT2G20390.1		cytochrome oxidase complex assembly protein	
Sapur.010G0280800.1	0.46414394	0.14668435	0.32008783	0.42266	0.67289819	0.74381862	grey	-0.19508724	0.03435648	GBL,NAP5,NAPP	AT2G20110.2	transcription activators	hb-associated protein	
Sapur.002G1254000.3	1.06181402	0.10705488	0.24810478	0.42015	0.67314102	0.74363225	grey	-0.04660137	0.95388329	GO:0003676	AT5G55500.4	AT-SRP40,ATRSP35,ATRSP46	arginine/serine-rich splicing factor 35	arginine/serine-rich splicing factor RSP41, putative
Sapur.019G2878800.1	0.15253888	0.39485676	0.67506146	-0.42391	0.67329692	0.7436265	grey	-0.17104529	0.02203362	GO:0007264;GO:0005525	AT5G45970.1	ARAC2,ATRAC2,ATROP7,RA	RAC-like 2	Rac-like small GTP-binding protein
Sapur.019G0122200.1	0.77749878	0.14166747	0.31042708	-0.42164	0.67360158	0.74366554	grey	-0.06996688	0.38410075		AT5G45681.1	AHP2-B12,PP2-B12	phloem protein 2-B12	phloem protein
Sapur.004G0960600.1	2.65788859	0.07004081	0.16829791	0.42158	0.67378665	0.74366554	grey	0.09687041	0.80655514					NA
Sapur.016G0202200.1	234.991626	0.04168482	0.09866887	-0.42117	0.67383526	0.74388537	grey	-0.05053426	0.52905444		AT5G37400.1		transmembrane protein, putative	
Sapur.004G1413000.2	0.16297569	0.32088787	0.76199149	-0.42112	0.67386478	0.74391098	grey	-0.08160864	0.30959042		AT2G28150.1	Domain of unknown function (DUF866)	auxin-regulated protein	
Sapur.005G0791200.1	12.0368813	0.04685152	0.11048355	-0.4212	0.67411023	0.74438018	grey	-0.20762164	0.03941882	GO:0016021;GO:0004659	AT2G26610.1	PrPRT1,PRT1	polyprenyl transferase	4-hydroxybenzoate polyprenyltransferase
Sapur.013G1661000.2	1.59572306	0.09626146	0.22863892	-0.42043	0.67417849	0.74441846	grey	-0.05129633	0.52345641	GO:0008289	AT1G79840.1	GL2	HD-ZIP IV family of homeobox-leucine zipper protein with lipid-binding START domain	homeobox leucine zipper protein glabra protein
Sapur.006G0275200.1	0.10758169	0.34538071	0.82336186	-0.41974	0.67488568	0.74511404	grey	-0.10301563	0.19108542	GO:0003723	AT4G04460.1	HEN4	RNA-binding KH domain-containing protein	heterogeneous nuclear ribonucleoprotein K, putative
Sapur.016G0883800.4	0.12637896	0.12819124	0.78263546	-0.41941	0.67496795	0.74519507	grey	0.09702456	0.22674758		AT3G37160.1	Transducin/WD40 repeat-like superfamily protein	transducin/WD40 domain protein	
Sapur.016G0893300.1	588.307104	0.01458931	0.03169229	0.41552	0.67498	0.74525786	grey	-0.04052856	0.54218004		AT3G60420.1	Ribosomal L18p/L5e family protein	50S ribosomal protein L5	
Sapur.010G0291900.4	0.08110546	0.47905184	0.14056655	0.41962	0.67536168	0.74525488	grey	-0.06347571	0.42965157	GO:0016746;GO:0008152	AT5G60950.1	Phosphoglycéglycerol acyltransferase family protein	1-acyl-sn-glycerol-3-phosphate acyltransferase	
Sapur.005G0950200.1	0.09287705	0.50684826	1.20888885	-0.41858	0.67520988	0.74579616	grey	-0.26392833	0.00897548		AT4G18770.1	AHM9|||AHM9|||	myb domain protein 98	Myb-like DNA-binding domain protein
Sapur.010G0290000.4	0.46141394	0.14668435	0.35033357	0.41859	0.67530792	0.74579616	grey	-0.03357429	0.65695154	GO:0008270;GO:0004089	AT4G20360.1	ATBCA4,BCA4,CA4	beta carbonic anhydrase 4	carbonic anhydrase
Sapur.017G0124000.1	1.6826675	-0.09218763	0.22038705	-0.41831	0.67571994	0.74593481	grey	-0.01806768	0.81937079		AT5G28580.1	Plant protein of unknown function (DUF247)	NA	
Sapur.009G1291000.1	0.32495824	0.12180783	0.27802426	0.41823	0.67628395	0.74681319	grey	0.06927652	0.38862834		AT3G26290.1	alpha/beta-hydrolase family protein	alpha/beta hydrolase family protein	
Sapur.15W0107800.1	2.99032706	-0.06572585	0.15762628	-0.41692	0.67672749	0.74807043	grey	-0.02562667	0.74891573	GO:0008270;GO:0003676				NA
Sapur.007G0266800.3	0.35681115	0.17237261	0.41357659	-0.41679	0.67683829	0.74808449	grey	-0.0288006	0.92373581		AT5G17330.1	Metal-dependent phosphohydrolase	HD family hydrolase	
Sapur.002G0685500.1	0.82008411	0.14208896	0.34148513	-0.41643	0.67742188	0.74767219	grey	-0.03560847	0.61758027	GO:0008270;GO:0005515	AT5G03340.1	RING/U-box superfamily protein	RING-U box protein family	
Sapur.008G0613000.1	91.6202033	0.02604442	0.06417974	-0.41575	0.67755167	0.74770629	grey	-0.05436147	0.48890021	GO:0006351	AT5G04570.2	Fer-red transport and vesicle trafficking protein	Fer-red transport and vesicle trafficking protein, putative	
Sapur.012G0927000.3	0.17072622	0.30155463	0.72565455	-0.41554	0.67774897	0.74792969	grey	-0.07580283	0.34563037		AT5G35180.1	Tetratricopeptide-repeat (TPR)-like superfamily protein	PPR containing plant protein	
Sapur.004G0752600.1	0.20378275	0.12180783	0.29206426	0.41524	0.67787	0.74807896	grey	-0.14087606	0.03944769	GO:0055114;GO:0016616;GO:0006694;GO:0003854;GO:0019752	AT4G25280.1	MDH	malate dehydrogenase	NAD-malate dehydrogenase
Sapur.006G0854500.1	0.05077823	0.54976171	1.32377634	0.41529	0.67843859	0.74809706	grey	-0.25860097	0.01037185	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP152A2	cytochrome P450, family 712, subfamily A, polypeptide 2	cytochrome P450 family protein	cytochrome P450 family protein
Sapur.016G0612000.2	2.47134214	0.08382021	0.20208853	-0.41484	0.67926174	0.74845344	grey	-0.02370873	0.78259856	GO:0016887;GO:0005524	AT5G06530.1		ABC-2 type transporter family protein	ABC transporter G family protein
Sapur.014G0316000.1	0.11219429	0.14668435	0.35263346	0.41468	0.67969154	0.74861809	grey	-0.07843284	0.33530119	GO:0016758;GO:0008152	AT3G15520.3	UGT88A1	UDP-glucosyl transferase 88A1	UDP-glucosyl transferase family
Sapur.006G1621000.1	0.22395636	0.22607519	0.54786459	0.41749	0.67957762	0.74921945	grey	0.07461556	0.35430616	GO:0005515	AT5G11890.2	Sterile alpha motif (SAM) domain-containing protein		
Sapur.004G0622800.1	0.07977549	0.12180783	0.29206426	0.41628	0.67964699	0.74938564	grey	0.18213047	0.02243152		AT5G49490.1			hypothetical protein
Sapur.017G1330800.1	0.78829554	0.10914185	0.26396221	-0.41337	0.67033207	0.74946843	grey	-0.04152459	0.65095511	GO:0016788	AT5G40990.1	GLIP1	GDSL lipase 1	GDSL esterase/lipase
Sapur.T036000.7	0.29466023	0.12180783	0.29206426	0.41329	0.67062393	0.74962571	grey	0.02872125	0.79392572	GO:0008270	AT5G07220.1	DHHC type zinc finger family protein	DHHC palmitoyltransferase	
Sapur.003G1617000.1	0.10127945	0.36146942	0.87477609	0.41263	0.67076124	0.74989268	grey	0.11452002	0.15127674	GO:0006629	AT4G20460.1	alpha/beta-hydrolases superfamily protein	triacylglycerol lipase	
Sapur.011G0264000.1	0.07187344	0.17237261	0.41357659	0.41259	0.67080604	0.75017389	grey	0.00269859	0.93673273		AT5G55230.1	alpha/beta-hydrolases superfamily protein	alpha/beta hydrolase family protein	
Sapur.016G2545400.2	0.94567015	0.13409781	0.32723818	0.41242	0.67094329	0.75208334	grey	0.00544947	0.9602592	GO:0055114;GO:0016491	AT5G17020.1	ATSRG1,SRG1	senescence-related gene 1	leucoanthocyanidin dioxygenase, putative
Sapur.012G0905600.1	7.68812592	0.06073864	0.16906618	0.41245	0.68002039	0.7509981	grey	0.01882776	0.93955139					hypothetical protein
Sapur.009G0284500.1	0.13846662	0.12180783	0.29206426	0.41167	0.68027221	0.75208473	grey	0.04663652	0.51389489		AT4G31980.1			NA
Sapur.005G0764600.1	28.5817562	0.02606691	0.06475723	0.412165	0.68021814	0.75208473	grey	0.05395588	0.55287297	GO:0005515	AT5G13140.1	ATRUB1,NEDD8,RUB1	related to ubiquitin 1	ubiquitin-NEDD8-like protein RUB1
Sapur.004G1650600.1	2.34727982	0.12180783	0.29206426	0.41146	0.68059127	0.75250426	grey	0.00247549	0.97453387		AT5G18240.1	EDL2	EDG-like 2	circadian clock coupling factor ZGT
Sapur.006G1438800.1	0.26177109	0.15203184	0.36957829	-0.41137	0.68079369	0.75283917	grey	-0.11002004	0.17015381					NA
Sapur.009G0541200.1	0.06117293	0.14668435	0.35263346	0.41081	0.68088952	0.75306684	grey	0.22970374	0.03884402		AT5G13180.1			NA
Sapur.009G0491600.1	283.376776	0.01809564	0.04608754	0.41073	0.68127048	0.75310339	grey	-0.03801814	0.63677053		AT3G12650.1		transmembrane protein, putative	
Sapur.003G1213000.2	0.45862913	0.15406487	0.37104607	0.41067	0.68136176	0.75346021	grey	-0.02047549	0.85553687		AT1G28100.1		PPR containing protein, putative	
Sapur.T057800.1	0.06493664	0.54288891	1.32336129	0.40391	0.68166178	0.75362321	grey	-0.19843773	0.01273695		AT2G17020.1	ATCRM1,ATKPO1,HET2,XPO1	exportin 1A	
Sapur.010G0470200.1	4.65614869	0.07491479	0.18188455	0.27717563	0.68168663	0.75362321	grey	-0.04624647	0.52364694	GO:0005515	AT2G37220.1	NB-ARC domain-containing disease resistance protein		
Sapur.004G1180000.1	2.83352448	0.06826273	0.16651928	0.40994	0.68185028	0.7581739	grey	0.02522339	0.75376701	GO:0016021	AT2G21680.1	ATRER1B,RER1B	endoplasmatic reticulum retrieval protein 1B	RER1A protein
Sapur.006G1371000.2	1.31735752	0.10165691	0.24808261	-0.40976	0.68198126	0.75393674	grey	-0.03209589	0.68969763		AT4G30260.1	VEL1	vernalization5/VIN3-like	protein vernalization insensitive protein
Sapur.016G2483000.1	0.46829217	0.14668435	0.35263346	-0.40972	0.68201833	0.75395462	grey	-0.05792037	0.47117616		AT5T3161.1	CLE3	CLAVATA/ESR-like 3	transmembrane protein, putative
Sapur.016G0941600.1	0.06909329	0.53615878	1.30924509	0.40958	0.68215912	0.75408624	grey	0.25118303	0.01507721	GO:0006468;GO:0006472	AT4G18750.1	CDC2,CDC2A,CDC2AAT,CDK	cell division control 2	NA
Sapur.003G0212000.1	0.07023856	0.45508182	1.10988164	0.40686	0.68233927	0.75246758	grey	0.22399116	0.05991048					plant-specific B3-DNA-binding domain protein, putative
Sapur.005G1115300.1	1.26669963	0.09439805	0.23067021	0.40919	0.68233116	0.75290808	grey	0.04602052	0.56642912		AT2G17310.1	Chaperone Dnaj-domain superfamily protein		AT hook motif protein
Sapur.T015500.1	0.00715717	0.37268817	0.90966024	0.40904	0.68251907	0.75241955	grey	0.12284854	0.12532366		AT2G47562.1			NA
Sapur.007G0470700.1	0.06863791	0.50453889	1.23414592	0.408748	0.68272456	0.75258447	grey	0.20931523	0.08514108		AT4G38040.1	Exostosin family protein		NA
Sapur.014G0750600.1	0.19316829	0.12180783	0.29206426	0.40747	0.68277936	0.75258447	grey	0.18712474	0.03945991	GO:0046872	AT5G61250.1	RING/U-box,C3HC4-type RING finger family protein	RING zinc finger protein, putative	
Sapur.012G0760600.1	6.82339635	-0.06610235	0.16198796	-0.40809	0.68329042	0.75300132	grey	0.07836658	0.82425735		AT4G36800.1	RCE1	RUB1 conjugating enzyme 1	NA
Sapur.007G0272900.1	0.15758855	0.07286202	0.17912764	0.407326	0.68328362	0.75380189	grey	0.03524351	0.66123395					NA
Sapur.014G0260600.1	0.12801012	0.31152179	0.86245339	0.407137	0.68397318	0.75380576	grey	0.17401672	0.02508966		AT4G42870.1	ATPAK2,PAK2	phosphatidic acid phosphophydrolase 2	Protein kinase superfamily protein
Sapur.005G1219000.1	575.588097	0.07260798	0.09160507	-0.40678	0.68417234	0.75407088	grey	-0.02961886	0.71269901	GO:0006468;GO:0006672	AT2G20370.1			NAD(P)-binding Rossmann-fold superfamily protein
Sapur.010G0300300.1	11.8814767	0.06259415	0.15397527	-0.40655	0.68439966	0.75420249	grey	-0.03749685	0.64126616	GO:0016757;GO:0000304	AT5G27620.1			leucoanthocyanidin reductase
Sapur.018G0799800.1	1.17604802	0.11076022	0.27461896	-0.40635	0.68482405	0.75430579	grey	-0.01100362	0.86862626					NA
Sapur.006G1651200.1	0.38969844	0.24726916	0.60806492	-0.4062	0.68491388	0.75404594	grey	-0.12691188	0.13074116	GO:0006355;GO:0003700	AT5G58160.1	PLICHI	Integrase-type DNA-binding superfamily protein	ethylene-responsive transcription factor ERF086
Sapur.016G2091000.1	0.13897815	0.31137822	0.76646234	0.405987	0.68575192	0.75461346	grey	0.08012316	0.31851995	GO:0005515	AT5G13340.1	Transducin/WD40 repeat-like superfamily protein	transducin/WD40 domain protein	
Sapur.016G0881200.2	0.74072511	0.14668435	0.35263346	0.40579	0.68676069	0.75462606	grey	-0.02053428	0.75834602		AT5G05420.1	CCT,CRP	RNA polymerase II transcription mediator	NA
Sapur.016G1080600.1	0.16898801	0.27030814	0.66234871	0.405725	0.68694466	0.75477427	grey	0.06004187	0.45562789		AT5G19150.3	BES1,BZR2	Brassinosteroid signalling positive regulator (BZR1) family protein	DUF822 family protein
Sapur.015G0950400.4	15.1129833	0.05504004	0.13479709	0.405348	0.68504751	0.75481573	grey	0.01982078	0.84410458		AT5G06860.1	DEX1,2	DUF96 2,3	NA
Sapur.T000500.1	0.08266124	0.52784709	1.3251888	0.40544	0.68515426	0.75493311	grey	0.16647803	0.03717325	GO:0016788	AT5G26670.1	RCE1	GDSL-like lipase/Acylhydrolase superfamily protein	GDSL-like lipase/Acylhydrolase family protein
Sapur.T055800.1	0.16129401	0.29141061	0.72004498	0.405426	0.68516446	0.75493311	grey	0.07810895	0.33086746	GO:0016788	AT5G45670.1		GDSL-like lipase/Acylhydrolase superfamily protein	GDSL-like lipase/Acylhydrolase family protein
Sapur.T191700.1	0.24349674	0.18783784	0.46344538	0.405311	0.68524974	0.75501146	grey	0.01982079	0.84410679	GO:0005515;GO:0006468;GO:0005524;GO:0004672	AT5G47570.1		Leucine-rich repeat protein kinase family protein	Leucine-rich repeat protein kinase family protein
Sapur.T129300.1	0.05806883	0.49905205	1.23538399	0.404673	0.68573207	0.75547784	grey	0.24960852	0.00162518	GO:0003677				NA
Sapur.T057500.1	0.24402701	0.15944746	0.42165628	0.404325	0.68604261	0.75587651	grey	-0.00928264	0.93834672		AT5G54750.2			NA
Sapur.01G0220800.1	0.48786261	0.15196156	0.37606561	0.404043	0.68161289	0.75593744	grey	-0.01694928	0.84046254	GO:0008146	AT5G76100.1	ATSOT16,ATSTA,CDB-7,SC	sulfotransferase 16	flavonol 3-sulfotransferase, putative
Sapur.01G0480800.2	0.25178215	0.15405924	0.38097374	0.403215	0.68637261	0.75615201	grey	-0.11239473	0.51638181		AT5T0120.79|120	79|120		79|120
Sapur.01G0179800.2	1.12750176	0.10414386	0.25836171	-0.40309	0.68681507	0.75633438	grey	-0.04514126	0.57415557		AT4G15240.1	UNC-50 family protein	UNC-50 family protein	UNC-50
Sapur.T013000.1	0.11357376	0.27237837	0.1836784	-0.4024	0.68682142	0.75682988	grey	-0.05662004	0.49348754		AT4G04640.1	ATNEK5,NEK5	NIMA-related kinase 5	NIMA-related kinase 5
Sapur.T123500.1	0.12415905	0.30648655	0.82026561	-0.40288	0.68703482	0.75751911	grey	-0.20828602	0.00931457					NA
Sapur.006G1338000.1	1.1143616	0.10320583	0.25269162	0.402678	0.68718139	0.75809387	grey	0.04484573	0.60820509		AT5G02730.1			hypothetical protein
Sapur.002G0604000.1	10.0174388	0.06506073	0.16158298	0.402514	0.68730549	0.75700022	grey	0.01824993	0.82530703					hypothetical protein
Sapur.019G0290900.1	0.08037629	0.52334691	1.30276328	0.401649	0.68794292	0.75725763	grey	0.20825541	0.08868342	GO:0005524;GO:0004386;GO:0006281;GO:0003678;GO:0000723	AT5G17030.1	PIF1 helicase		DNA helicase
Sapur.016G1812000.1	3.60898123	-0.07316551	0.17728029	-0.40161	0.68809028	0.75829524	grey	0.01589731	0.88329651	GO:0008641	AT1G8A1,MOSL,UBA1	ubiquitin-activating enzyme 1	ubiquitin-activating enzyme E1	ubiquitin-activating enzyme 11
Sapur.01G0251500.1	0.11050223	0.34603539	0.86319163	0.401537	0.68823659	0.75765565	grey	0.07829092	0.33972642	GO:0004674;GO:0048544;GO:0006468;GO:0004672	AT5G11330.1	S-locus lectin protein kinase family protein		NA
Sapur.01G0280600.1	0.51219384	0.15944746	0.42165628	0.401446	0.68859045	0.75774653	grey	0.07313437	0.64410244	GO:0005515	AT5G50620.1			histone deacetylase complex subunit SAP30 Sin3-binding protein
Sapur.15W0052700.1	0.19407115	-0.21644167	0.54832047	-0.4002	0.69008423	0.75869381	grey	-0.12101653	0.12794187	GO:0055114;GO:0006468;GO:0005524;GO:0004672	AT4G37530.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.01T0131300.1	0.18256419	0.35877729	0.89662246	-0.40014	0.69070359	0.75231282	grey	-0.10794906	0.20582284		AT1G14140.1	RAL1L2	RAV like 2	NA
Sapur.007G0250500.2	0.13761467	0.30190368	0.76023749	0.39933	0.69649891	0.75392728	grey	-0.00178625	0.98221709	GO:0005085;GO:0022857;GO:0016021	AT4G36670.1	Major facilitator superfamily protein	sugar porter (SP) family MFS transporter	
Sapur.006G2300300.1	0.12749664	0.27237837	0.1836784	0.398854	0.68736630	0.75535057	grey	-0.02383092	0.76394583	GO:0003676	AT5G14100.1	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in nucleolysin TIA-1 (p40-TIA-1)-like protein	
Sapur.15W0033400.1	0.10116232	-0.13292929	0.82421463	-0.39918	0.68791752	0.75350927	grey	-0.23549085	0.02987602					NA
Sapur.01E0280800.1	0.19000738	0.25384261	0.5408328	0.399103	0.68881722	0.75386724	grey	0.06487043	0.43912779	GO:0005515	AT1G09100.1	AtRLP9,RLP9	receptor like protein 9	NA
Sapur.008G0751005.1	640.367602	0.01472876	0.03176052	0.398884	0.68897807	0.75919392	grey	-0.04607029	0.65828657		AT5G18010.1	PDC83	phosphoinositide-phospholipase C family protein	carbohydrate-binding module family 43 protein
Sapur.005G0228800.1	0.41249006	0.10168534	0.40400195	0.388678	0.69013059	0.75965589	grey	-0.00797213	0.92108383		AT4G12010.1	Disease resistance protein (TIR-NBS-LRR class) family		NA
Sapur.T111600.1	0.05874934	0.12180783	0.29206426	0.388176	0.69025989	0.75968706	grey	0.22071758	0.05657776					NA
Sapur.005G0379000.3	0.16067217	0.24523627	0.61628207	0.388334	0.69038166	0.75984551	grey	0.06324818	0.41307738	GO:0003127;GO:0008270;GO:0008188;GO:0006886	AT4G32640.1	Sec23/Sec24 protein family	protein transporter Sec24-like CEF protein	
Sapur.002G1391300.1	0.95157564	0.26276629	0.67268129	0.3882	0.69061588	0.76011914	grey	-0.09724385	0.23159827	GO:0016757;GO:0000304	AT5G14140.1	GAUT8,QUA1	Nucleotide-diphosphо-sugar transferases superfamily protein	CAZy family GT8 protein
Sapur.014G0330800.1	0.26170328	-0.19801134	0.50160726	-0.39789	0.69070751	0.76018949	grey	-0.06270635	0.43529491					NA
Sapur.016G1388800.2	17.9581846	0.06011583	0.14021184	0.391774	0.69111324	0.76061648	grey	-0.04501653	0.57329888	GO:0008152;GO:0004807	AT1T7MC,CYTOTP,TPI	triosephosphate isomerase	triosephosphate isomerase	
Sapur.T000700.1	0.11978293	0.27160746	0.82343504	0.397311	0.69137809	0.76061648	grey	0.46385657	9.45E-10	GO:0055114;GO:0016491	AT4G38570.1	PDE181,SPC1,PCS1	zeta-carotene desaturase	NA
Sapur.T023300.1	0.17521303	0.27237837	0.1836784	0.397124	0.69185548	0.76073285	grey	0.03219835	0.67658884	GO:0005085;GO:0016021	AT5G26120.1	Auxin-efflux carrier family protein	auxin efflux carrier family protein	
Sapur.013G1417000.4	1.65210538	0.11553386	0.29088749	0.397109	0.69187159	0.76076285	grey	0.05187573	0.51891885		AT2G43650.1	EMB2777	Sec31/Lst3 ribonucleoprotein (Ltp) family protein	Sec31/Lst3 ribonucleoprotein (Ltp) family protein
Sapur.002G0548000.1	8.44579871	0.07840507	0.19020812	-0.39476	0.69154656	0.76086523	grey	-0.07735275	0.73006755		AT5G05550.1	Hypoxia-responsive family protein	hypoxia induced protein	
Sapur.014G0017000.1	0.30080309	0.05185972	0.49198481	-0.39608	0.69188177	0.76108234	grey	-0.00375522	0.92348124					NA
Sapur.T108600.1	0.06706473	0.48669988	1.22833851	0.396184	0.69198515	0.76141282	grey	0.18964232	0.07401658		AT5G17020.1	ATCRM1,ATKPO1,HET2,XPO1	exportin 1A	NA
Sapur.006G1724000.1	0.16167934	0.12180783	0.29206426	0.39667	0.69205195	0.76146771	grey	0.17205147	0.18123668		AT1G70200.1	ABI2	abscisic-conjugating enzyme 8	abscisic-conjugating enzyme E2
Sapur.013G1266000.3	0.38150679	0.15178688	0.38362532	-0.39562	0.69238547	0.76180287	grey	-0.07860343	0.31861694	GO:0006468;GO:0006672	AT4G00720.1	ASKTHETA,ATSGK2,SGK2	shaggy-like protein kinase 32	shaggy-related kinase
Sapur.005G0261000.1	2.12431644	0.07735176	0.18646941	0.395123	0.69268006	0.76230149	grey	0.01120129	0.88925659	GO:0005515;GO:0005622	AT5G01810.1	LIP1	Ras-related small GTP-binding family protein	Ras-related small GTP-binding family protein
Sapur.005G1564000.3	2.98004712	0.07377749	0.18669571	0.395175	0.69271704	0.76231873	grey	0.03808834	0.70178767	GO:0008008;GO:0008152

Sapur.008G125600.1	592.5965459	-0.016091463	0.045559139	-0.37127	0.710438162	0.778150476	grey	-0.036511565	0.649840211	ATSG05440.1	SDE3	P-loop containing nucleotide triphosphate hydrolases superfamily protein	RNA helicase
Sapur.006G135800.1	25.25023875	0.189382523	0.510397307	0.371049	0.710608872	0.778279421	grey	-0.036666618	0.6484525	ATSG15450.1		Senescence/dehydration-associated protein-related	senescence-associated protein
Sapur.001G111400.1	456.9129601	0.027561924	0.060802307	0.371046	0.710609295	0.778279421	grey	-0.190785259	0.016682726	GO:0005515		Proteasome component (PC) domain protein	26S proteasome non-ATPase regulatory subunit 13
Sapur.006G085500.1	20.60851833	0.056469731	0.152338628	0.370686	0.710871738	0.778548027	grey	0.057808364	0.47149521				
Sapur.001G363000.1	0.152663664	0.362744827	0.70902783	0.37057	0.710957945	0.778616616	grey	-0.013670201	0.865009842	ATSG37088.1	RTI1/9	ROTUNDIFOLIA like 9	DnaJ/J3
Sapur.001G222900.1	0.078626778	0.399552761	1.079385543	0.370168	0.711275668	0.778919112	grey	0.144851509	0.07028759				transglutaminase family protein
Sapur.006G005000.2	0.412027085	0.118780711	0.375082751	0.37	0.711382308	0.779029814	grey	0.032047722	0.690298195	GO:0006508,GO:0004190		Eukaryotic aspartyl protease family protein	aspartic proteinase Asp1, putative
Sapur.008G041050.2	0.106181217	0.121237381	0.368440834	0.369901	0.711450049	0.779084766	grey	0.118519309	0.139186699	ATSG79275.1	ECT8	evolutionarily conserved C-terminal region 8	YTH domain protein
Sapur.003G076300.1	0.07762418	0.424885623	1.148815881	0.369847	0.711468832	0.779103635	grey	0.199511884	0.012240363	GO:0005737,GO:0000045		Ubiquitin-like superfamily protein	gabaA/gamma-aminobutyric acid receptor-associated protein, putative
Sapur.006G064700.2	1.978238373	0.734218308	0.181063126	0.369362	0.711816919	0.779479212	grey	0.010373525	0.891289195	GO:0051082,GO:0016272,GO:0006457		PREFOLDIN 5	prefoldin subunit
Sapur.005G067300.1	300.7849293	0.019381146	0.052487548	0.36929	0.711911	0.779480066	grey	0.003586544	0.964441853	GO:0008270		RING/FYVE/PHD zinc finger superfamily protein	zinc finger C3HC4 type family protein
Sapur.006G086800.1	195.0107223	0.045179519	0.123860369	0.369108	0.712046896	0.779607722	grey	0.025156682	0.7795624	GO:0004568,GO:0005634,GO:0006027,GO:0030246		Concanavalin A-like lectin protein kinase family protein	lectin-domain receptor kinase
Sapur.016G052500.1	15.18049453	0.041659284	0.11288171	0.369053	0.712088552	0.779622522	grey	0.034654325	0.666557781	GO:0007165,GO:0005515,GO:0043531		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.001G054500.1	68.01225641	0.140124227	0.379719454	0.36902	0.712132226	0.779622522	grey	-0.04857068	0.542451115				NA
Sapur.003G058800.4	0.30868664	0.175476322	0.475736345	0.368821	0.712261472	0.779760218	grey	0.435604194	1.16E-08	GO:0016787,GO:0008152		Peptidase M20/M25/M40 family protein	M20 peptidase acetylornithine deacetylase
Sapur.006G148800.2	0.153968182	0.054953627	0.150233612	0.368463	0.712539816	0.780361914	grey	-0.023785934	0.777777546		ATPRD2,MPS1,PRD2	multispar spindle 1	recombination initiation defect 2 protein, putative
Sapur.005G068800.1	211.4312923	0.028325455	0.076891458	-0.36838	0.712588171	0.780606235	grey	-0.054080686	0.501133977				hypothetical protein
Sapur.006G239600.1	0.168764881	0.215662605	0.572018897	0.36827	0.712671761	0.78031332	grey	-0.034193991	0.670727282			Nucleotide/sugar transporter family protein	triose-phosphate transporter family protein
Sapur.019G001180.1	0.132261173	0.067044832	0.178108429	0.367891	0.712904789	0.780300861	grey	0.024893039	0.630280595				NA
Sapur.002G049000.2	0.27005869	0.202891056	0.551627914	0.367804	0.713019247	0.780440888	grey	-0.000434165	0.995738832	GO:0016020,GO:0006810,GO:0005215	ATNRAMP1,NRAMP1,PMIT1	natural resistance-associated macrophage protein 1	nramp metal transporter
Sapur.004G284800.1	0.061112236	0.466239946	1.322868487	0.367611	0.713154561	0.780785386	grey	0.12957565	0.038287376	GO:0005887,GO:0050832		Polyketide cyclase/dehydrase and lipid transport superfamily protein	pathogenesis-related protein Bet V I family protein
Sapur.017G125500.1	58.84043858	-0.091302558	0.24872421	-0.3671	0.713547143	0.780931361	grey	-0.041178027	0.60860494			Heavy metal transport/detoxification superfamily protein	hypothetical protein
Sapur.006G126200.1	3.796862269	0.066282128	0.182261148	-0.3666	0.713870739	0.781338188	grey	-0.013189511	0.832131554				glycosyomal processing protease, glycosyosmal protein
Sapur.019G144500.1	0.193010156	0.189505248	0.517162546	0.366433	0.714042252	0.781399379	grey	0.145926635	0.06820975	GO:0007186,GO:0005834,GO:0004871	ATCOL2,COL2	G-protein gamma subunit 2	guanine nucleotide-binding protein subunit gamma 2, putative
Sapur.004G268000.1	0.139608201	0.139087121	0.381287977	0.365879	0.714455136	0.781545499	grey	0.047439248	0.55488077			RHSB	sulfoquinovose glycosyltransferase KATAMARI protein
Sapur.011G123600.1	17.16367595	0.038262884	0.099224464	0.365665	0.714615287	0.781974724	grey	0.020845157	0.831818872		ARP2	amino acid permease 2	amino acid permease
Sapur.019G076100.1	31.18024818	-0.033489395	0.091639709	-0.36547	0.714764196	0.782111791	grey	0.00723608	0.928446667	GO:0005524	CHR42	chromatin remodeling 42	NA
Sapur.014G049100.1	16.2222964	-0.033588167	0.089667719	-0.3651	0.715019776	0.782358294	grey	0.062129053	0.439216568		CHCL,NB133,TFC 0,TTN1	ARM repeat superfamily protein	beta-tubulin folding cofactor D
Sapur.010G159000.1	1.634524287	0.107759794	0.293368497	0.36482	0.715270310	0.782551511	grey	-0.002264548	0.975646111				transmembrane protein, putative
Sapur.005G109500.1	6.648587358	0.029445145	0.136250604	0.364683	0.715348175	0.782647223	grey	0.02093621	0.79067777	GO:0006468,GO:0005634,GO:0004672	ATSGT080.1	MAPKKK19	mitogen-activated protein kinase kinase kinase 19
Sapur.012G026200.2	8.860649029	-0.032835346	0.090125505	-0.36453	0.715661484	0.782731328	grey	-0.001533857	0.443925289		ATSBHC1,BBR,BPC1	basic pentacysteine1	GAGA-binding transcriptional activator
Sapur.005G065900.1	0.431117972	0.143842301	0.394184813	0.364419	0.715545481	0.782785386	grey	0.0475661	0.578207076	GO:0046983,GO:0003677	AGL62	AGAMOUS-like 62	MADS box protein, putative
Sapur.001G171200.2	0.072523228	0.474511266	1.303517126	0.364303	0.715615148	0.782853669	grey	0.198738873	0.012596519	GO:0003151,GO:0003677		NAC domain containing protein 90	NAC transcription factor
Sapur.006G012600.1	0.074605214	0.148428604	1.223873212	0.364242	0.715673139	0.782877649	grey	0.195662516	0.014427155	GO:0016020,GO:0009570	ATGLR2,7,GLR2.7	glutamate receptor 2.7	glutamate receptor
Sapur.006G190200.1	49.0854672	0.039786812	0.109256559	0.364159	0.715738919	0.782906517	grey	0.030695539	0.70275486			myb-like transcription factor family protein	MYB-like DNA-binding domain protein
Sapur.006G088000.5	4.987004209	0.057494494	0.157829459	0.363968	0.715758873	0.782906517	grey	-0.026025625	0.717485558	GO:0006367	TAF13	TBP-associated factor 13	transcription initiation factor TFIID subunit
Sapur.003G179100.1	0.17652276	-0.265202797	0.728468204	-0.36404	0.715826536	0.782952546	grey	0.106645814	0.183721162	GO:0006629		alpha/beta-Hydrolases superfamily protein	phospholipase A(1)
Sapur.005G175800.1	0.152836609	0.318301607	0.874050457	0.364002	0.715856609	0.782970285	grey	0.078868801	0.377781823				NA
Sapur.017G087600.1	0.58855764	0.131589912	0.367236478	0.363706	0.716074224	0.783151835	grey	0.052850557	0.543829169	GO:0008270,GO:0005622,GO:0005515	ATCO3,2,CO3,2	CONSTANS-like 2	constans protein
Sapur.012G045900.2	0.272593982	0.443624582	1.210805783	0.363685	0.716093542	0.783151835	grey	0.081627248	0.309528559	GO:0017279,GO:0005958		ADP-glucose pyrophosphorylase family protein	mannose-1-phosphate guanyltransferase
Sapur.014G130704.2	0.080426754	0.144255775	1.135588645	0.363551	0.716417126	0.783404241	grey	0.177539237	0.024856569	GO:0005985,GO:0016021		Major facilitator superfamily protein	sugar porter (SP) family protein
Sapur.003G129900.3	0.115033578	0.313237088	0.862376638	-0.36323	0.716435581	0.783469431	grey	-0.210166118	0.008246073		ATG11780.1	oxidoreductase, 2OG-Fe(II) oxygenase family protein	alpha-ketoglutarate-dependent dioxygenase alkB, putative
Sapur.011G096100.1	1.484779886	0.085849836	0.236375275	-0.3622	0.716708008	0.783469431	grey	0.153786104	1.32E-04	GO:0016491	ATC27270.1	Cytochrome reductase family protein	sucrose synthase/sucrase
Sapur.T002S001.1	19.01164288	0.030161778	0.083163977	0.362043	0.716723395	0.783571891	grey	0.053206459	0.492252135				NA
Sapur.006G092000.1	0.462147468	0.122761463	0.3382924	0.36284	0.716847088	0.783283315	grey	-0.016455568	0.872267728	GO:0045454	ATPDL5-1,PDL5-1	PDI-like 5-1	protein disulfide-isomerase
Sapur.017G043600.1	2.084691181	0.084515851	0.23215049	-0.3625	0.716890068	0.7839254	grey	-0.054675596	0.496429954				NA
Sapur.004G146900.1	40.02158213	0.052764694	0.072939872	0.362048	0.716892867	0.7839254	grey	-0.061808864	0.383809943		ATB6H2,B-BRX-LIKE2	DZIC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein	b-box radio-like protein
Sapur.008G131600.1	0.478557873	0.135219734	0.373168871	0.362357	0.717085011	0.78402832	grey	0.006973379	0.930926666		BHLH82	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	basic helix loop helix protein, putative
Sapur.016G051400.1	12.76218507	0.069263656	0.19110109	0.362049	0.717157323	0.78410964	grey	-0.050293654	0.529177837	GO:0007165,GO:0005515,GO:0043531		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.018G017300.1	94.81411334	0.057450231	0.158851	0.362039	0.717271761	0.784105564	grey	0.024123575	0.673602973	GO:0005160	ARR12,RR12	response regulator 12	NA
Sapur.006G107300.1	0.112059037	0.327004816	0.90620694	-0.36188	0.71744447	0.784180854	grey	-0.17928823	0.024655345				hypothetical protein
Sapur.009G017500.4	1.148291559	0.055365641	0.153561568	0.361565	0.717527291	0.784371308	grey	0.004627121	0.953739166			Major facilitator superfamily protein	plant/T1D6-50 protein
Sapur.006G190900.1	0.12155238	0.296151144	0.819662943	0.361748	0.717540615	0.784371308	grey	0.09850956	0.2194054		ATG37195.1		transmembrane protein, putative
Sapur.T004S001.1	0.83132673	0.385885834	1.068866158	0.361461	0.717755091	0.784634499	grey	0.041439422	0.633387511				NA
Sapur.011G105800.2	0.109999942	0.207755961	0.823882273	0.361396	0.717809369	0.78481092	grey	-0.271320105	0.000591239		ATG12940.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase family protein	hypothetical protein
Sapur.006G025600.1	155.6203804	0.031453494	0.088623985	0.361303	0.717873188	0.784621314	grey	0.027882508	0.727925711		ATCYP62,CYP68	cytochrome C oxidase subunit 6b	cytochrome C oxidase subunit 6b
Sapur.016G106600.1	691.4629515	0.01717331	0.047577586	0.360992	0.718105309	0.78485894	grey	0.026499614	0.741832322	GO:0009378,GO:0006310,GO:0006281,GO:0005524		Nucleotide/sugar transporter family protein	integral membrane-like protein
Sapur.005G088000.1	425.4026745	0.014291627	0.039605166	0.360903	0.718171713	0.78485532	grey	-0.031885229	0.825227733		ATG5846.1	Protein of unknown function (DUF530)	NA
Sapur.008G051150.1	0.158884827	-0.156800613	1.044376811	-0.3601	0.718394487	0.7851202	grey	-0.110693576	0.16830775		ATG5730.1	Chaperone DnaJ-domain superfamily protein	AT hook motif protein
Sapur.006G194900.1	1395.100742	-0.013512108	0.037501766	-0.36031	0.718616937	0.78530597	grey	0.002717064	0.973058062	GO:0016779,GO:0004631,GO:0003723,GO:0006512,GO:0005634	ATGD3510.5	HPAP,PAP(V)	poly(A) polymerase
Sapur.013G308000.1	0.303129202	0.127549494	0.354129004	0.359989	0.718687813	0.785330597	grey	0.047397416	0.632093942	GO:0005524,GO:0016887,GO:0140187	FAB10	FORMIN AFH10 PROTEOLIGATE CELLS 1A	phosphatidylinositol-4-phosphate 5-kinase
Sapur.001G152400.1	0.110761872	0.296104693	0.823321807	0.360176	0.718715759	0.785370371	grey	0.064609487	0.419439865	GO:0005515,GO:0016020		Integrase-type DNA-binding superfamily protein	ethylene-responsive transcription factor ERF021
Sapur.006G086400.1	0.968805544	0.107189144	0.297605834	-0.36	0.718843	0.785480704	grey	-0.058204667	0.46672031				hypothetical protein
Sapur.013G197000.1	0.367443864	0.161059	0.447423645	0.35987	0.718869738	0.785480704	grey	-0.005323515	0.948231426	GO:0008270,GO:0005515	ATG6490.1	RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.006G140100.1	0.975319648	0.080188128	0.222675522	0.359457	0.719028179	0.785622522	grey	0.020291679	0.974302222		ATG4530.1	Tetratricopeptide repeat (TPR)-like superfamily protein	O-linked N-acetylglucosamine transferase, rgd protein%2C putative
Sapur.010G012300.1	0.082719015	0.408472085	1.132419021	0.35887	0.719024646	0.786333737	grey	0.008973379	0.919036666		MPK16	mitogen-activated protein kinase 16	MAP kinase
Sapur.005G135500.1	28.84373815	0.025604183	0.071181444	0.358226	0.719096458	0.786387923	grey	-0.035237108	0.600365041	GO:0005515		DNA/RNA-binding protein	NA
Sapur.003G152900.1	543.4023816	0.012543073	0.035060682	0.357753	0.720527968	0.787116585	grey	-0.051739734	0.519513406			sequence-specific DNA binding;sequence-specific DNA binding transcription factors	NDX1 homeobox protein
Sapur.012G031900.3	0.637045753	0.093009593	0.305507079	0.356797	0.721439352	0.787872726	grey	0.008956961	0.911350082		ATG1060.1	WAPL (Wings apart-like protein regulation of heterochromatin) protein	wings apart-like protein regulation of heterochromatin protein
Sapur.016G230105.2	0.106079663	0.121182859	0.930650934	0.356664	0.721542121	0.787917813	grey	0.068656208	0.315514376		ATG2245.1	DNA heat shock N-terminal domain-containing protein	heat shock protein-binding protein, putative
Sapur.004G070300.1	0.86068848	0.104680426	0.293121375	-0.35664	0.721639373	0.787917813	grey	-0.015129706	0.85821365				NA
Sapur.003G062400.2	0.158546813	0.218062572	0.614064946	0.35659	0.721681215	0.787924499	grey	0.011132606	0.897072083				transmembrane protein, putative
Sapur.004G060900.1	0.141096855	0.268861666	0.752278517	0.355977	0.721857908	0.78849229	grey	0.03080874	0.70841673		ATG2180.1		hypothetical protein
Sapur.001G075600.1	0.151139267	0.218283735	0.613344024	0.355484	0.722227227	0.788816688	grey	0.012302026	0.875882399	GO:0005739,GO:0006129	ATCYP62,CYP68	cytochrome C oxidase subunit 6b	cytochrome C oxidase subunit 6b
Sapur.006G067000.1	1128.251999	-0.022132893	0.062270746	-0.35529	0.723375756	0.78892642	grey	-0.04882665	0.543374474		ATG28315.1	Nucleotide/sugar transporter family protein	integral membrane-like protein
Sapur.009G067500.1	0.079696035	-0.021208754	0.061180756	-0.35429	0.723472128	0.788956988	grey	-0.281289162	0.020383743				NA
Sapur.T021S00.1	0.064993257	0.409882021	1.154278315	0.353185	0.724145121	0.78956988	grey	-0.17900326	0.024888407		ATG35700.1	Fimbrin-like protein 2	FIM2
Sapur.018G064400.2	0.138697762	0.281279047	0.793238647	-0.3546	0.723891833	0.789300018	grey	-0.137827622	0.085178318		ATG3748.1		hypothetical protein
Sapur.014G068700.1	1.547770866	0.057969276	0.211242124	0.354091	0.723235367	0.789773321	grey	0.016860324	0.832025546	GO:0006887,GO:0000145	ATEXO70G1,EXO70G1	exocyst subunit exo70 family protein G1	exocyst subunit exo70 family protein
Sapur.006G034000.1	51.03412604	0.034063243	0.096195535	0.353986	0.723349729	0.789830904	grey	0.019233029	0.811127013		ATG5846.1	Gibberellin-regulated family protein	gibberellin-regulated protein
Sapur.001G132200.1	8.782925979	0.047760483	0.134916018	0.353687	0.723438186	0.789904412	grey	0.018235655	0.820979089		ATG4172.1		COP1-interacting-like protein
Sapur.001G160900.1	765.2893259	0.015159968	0.038165143	-0.35348	0.723729998	0.790106948	grey	-0.008829517	0.314259089		ATG2810.1	Pyridoxal-5'-phosphate-dependent enzyme family protein	threonine synthase
Sapur.007G009900.2	1.109413024	0.086880989	0.245080935	-0.3523	0.723819143	0.790355159	grey	-0.05622233	0.484100075		ATG6260.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase family protein	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein
Sapur.001G131900.1	0.216318147	0.17780862	0.50347507	0.351612	0.723866939	0.790377374	grey	0.002804045	0.972196248	GO:0006468,GO:0004672	ATCDPK3,ATCPKL,CPK6	Calcium-dependent protein kinase family protein	calcium-dependent kinase
Sapur.006G000300.1	0.079876763	0.321110001	0.9054021171	0.351372	0.724039979	0.790707226	grey	0.116777009	0.145252229	GO:0016787,GO:0006462		RING/U-box superfamily protein	zinc finger protein, putative
Sapur.009G074200.1	50.86731729	0.161928365	0.459783032	0.352184	0.724700205	0.791125675	grey	0.030057588	0.627204848		ATG15220.1	Plant basic secretory protein (BSP) family protein	peptidase
Sapur.001G088300.1	0.150208301	0.201208317	0.572000737	0.35146	0.724868693	0.791263526	grey	-0.164483816	0.019001189	GO:0016157,GO:0047262	GALT12,IRX8,LGT6	galactanyltransferase 12	GT-family GTB glycosyltransferase
Sapur.008G048700.1	29.60761201	0.046230053	0.131353223	0.35162	0.724874343	0.791263526	grey	-0.012170748	0.880176647		ATG2110.1	Disease resistance-responsive (dirigent-like protein) family protein	disease resistance response protein
Sapur.008G192600.8	0.152598815	-0.40157659	1.142274	-0.35187	0.724939103	0.791288115	grey	-0.180317647	0.019324946		ATG5510.1	NscG family	NscG family protein
Sapur.003G049800.1	471.9792576	0.014591165	0.03774331	0.350562	0.725615106	0.791854984	grey	0.014531187	0.505595457		ATG4010.1	CTC-interacting domain 4	CTC-interacting domain
Sapur.012G089300.1	105.7207063	0.029665466	0.084626169	0.350901	0.725682279	0.791929945	grey	0.014177793	0.861018149	GO:0008270,GO:0005515	ATG1580.1	RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.016G307900.1	-0.09851854	0.467968759	1.136238288	-0.35078	0.725754564	0.792067924	grey	-0.047276148	0.528386613		ATG4297.1	amino acid permease 7	transmembrane amino acid transporter protein
Sapur.016G136300.1	0.260414241	0.225411964	0.642852485	-0.35064	0.725859594	0.792152887	grey	-0.007393546	0.124949076	GO:0055114,GO:0020037,GO:0006979,GO:0004601	ATG2410.1	root hair specific 18	peroxidase
Sapur.016G051600.1	107.5460174	0.010191665	0.030078293	-0.34973	0.726029256	0.792833273	grey	-0.046836106	0.524282232	GO:0005852,GO:0005737,GO:0003743	ATG2572.1	Ribosomal protein L18ae/LX family protein PAF67	NA
Sapur.019G113300.1	1.564451391	-0.079060473	0.20295451	-0.34965	0.726595125	0.792858444	grey	-0.012555611	0.875977578	GO:0006412,GO:0005840,GO:0003735	RPL10B	Ribosomal protein L16p/L10e family protein	60S ribosomal protein L10
Sapur.006G024100.1	344.8567365	0.007024811	0.020273688	-0.34913	0.726894027	0.793227211	grey	-0.02809402	0.513818272				small multidrug resport protein, putative
Sapur.016G061000.1	0.387261306	0.13270003	0.380290451	0.348942	0.727121281	0.793362273	grey	0.04661872	0.57908146		ATG4888.1	RNA-like superfamily protein	F-box protein
Sapur.003G078000.1	0.070681245	0.424863897	1.219160877	0.348587	0.727399288	0.793426861	grey	0.178816751	0.032438866		ATG3260.1	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing-like protein
Sapur.012G020800.2	0.152612658	0.120510511	0.661390779	0.348524	0.727464748	0.793652441	grey	0.00695775	0.448211276		ATG2290.1	Endoplasmic reticulum vesicle transporter protein	endoplasmic reticulum vesicle transporter
Sapur.014G037400.1	0.420610574	0.132152118	0.379398835	0.348323	0.727597285	0.793783786	grey	0.045757131	0.589329981	GO:0005634	ATG2140.1	magc nash family protein	magc nash-like protein
Sapur.T033S00.1	60.16451124	0.027513231	0.078617035	0.34831	0.727607051	0.793783786	grey	0.06281084	0.437966967		ATG7920.1	PLATZ transcription factor family protein	NA
Sapur.001G030800.1	9.262559946	0.03297766	0.094689369	0.348292	0.727630804	0.793783786	grey	-0.004439435	0.956038254		ATG7630.2	ARM repeat superfamily protein	NA
Sapur.008G031200.5	0.68232509	0.034911154	0.100079216	0.348215	0.727634044	0.793796634	grey	0.075648531	0.3391497		ATG3220.2		DUF410 family protein
Sapur.006G040100.1	0.067981407	0.487035187	1.405518907	0.347651	0.728102067	0.794156496	grey	0.211892762	0.007719152				NA
Sapur.006G061600.1	1.101015497	0.295495466	0.851682429	0.347526	0.728189	0.794441945	grey	0.079629189	0.832021665		ATG2240.1		NA
Sapur.019G051200.1	0.168585137	0.218800195	0.630289594	0.347142	0.728649198	0.794574843	grey	-0.031439066	0.695885617	GO:0000160	ABR17,RR17	response regulator 17	NA
Sapur.004G330600.1	0.394620868	0.114267	0.329288745	0.34888854	-0.2466	0.728898648	0.794863335	grey	0.005208313	0.985406583	EMB3006	embryo defective 3006	hypothetical protein
Sapur.009G009600.2	0.526137747	0.114147	0.329288745	0.346547	0.728931553	0.794966027	grey	0.012145665	0.791695206				cytochrome B561, amino-terminal protein
Sapur.012G027800.1	0.364685679	0.136090764	0.392736237	-0.34654	0.728939188	0.794966027	grey	-0.059357516	0.42267742		ATG4692.1	Protein of unknown function (DUF302)	plant/T1N15-5-5 protein
Sapur.005G136600.1	0.142209002	0.213188937	0.617487157	-0.3463	0.729174014	0.795135399	grey	-0.154184704	0.053810654		ATG8910.1	hydroxyproline-rich glycoprotein family protein, putative	hydroxyproline-rich glycoprotein family protein
Sapur.008G157400.1	0.281740607	0.050011443	0.170558959	0.34599	0.729350457	0.795388464	grey	-0.063501984	0.439022622				hypothetical protein
Sapur.019G107300.1	0.141903163	0.409267	1.185966	0.345459	0.729528233	0.795388464	grey	0.052572559	0.515262487	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATG8850.1	Leucine-rich repeat receptor-like protein kinase family protein	receptor kinase, putative
Sapur.T145Z00.1	0.13550112	0.223461227	0.6459858	0.345888	0.729419453	0.795388886	grey	0.008042601	0.917788478				NA
Sapur.001G180400.2	0.230210169	0.055809283	0.161899898	0.345264	0.729862126	0.795485135	grey	-0.018146395	0.882955253	GO:0016021	ACY9-2	Cytochrome b561/ferric reductase transmembrane protein family	cytochrome protein b561
Sapur.008G139900.1	0.79455891	0.119373876	0.345316024	-0.34567	0.729589921	0.795518315	grey	-0.078147273	0.325887945		ATG4590.3	DYNAMIN-like 1D	dynamin-like protein
Sapur.003G094400.1	1.505132004	0.078158261	0.226811928	0.344861	0.729681621	0.795518315	grey	-0.041892839	0.630152212	GO:0003676	ATG7370.1	Glycosyltide-binding protein 1B	glycosyltide-binding protein 1B
Sapur.005G061600.1	0.321938134	0.153365801	0.44974726	0.345416	0.729378134	0.795474988	grey	0.040088847	0.545107761	GO:0016021,GO:0005198,GO:0008272,GO:0005085,GO:0016020,GO:0008271	ATG3108.1	sulfate transporter 2;1	sulfate/bicarbonate/oxalate exchanger and transporter sat-1
Sapur.001G344600.1	11.61355155	0.026838844	0.078031163	0.34503	0.729862324	0.795751754	grey	0.02806064	0.734365683		ATG6060.1		hypothetical protein
Sapur.016G165900.2	0.05871507	0.426301085	1.234600275	0.345295	0.729872737	0.795751754	grey	0.207739694	0.009353305		ATG7060.1		hypothetical protein
Sapur.005G138700.1	0.159449566	0.06087728	0.167986449	0.345253	0.729904074	0.795750126	grey	0.00236362	0.976558576				NA
Sapur.V004S001.1	9.11809404	0.066480606	0.19271527	-0.34502	0.730127537	0.795863642	grey	-0.006842624	0.937455	GO:0043565,GO:0006355,GO:0003700	ATG6830.1	Atb2P70,b2P70	bZIP transcription factor
Sapur.002G051000.2	0.56637948	0.112679497	0.32634315	-0.34497	0.730115744	0.795881748	grey	-0.071812514	0.36236453	GO:0005515	ATG4250.1	Galactose-oxidase/kelch repeat superfamily protein	F-box/kelch-repeat plant protein
Sapur.T075W01.1	25.34670872	0.024387076	0.069420179	0.34187	0.730487108	0.795916412	grey	-0.019797435	0.680974138	GO:0006810,GO:0016020,GO:0016740,GO:0005506	ATG3970.1	cytochrome P450, family 82, subfamily C, polypeptide 2	cytochrome P450
Sapur.010G062700.4	0.114282249	-0.311319469	0.908358811	-0.34683	0.730222797	0.795965977	grey	-0.140125748	0.080051611	GO:0016021,GO:0006810	ATG2040.1	Major facilitator superfamily protein	folate/biopterin transporter
Sapur.003G041100	24.84978887	0.022731292	0.064936514	0.34477	0.730250548	0.795964556	grey	-0.018802163	0.67425755		ATG4180.1	DNAse I like superfamily protein	NA
Sapur.002G101100.1	5384.688339	0.009195452	0.026575982	-0.34471	0.730313121	0.795965734	grey	-0.04934986	0.61956	GO:0003723,GO:0016776	ATG4760.1	PAB8,PABP8	polyadenylate binding protein, animal type 1, 2, 3, 4; family protein
Sapur.010G011200.3	0.118896667	0.231434088	0.66865112	0.344061	0.730423412	0.796017251	grey	-0.141139426	0.070076164	GO:0007165,GO:0005515,GO:0043531	ATG6830.1	Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.T112T00.1	0.79148401	0.091124039	0.264897026	0.343998	0.730848041	0.796496248	grey	0.080539852	0.315925254		ATG4790.1	PLATZ transcription factor family protein	NA
Sapur.003G137200.1	0.408673913	0.129373188	0.376788187	0.343887	0.730839337	0.796560342	grey	-0.000568887	0.994179518	GO:0008270,GO:0005515	ATG6530.2	BB,BB2	RING/U-box superfamily protein
Sapur.005G188300.1	16.93673	-0.018030274	0.05019071	-0.34385	0.730926214	0.796561661	grey	-0.017869139	0.827909				NA
Sapur.V012S400.1	0.143342861	0.257282204	0.748538661	0.343727	0.731051453	0.796633737	grey	-0.40765699	6.48E-10		ATG6820.1		stress up-regulated Nod 19 protein
Sapur.012G046700.1	0.213597941	0.184200305	0.536236393	-0.34368	0.731169712	0.796687934	grey	-0.132745619	0.185601314	GO:0016593,GO:0016570,GO:0006368	ATG7480.1	VIP4	leo1-like family protein
Sapur.V5WG001900.1	0.113762293	0.296837549	0.86372895	0.34367	0.731096631	0.796633737	grey	0.081606848	0.309620931	GO:0048500,GO:0008312,GO:0006614	AT

Sapur.03G115800.5	0.09317649	-0.32579665	1.019161821	-0.32127	0.74806698	0.81585918	grey	-0.51922667	3.20E-12	GO:0006508,GO:0004195	AT3G17180.1	scp33	serine carboxypeptidase-like 13
Sapur.0806G05100.1	0.12668988	-0.27010269	0.84132259	-0.32105	0.74817116	0.81174107	grey	-0.13446765	0.09314775	GO:0008270	AT5G55915.1		zinc ion binding
Sapur.0170G08100.1	1.125867517	-0.27386757	0.240261189	-0.32079	0.74892737	0.81104352	grey	-0.00174827	0.98299837	GO:0016758,GO:0008152	AT4G14090.1		UDP-glycosyltransferase superfamily protein
Sapur.0910G094600.1	1.073423234	-0.07586255	0.236966489	-0.32066	0.74846411	0.81086016	grey	0.00671804	0.93462162	GO:0004683,GO:0005516,GO:0004672	AT4G27300.1		S-locus lectin protein kinase family protein
Sapur.0951G084000.1	0.09653984	-0.26233805	0.931634736	-0.32065	0.74867655	0.81086016	grey	-0.13229373	0.12718391		AT5G51320.1		transmembrane protein, putative
Sapur.0D2G05300.3	0.21074954	0.182497427	0.589299129	0.32065	0.74853983	0.81201337	grey	0.09475231	0.93585016	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G08950.1		Leucine-rich repeat receptor-like protein kinase family protein
Sapur.0D2G054400.1	529.4887756	0.019378769	0.060492936	0.32057	0.74858446	0.81052827	grey	-0.00401579	0.95429015	GO:0043565,GO:0006355,GO:0003700	AT4G03700.1	SUE3,VIP1	NDP transcription factor, putative
Sapur.0170G06300.7	1.921395563	0.262451545	0.195007755	0.32049	0.74885355	0.81202027	grey	0.022104621	0.68995209	GO:0016755,GO:0006508	AT3G07705.2		CCR4-NOT transcription complex subunit, putative
Sapur.0D7G101000.1	0.47747969	0.110850748	0.346534654	0.319884	0.74905443	0.81251653	grey	-0.07087812	0.37707411	GO:0008234,GO:0006508	AT5G09730.2		Cysteine proteinases superfamily protein
Sapur.0170G03400.3	0.157233843	0.279066347	0.661217	0.319876	0.74954812	0.81284647	grey	-0.00463579	0.12806464	GO:0006355,GO:0003723	AT5G11181.1		NOL1/NOP2/sun family protein / antitermination NusB domain-containing protein
Sapur.0K1G108800.1	5.220271301	0.164984044	0.129828715	0.319606	0.74926983	0.81268721	grey	0.00623753	0.93820124		AT5G27760.1		Hypoxia-responsive family protein
Sapur.0910G196100.2	0.064502517	-0.42076385	0.318204653	0.319347	0.74962299	0.81301527	grey	0.13362847	0.09126759	GO:0008400	AT4G14520.1	SBP1	selenium-binding protein 1
Sapur.0180G102000.3	0.200071151	0.156311171	0.489840038	0.318902	0.74980514	0.81358743	grey	-0.15562087	0.05162382	GO:0007165	AT5G54100.1	ATSOS2,CIPK24,SNRK2.11.5	Protein kinase superfamily protein
Sapur.0D5G112500.1	0.064245668	0.190301238	0.420620106	0.318824	0.74989604	0.81366182	grey	0.20600306	0.09843855		AT2G20200.1		Transmembrane emp24-gp25 superfamily protein
Sapur.0D4G062700.1	107.2998177	0.020093475	0.065698548	0.318721	0.74983459	0.81325011	grey	0.01941114	0.88932079				hypothetical protein
Sapur.0D7G108400.3	12.91284	0.192827817	0.015969361	0.318675	0.75039736	0.81371776	grey	0.05235174	0.87650126		AT2G21810.1		Zinc finger C-x8-C-x5-C-x3-H type family protein, putative
Sapur.0D6G087200.2	2.508959279	-0.049732486	0.156239556	-0.31831	0.75250416	0.81339959	grey	-0.06204062	0.44000153	GO:0031931,GO:0031929	AT8G07530.1	ATRAPTOR1B,RAPTOR1,RAI	HEAT repeat ;WD domain, G-beta repeat protein protein
Sapur.7G8100.1	93.97619227	0.223868996	0.075009428	0.318213	0.75332157	0.81392161	grey	0.06199875	0.46048341	GO:0016853,GO:0005975	AT5G27330.1		Galactose mutarotase-like superfamily protein
Sapur.0D6G082100.4	2.123619986	0.262396626	0.186146471	0.318011	0.75047026	0.81171811	grey	0.01737206	0.82602671		AT5G45410.1		RING/U-box superfamily protein
Sapur.0150G021000.1	0.10944844	0.290054615	0.912405561	0.317901	0.75050161	0.81195789	grey	0.05138741	0.5227476		AT5G43760.1		DNAse I-like superfamily protein
Sapur.7G8300E.1	0.15327316	0.218600127	0.546469008	0.31474	0.75150128	0.81494969	grey	0.06343126	0.4396446				hypothetical protein
Sapur.0120G097800.1	3.088142655	0.067669513	0.213239364	0.317274	0.75103541	0.81420432	grey	0.02962958	0.71352879		AT5G10170.1	ATFLA11,FLA11	FASCICLIN-like arabinogalactan protein 11
Sapur.0961G147500.1	15.45241422	0.058402009	0.096839366	0.317116	0.75115723	0.81408053	grey	0.05750197	0.47281527		AT2G27210.1		Family of unknown function (DUF568)
Sapur.0120G076500.1	391.0046577	0.151736365	0.043342611	0.316925	0.75130076	0.81403172	grey	-0.01809966	0.87348587		AT5G63470.1	NF-YC4	nuclear factor Y, subunit C4
Sapur.0D6G165000.2	0.166817469	0.190301238	0.420620106	0.316819	0.75132783	0.81466952	grey	0.14282646	0.06347957		AT2G25780.1		
Sapur.0150G170000.2	0.12558665	-0.25196799	0.795890105	-0.31658	0.75155811	0.81469952	grey	0.10381458	0.19570802	GO:0006468,GO:0006672	AT5G18630.2		Protein kinase superfamily protein
Sapur.1S2G207500.1	0.05462232	0.469660925	1.422187497	0.316161	0.75187933	0.81495589	grey	0.23839899	0.00264194				
Sapur.0D6G101100.3	0.80628212	0.138526148	0.317486079	0.315284	0.75250607	0.81508861	grey	-0.41570008	6.13E-08		AT5G40770.1		HD domain-containing metal-dependent phosphohydrolase family protein
Sapur.0120G074000.1	52.30746394	0.064032812	0.203280433	0.315028	0.75274008	0.81581692	grey	0.02157965	0.75231463	GO:0006468,GO:0006672	AT5G47570.1		Leucine-rich repeat protein kinase family protein
Sapur.0D5G181000.4	23.02661777	0.192827817	0.161604042	0.314905	0.75282514	0.81586594	grey	0.02362748	0.68462244		AT2G44661.1		RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.0D3G144800.1	682.2386587	-0.01012291	0.032445426	-0.31477	0.75269304	0.81591692	grey	-0.05321545	0.10557369		AT4G01000.1		Ubiquitin-like superfamily protein
Sapur.0D5G173000.1	288.8844873	-0.014152	0.046469508	-0.31474	0.75290549	0.81591692	grey	-0.05682036	0.45168731		AT5G58310.1		
Sapur.0170G029900.1	0.15389608	0.267303501	0.835235391	0.314569	0.75308204	0.81609628	grey	0.03330611	0.77202246	GO:0010247,GO:0006468,GO:0005524,GO:0004672	AT5G66930.1		Protein kinase superfamily protein
Sapur.0D2G082200.2	2.248303014	0.174949736	0.553316049	0.314226	0.75368761	0.81648831	grey	0.03884766	0.70146866		AT5G58190.1	ECT5	evolutionarily conserved C-terminal region 5
Sapur.0D6G141900.6	0.10273823	0.336344652	1.070023847	0.31407	0.75468158	0.81803676	grey	0.11087833	0.16684561		AT5G28030.1		Acyl-CoA N-acyltransferases (NAT) superfamily protein
Sapur.0D5G057000.1	0.051160094	0.090605257	0.288437532	0.313967	0.75452552	0.81802607	grey	0.22477366	0.06661861	GO:0003677			B-DNA-binding domain protein
Sapur.0140G063000.6	0.156386015	0.245067251	0.770288518	-0.31293	0.75433846	0.81718733	grey	0.14541895	0.06920192	GO:0055085,GO:0016021			Major facilitator superfamily protein
Sapur.0D3G054000.5	0.32429294	0.148077405	0.473338226	-0.31284	0.75485045	0.81768013	grey	-0.06953748	0.38686312	GO:0005634	AT5G17690.1	NDF1	plastidic glucose transporter
Sapur.0D6G186100.1	0.06602798	0.190301238	0.420620106	0.31169	0.75485446	0.81823467	grey	0.14282646	0.07437956		AT2G25780.1		digestive organ expansion factor-like protein
Sapur.0D6G054000.2	12.54130176	0.078324977	0.230682317	0.312465	0.75487261	0.81769524	grey	0.03926955	0.6245549		AT5G07370.1	ATSIR.1	Protein of unknown function (DUF3677)
Sapur.7I0S000.1	0.417819034	0.192827817	0.34362868	0.31325	0.75477662	0.81758527	grey	-0.02915668	0.75157174	GO:0008270,GO:0008022,GO:0006625,GO:0005779	AT4G34660.1	APM4,ATPDX12,PDX12	PRP38 family protein
Sapur.0D6G094500.1	16.13794247	0.027233346	0.087233435	0.311225	0.75486945	0.81760439	grey	-0.01403881	0.86154148	GO:0006468,GO:0006672	AT5G29730.1		peroxin-12
Sapur.0180G094000.5	546.9110176	0.078324977	0.018326147	0.31229	0.75494539	0.81760257	grey	-0.06138051	0.45027257	GO:0006352,GO:0005634	AT5G17120.2	STG1,TAF1D,TAF1H15	Leucine-rich repeat transmembrane protein kinase
Sapur.0D5G143300.2	1.344278215	0.067663916	0.216793998	0.312112	0.75495561	0.81760257	grey	0.02238982	0.78081981	GO:0003993	TBP-associated factor 1H15		transcription initiation factor TFIID subunit
Sapur.0D6G146800.1	0.363968819	0.214828215	0.39027525	-0.31204	0.75501323	0.81768794	grey	-0.05438905	0.48362888		GO:0008270		histidine acid phosphatase family protein
Sapur.0B6G109800.3	11.02604162	0.039247884	0.125837715	0.311893	0.75512951	0.81775022	grey	0.02447746	0.76093726	GO:0008017,GO:0007010	AT4G24764.1	ATMAPT0-2,MAPT0-2	NADP(H)-dependent oxidoreductase superfamily
Sapur.0D5G146300.1	280.2793041	0.078324977	0.018326147	0.31178	0.75524176	0.81783005	grey	-0.01377141	0.65826864	GO:0042588,GO:0005506	AT2G05610.1	ATDEF1,PDF1A	microtubule-associated proteins 70-2
Sapur.15W0S85400.2	0.10232208	0.301316526	0.966832966	0.311653	0.75526147	0.81793768	grey	-0.08261552	0.30364187		AT5G18900.2		peptide deformylase
Sapur.0D5G012400.1	0.10600058	0.223161873	0.7176324	-0.31087	0.75582701	0.81842631	grey	-0.16924252	0.03664026		AT5G68810.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.0D6G028300.1	2.484667578	0.190301238	0.420620106	0.31069	0.75602507	0.81856763	grey	0.01606505	0.84168254	GO:0006468,GO:0005634,GO:0004672	AT5G62460.1		Zinc finger C-x8-C-x5-C-x3-H type family protein
Sapur.0961G164100.1	0.25868346	0.175835538	0.566838045	0.310291	0.75634006	0.81881469	grey	0.03485234	0.61811264	GO:0051259,GO:0051087,GO:0006457	AT5G04330.1		Cochaperin A-like domain family protein
Sapur.0D5G113200.1	0.118573224	0.192827817	0.93486288	0.31053	0.75669541	0.81910852	grey	0.09996607	0.21533808		AT5G10260.1		DNA heat shock N-terminal domain-containing protein
Sapur.0D2G058000.2	0.09065168	-0.43602764	1.4076225	-0.30977	0.75673936	0.81926146	grey	0.17458991	0.02874673	GO:0005515	AT1G30670.1		Wound-responsive family protein
Sapur.0D5G118800.1	13.75478619	0.192827817	0.161604042	0.309655	0.75682306	0.81922886	grey	0.01509247	0.84283557		AT5G44661.1		DNA-binding bromodomain-containing protein
Sapur.0180G070300.1	0.09602679	0.281450077	0.908463263	0.309474	0.75690641	0.81941955	grey	0.05774272	0.47231056				RNA-binding family protein
Sapur.0D5G075700.1	27.11185645	-0.020451396	0.066115301	-0.3064	0.75727464	0.81964019	grey	-0.03779041	0.82672513		AT4G37760.1		DNAse I-like superfamily protein
Sapur.0D5G205300.1	0.92898655	-0.089661222	0.291212984	-0.30871	0.75753885	0.81938589	grey	-0.05239489	0.50782517				
Sapur.0D2G023200.2	0.38821938	0.115329784	0.373036896	0.308629	0.75780481	0.81981588	grey	-0.0887703	0.93193038	GO:0006355,GO:0003677	AT5G16400.1	BLH7	BELL-like homeodomain 7
Sapur.0D6G087000.2	0.487937944	-0.047487736	0.348364707	-0.30892	0.75783604	0.82000012	grey	-0.05968904	0.45773156		AT5G59180.1	AKIA	ARM repeat-containing protein interacting with ABI2
Sapur.0D3G040000.1	44.08951517	0.035364885	0.114660177	0.308219	0.75795429	0.82064886	grey	0.01105544	0.69803006		AT5G14170.1		Plant protein of unknown function (DUF936)
Sapur.0140G139000.1	35.76115508	0.078324977	0.018326147	0.3079	0.75816855	0.82066265	grey	0.09992052	0.21309695		AT5G58310.1		ARM repeat superfamily protein
Sapur.0180G016000.2	0.272375474	0.149934681	0.487313916	0.307087	0.75821146	0.82061794	grey	-0.00614708	0.93092322		AT5G53480.1		Protein of unknown function (DUF3639)
Sapur.0D5G115300.1	10.0208624	0.043468826	0.141217569	0.307069	0.75831007	0.82061794	grey	-0.04432685	0.53285655	GO:0004674,GO:0006468,GO:0004672	AT4G13280.1	ARK1,BRK1	receptor kinase 1
Sapur.0170G054500.1	0.77367289	-0.09073827	0.295054383	0.307651	0.75834776	0.82065287	grey	-0.05867018	0.45638349	GO:0008270	AT5G18620.1		DHHC-type zinc finger family protein
Sapur.0D6G087000.1	0.08806687	0.077324977	0.251164569	0.307363	0.75847008	0.82081246	grey	-0.01377141	0.65826864		AT5G07010.1	CYP07B3	cytochrome P450, family 7, subfamily B, polypeptide 3
Sapur.0D5G060800.1	0.21607226	-0.19402903	0.631672022	-0.30717	0.75871518	0.82094254	grey	-0.0873305	0.27679714		AT5G13130.1		
Sapur.0D5G096900.1	5.812133223	0.159329784	0.518126149	0.306536142	0.75877722	0.82083187	grey	-0.16648956	0.03760107		AT5G50580.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.0D2G047800.2	0.07661073	0.351269439	1.144346439	0.306961	0.75887239	0.82104725	grey	0.23999216	0.02246372	GO:0016773,GO:0016020,GO:0005524	AT2G42880.1	ATMPK20,MPK20	MAP kinase 20
Sapur.0140G135200.1	0.177185492	0.170083959	0.554155541	-0.3069	0.75899141	0.82105623	grey	-0.12912054	0.10703958	GO:0016757,GO:0047262	AT5G58790.1	GALT15	galactosyltransferase 15
Sapur.0D6G112900.1	1.125001256	0.192827817	0.269054962	0.306751	0.75902661	0.82151989	grey	-0.00692162	0.91396753		AT5G51230.1	ATCSLC1,CAS1,SOS3	Calcium-binding EF-hand family protein
Sapur.15W0S135700.1	1.97358576	0.060342193	0.197068825	0.306202	0.75945093	0.82157526	grey	-0.00351866	0.96114387		AT5G26660.1		Glycosyl hydrolases family 32 protein
Sapur.0D5G127800.1	0.344869016	0.192827817	0.161604042	0.306174	0.75947265	0.82157526	grey	0.01509247	0.84283557				
Sapur.0B6G058100.2	0.17490630	0.185760888	0.606768508	0.306115	0.75957329	0.82179575	grey	-0.23457287	0.03105788		AT2G40316.1		
Sapur.0D5G036300.1	2.138415651	0.049660608	0.162260818	-0.3061	0.75957268	0.82179575	grey	-0.03779041	0.82672513		AT4G37760.1	TBL25	TRICHOME BIREFRINGENCE-LIKE 25
Sapur.0D6G063000.1	0.96513377	-0.073085218	0.238940603	-0.30587	0.75970175	0.82174186	grey	-0.03276155	0.68376713				
Sapur.0D6G049400.1	83.48311186	0.192827817	0.161604042	0.305362	0.75974057	0.82158224	grey	-0.04553765	0.57318378		AT2G03870.1		Small nuclear ribonucleoprotein family protein
Sapur.0D3G076000.1	172.8997069	0.091668383	0.300211084	0.305346	0.76032324	0.82220549	grey	0.09527492	0.01208488	GO:0005085,GO:0016020,GO:0008811,GO:0005216	AT3G45180.1	ATCNGC2,CNGC2,DND1	Cyclic nucleotide-regulated ion channel protein, putative
Sapur.0D6G070000.1	0.12920027	0.206857984	0.671232883	0.305243	0.76031052	0.82237814	grey	-0.16689646	0.03715187	GO:0043565,GO:0006355,GO:0005634,GO:0003700	AT3G07930.1	AT-HSFA8,HSFA8	heat shock transcription factor A8
Sapur.0D5G084800.1	0.11692874	-0.27793231	0.902768733	-0.30516	0.76029245	0.82237814	grey	-0.17799104	0.03272682		AT5G08520.1		Duplicated homeodomain-like superfamily protein
Sapur.0B6G117600.1	1.892706759	0.078151994	0.252329245	0.305014	0.76033545	0.82231637	grey	0.00585786	0.94196456				
Sapur.0D6G090900.1	0.10157336	-0.3237595	1.062839384	-0.3042	0.76063108	0.82268896	grey	-0.24231931	0.00214618				
Sapur.0D3G090000.1	248.6579915	0.010208409	0.034551562	-0.30414	0.76100146	0.82266644	grey	-0.04180618	0.63112112	GO:0009228,GO:0006789	AT5G22940.1	TH-1,THI1,THIE	thiamin biosynthesis protein, putative
Sapur.0D6G158300.1	0.23021733	0.138245914	0.455232888	0.304123	0.76103388	0.82366644	grey	0.02104537	0.78196969	GO:0016829,GO:0016114	CL84,CBL3,GCPE,HDS,ISPG	4-hydroxy-3-methylbut-2-enyl diphosphate synthase	4-hydroxy-3-methylbut-2-enyl diphosphate synthase
Sapur.0D1G151200.7	0.223498255	0.142318633	0.471270966	0.303899	0.76120507	0.82124844	grey	-0.00105588	0.99438793	GO:0016020	AT3G18865.2		Integral membrane Yip1 family protein
Sapur.0D6G077000.1	0.085686553	0.208881515	0.688267114	-0.3038	0.76122353	0.82208081	grey	-0.22629624	0.00429187		AT5G61667.1		Protein of unknown function, DUF538
Sapur.0170G129900.1	4.986748571	0.046525755	0.15228968	0.303722	0.76130975	0.82221665	grey	0.05891866	0.12727227	GO:0006950	GO:0032270.2		Adenine nucleotide alpha hydrolases-like superfamily protein
Sapur.0D6G030300.4	0.095218604	-0.206297004	0.679884355	-0.30394	0.76144186	0.82290456	grey	-0.04553765	0.57318378		AT4G22170.1		HCCD conserved family
Sapur.0170G073800.3	0.07966038	-0.396477588	1.306138919	-0.30355	0.76147257	0.82305014	grey	0.19986722	0.01208488	GO:0005085,GO:0016020,GO:0008811,GO:0005216	AT3G07230.2	ATCNGC2,CNGC2,DND1	Cyclic nucleotide-regulated ion channel family protein
Sapur.0140G109000.1	0.23693001	-0.165079979	0.543950436	-0.30348	0.76152538	0.82330884	grey	-0.0688993	0.39129317	GO:0003676	AT5G23840.1	ATSRP34,SR1,SRP34	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.0D5G067000.1	0.87346912	-0.015715435	0.052061381	0.302729	0.76290645	0.82380172	grey	0.08017008	0.91931556	GO:0005515,GO:0006096,GO:0004743,GO:0000287	AT4G26700.1	PKP-ALPHA,PKP1	Pyruvate kinase family protein
Sapur.0G6G182200.1	40.6348866	-0.044967797	0.148849363	-0.30251	0.76226935	0.82402018	grey	-0.01669716	0.83558272	GO:0005515,GO:0006468,GO:0006672	AT5G48840.2		Leucine-rich repeat transmembrane protein kinase
Sapur.0D5G111900.1	3.627594	0.152808649	0.501968409	0.301905	0.76224534	0.82402834	grey	-0.00919304	0.93070613		AT2G37020.1		PLATZ transcription factor family
Sapur.0D5G043800.1	5.581612441	-0.037544316	0.124337469	-0.30195	0.76268394	0.82457112	grey	-0.08509803	0.91490158	GO:0006468,GO:0005524,GO:0004672	AT5G49160.1	WNK7	Protein kinase superfamily protein
Sapur.0D6G030500.1	4.29660163	0.059329922	0.131215435	0.301166	0.76319128	0.82484009	grey	0.02720275	0.92692046				Serine/Threonine kinase domain protein
Sapur.0D6G069500.2	0.229436656	0.210135829	0.698923861	-0.30066	0.76367631	0.82547358	grey	0.0455897	0.57073428	GO:0007264,GO:0005525	AT4G08670.1	ARF-GAP	ADP-ribosylation factor-like A1C
Sapur.0D6G130000.1	0.21562751	0.175767284	0.584607157	-0.30069	0.76372426	0.82408009	grey	-0.02779235	0.80249912		AT4G11140.1	ATRAN11,WD11	Transducin/WD40 repeat-like superfamily protein
Sapur.0D1G151300.4	0.20085355	0.176264221	0.587105364	0.300192	0.76403852	0.82582497	grey	-0.19128225	4.42E-05	GO:0004683,GO:0006672	AT2G45510.1	ATPRKY,PERK1	proline extension-like receptor kinase 1
Sapur.0D6G084000.1	10.44794874	0.050238861	0.167027525	0.299719	0.76439143	0.82611189	grey	0.01498407	0.83141409	GO:0016020,GO:0015686,GO:0008519,GO:0072488	AT4G28280.1	AMT2,AMT2.1,ATAMT2	ammonium transporter 2
Sapur.0D6G223100.1	711.5837537	0.223960823	0.07480188	0.299626	0.76465476	0.82640853	grey	-0.00104125	0.98905101	GO:0055114,GO:0020037,GO:0009779,GO:0004601	AT5G42180.1		Peroxidase superfamily protein
Sapur.0D1G074700.1	924.2048872	0.014288426	0.047778797	0.299054	0.76489908	0.82665982	grey	0.02597614	0.76921857		AT2G28840.1		
Sapur.0D6G111000.2	1.728852528	0.061215134	0.205079659	0.298953	0.76528621	0.82697279	grey	-0.17585007	0.02692197	GO:0055092,GO:0008834	AT1T9E6,TP9E	UDP-Glycosyltransferase / trehalose-phosphatase family protein	trehalose-6-phosphate synthase
Sapur.0D1G111700.4	0.228743403	0.050056447	0.502650031	-0.29851	0.76531735	0.82697685	grey	-0.05723923	0.48819627		AT5G19003.2	VPS25	K2/DP family winged-helix DNA-binding domain
Sapur.0D6G087000.1	0.955149097	0.206368881	0.692746412	0.298581	0.76541244	0.82762421	grey	-0.02616146	0.74402949		AT5G47620.1		Lysine-related protein
Sapur.7I1I5S00.1	6.87779648	-0.071457403	0.239626429	-0.29821	0.76564258	0.82770185	grey	-0.00456188	0.95478182		AT4G17900.2		PLATZ transcription factor family protein
Sapur.0D6G089400.1	0.150455001	0.159329922	0.131215435	0.301166	0.76571242	0.82736584	grey	0.01109131	0.88923152		AT1G77240.1		PPPDE peptidase domain protein, putative
Sapur.0D1G084800.15	0.096609768	0.207301453	0.695923861	-0.30066	0.76367631	0.82547358	grey	0.0455897	0.57073428	GO:0007264,GO:0005525	AT4G08670.1	ARF-GAP	P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain
Sapur.0D6G130000.1	0.18861388	0.175767284	0.584607157	-0.30069	0.76372426	0.82408009	grey	-0.02779235	0.80249912		AT4G11140.1	AENODL1,EIL7,NOD1,L18	early nodulin-like protein 18
Sapur.0D1G127500.2	0.22640615	-0.154285265	0.518765988	-0.29741	0.76615875	0.82768822	grey	-0.09797989	0.24269594	GO:0055114,GO:0004471,GO:0051287	AT4G00570.1	NAD-ME2	NAD-dependent malic enzyme 2
Sapur.7I0R700.8	0.0944892	0.337561244	1.135016677	0.297406	0.76615245	0.82768822	grey	-0.02492714	0.75649853	GO:0006950	AT5G14680.1		Adenine nucleotide alpha hydrolases-like superfamily protein
Sapur.0D3G092000.1	0.270071504	0.208081837	0.474747984	-0.29738	0.76617925	0.82768822	grey	-0.11027839	0.18917653				plant-specific B2-DNA-binding domain protein, putative
Sapur.0B6G106000.1	1.00066276	-0.089592523	0.30178853	-0.29687	0.76656439	0.82853725	grey	0.18333752	0.02154351	GO:0006468,GO:0004672	AT3G17220.1		Protein kinase superfamily protein
Sapur.0G6G114500.2	0.842687714	0.208081837	0.27053704	0.296647	0.76681179	0.82854744	grey	0.01881179	0.83717347	GO:0006457,GO:0005515	AT3G18130.1	ATPUB13,PUB13	plant U-box 13
Sapur.0D6G134000.1	0.064228892	0.488379881	1.647304202	0.29635	0.76686242	0.82842668	grey	0.02118129	0.00742113	GO:0055085,GO:0046873,GO:0003001,GO:0016020	AT3G12750.1	ZIP1	zinc transporter 1 precursor
Sapur.0D6G153300.1	1.400874028	0.267601053	0.9027	0.295622	0.76722722	0.82888519	grey	0.00970137	0.92888519				
Sapur.0B6G150500.4	9.050110261	0.027345019	0.092451176	0.295681	0.76747253	0.82892794	grey	0.02597639	0.74674608	GO:0016746,GO:0008152	AT5G05580.1	ATS1,EMB3395,LPAT1	Phospholipid/glycerol acyltransferase family protein
Sapur.0B6G077100.4	0.079669418	0.207301453	0.695923861	-0.29576	0.76819469	0.82933164	grey	-0.01118129	0.83717347	GO:0016567	AT1G78390.1	ATG8B,ATG8B,GABI-LIBB	Ubiquitin-like superfamily protein
Sapur.0D6G137000.1	0.089036673	0.411316205	1.393315461	0.295207	0.76836003	0.82910735	grey	0.13517162	0.09142839	GO:0006355,GO:0003677	AT4G27410.2	ANAC072,RD26	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
Sapur.0D6G098800.1	0.262468635	0.110715255	0.376579331	0.294987	0.76853207	0.82924966	grey	-0.16248694	0.04303604		AT2G01050.1	ANK10,NAK10	ANK10 family;NAK10 N-terminal acetyltransferase
Sapur.0D6G090100.1	1082.542889	0.014565054	0.049246795	0.294782	0.76892037	0.82948805	grey	0.06019364	0.93667513	GO:0006468,GO:0004672	AT5G15150.1	FER	Malectin/receptor-like protein kinase family protein
Sapur.0B6G193200.5	0.100906387	0.253502897	0.801176239	-0.29477	0.76918731	0.82988805	grey	-0.19344296	0.05159618	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT4G17445.1	RPL18F	Ribosomal protein L18 family
Sapur.0B6G198500.1	0.096198501	0.266735164	0.842351814	1.212825	-0.29474	0.76919159	grey	-0.28732258	0.00266466	GO:0055085,GO:0003700	AT5G05580.1		Integrase-type DNA-binding superfamily protein
Sapur.0D3G167000.2	0.092941008	0.33452946	1.136357861	0.294387	0.76846378	0.82974284	grey	0.1191569	0.13717394	GO:0006355,GO:0005634,GO:0003700	AT5G69120.1	AGL7,AP1	K-box region and MADS-box transcription factor family protein
Sapur.0130D064000.1	0.144663868	0.207301453	0.695923861	-0.29367	0.76866479	0.83013146	grey	0.04801573	0.54386751	GO:0008270,GO:0046872	AT1G66370.1		C2H2 and C2HC zinc fingers superfamily protein
Sapur.0D7G027000.3	2.881442395	-0.064814025	0.159616117	-0.29348	0.76915197	0.8309135	grey	0.02006219	0.80304546		AT4G36800.1	RCE1	RUB1 conjugating enzyme 1
Sapur.0D6G027800.1	0.07721954	0.296264691	1.011819219	-0.29328	0.76960397	0.83084764	grey	0.17606197	0.03429254		AT5G17030.1		transmembrane protein, putative
Sapur.0D1G012300.1	0.152792245	0.187120356	0.639050216	0.29281	0.76966731	0.83088999	grey	0.04384644	0.58557027				
Sapur.0D6G025200.1	0.158446819	0.207301453	0.695923861	-0.29276	0.76970605	0.83090479	grey	0.00713716	0.92938064	GO:0016567,GO:0004842,GO:0005515	AT5G45850.1	ATPUB14,PUB14	plant U-box 14
Sapur.0D6G075100.3	48.54915129	-0.019166622	0.065431415	-0.29257	0.76984469	0.83102355	grey	-0.03251212	0.86152889		AT4G09600.1	ATMES12,MES12	methyl esterase 12
Sapur.0120G032800.1	0.168892473	0.220693423	0.75146891	0.291987	0.77029211	0.83148766	grey	0.01822686	0.83093384		AT4G33170.1	ATFLA11,FLA11	FASCICLIN-like arabinogalactan protein 11
Sapur.0140G074000.1	0.077726064	0.151631858	1.147675068	0.291915	0.77031421	0.83159553	grey	0.11372629	0.15809403	GO:0016020,GO:0009470	AT1G05200.1	ATGLR2.7,GLR2.7	glutamate-gated kainate-type ion channel receptor subunit GluR5
Sapur.0D6G030400.1	0.123257644	0.256838391

Sapur.010G024000.1	3.75968819	-0.06732889	0.24702308	-0.27217	0.78548703	0.84422217	grey	-0.01376348	0.86415754		AT2G45400.1		MeaS nucleotide pyrophosphohydrolase domain protein
Sapur.003G042400.1	0.08616014	-0.39188752	1.08206209	-0.27205	0.78556183	0.84429965	grey	-0.21004315	0.08815786	GO:0003677	AT1G53800.2		plant(?)BAD-4 protein, putative
Sapur.002G058600.2	0.08319739	0.27817876	1.02251146	-0.27182	0.78579388	0.84443095	grey	0.10403911	0.14483015	GO:0017156,GO:0046658	AT4G20160.3	ATPCAP1,PCAP1	plasma-membrane associated cation-binding protein 1
Sapur.010G018900.2	0.08948067	0.20208409	1.07469894	-0.27182	0.78578459	0.84463237	grey	0.12388321	0.12517182		AT5G01520.1		RING/U-box superfamily protein
Sapur.004G139300.1	438.123303	0.09020532	0.03423680	0.27142	0.78605194	0.84717067	grey	-0.05708849	0.98245671	GO:0009378,GO:0006310,GO:0006281	AAA-type ATPase family protein		
Sapur.005G132300.1	0.05945623	0.41412965	1.52797056	0.27109	0.78628847	0.84503103	grey	0.16945171	0.03385557		AT1G22110.1		structural constituent of ribosome
Sapur.002G201400.1	0.34799184	0.13387714	0.49400923	-0.27098	0.78684752	0.84562098	grey	-0.10834607	0.28891963		AT1G42440.1		Lateral organ boundaries (LOB) domain family protein
Sapur.001G033800.2	0.46526647	0.08182076	0.14168165	-0.27050	0.78677327	0.84540927	grey	0.22248215	0.77981662		AT2G20260.1		Acyl-CoA N-acyltransferases (NAT)-superfamily protein
Sapur.002G084400.2	0.08693681	0.27413263	1.01431422	0.270244	0.78693469	0.84555561	grey	0.07101771	0.37667769	GO:0006296,GO:0006996,GO:0000347	AT4G26420.2	PGI,PGI1	phosphoglucose isomerase 1
Sapur.014G136600.2	0.56279666	0.08462392	0.87878205	0.270325	0.78697483	0.84558582	grey	0.3961178	1.8267E-05		AT2G27230.3		SPT2 chromatin protein
Sapur.159G107000.1	0.28085093	0.13613922	0.50400627	-0.27011	0.78707276	0.84608923	grey	-0.10823202	0.17246263	GO:0003824	AT3G18030.1	ATHAL3,ATHAL3A,HAL3,HAL	HAL3-like protein A
Sapur.005G135200.1	0.26474937	0.15400007	0.57006619	-0.27007	0.78708547	0.84608923	grey	-0.02924591	0.73616232		AT1G77120.1		DNAse I-like superfamily protein
Sapur.011G050900.1	0.14033601	0.17994909	0.66442244	-0.27002	0.78714294	0.84562839	grey	-0.15852083	0.04727185		AT4G21780.1		
Sapur.003G232000.1	56.1373036	0.09422300	0.14956509	-0.27002	0.78723492	0.84568709	grey	-0.01397192	0.81938814				
Sapur.009G019400.1	1.1187729	0.01567228	0.05814579	0.269643	0.78743573	0.84590136	grey	-0.01186439	0.86980113	GO:0016747,GO:0008610,GO:0016020,GO:0006633	AT2G28630.1	KCS12	3-ketoacyl-CoA synthase 12
Sapur.005G050600.1	0.07947812	-0.32182314	1.30837182	0.269372	0.78763248	0.84609367	grey	0.30728777	9.10E-05		AT3G13410.1		transmembrane protein, putative
Sapur.003G113900.1	0.19881786	0.14309864	0.53101564	0.269314	0.78768266	0.84611825	grey	-0.08160864	0.30959094				hypothetical protein
Sapur.T081100.1	0.10991478	0.20481664	0.76077485	0.269212	0.78776118	0.84617209	grey	0.02968441	0.71287851	GO:0009733	AT2G18321.1		SAUR-like auxin-responsive protein family
Sapur.018G022200.3	2.36425349	0.09127456	0.16619858	0.269157	0.78778939	0.84617279	grey	-0.42266249	0.48867109	GO:0009506	AT4G22160.1		Phos (PP) domain-containing protein
Sapur.003G079000.2	0.09332674	-0.28118839	1.07091928	-0.26906	0.78788455	0.84620807	grey	-0.19688104	0.01349337		AT4G22670.1	AtHsp1,HIP1	HSP70-interacting protein 1
Sapur.019G077800.1	25.6261509	0.08172888	0.12956788	-0.26886	0.78802928	0.84631957	grey	-0.00985572	0.94245425	GO:0006412,GO:0005840,GO:0005622,GO:0003735	AT3G20120.1		Ribosomal L18p/L5e family protein
Sapur.T183300.1	0.16237052	0.19200889	0.71488576	0.268855	0.78804126	0.84630365	grey	0.07047564	0.38047261		AT1G70320.1	ATCIMS,ATCIMS2,HIT2,XPO	exportin 1A
Sapur.009G067100.4	0.36484412	0.13828791	0.47813957	0.268615	0.78832727	0.84661464	grey	0.12375095	0.00108299	GO:0005515	AT1G68320.1	MTMC7T5.1-NTMC2T7-PK1.1	Calcium-dependent lipid-binding (CaLB domain) family protein
Sapur.016G187100.1	0.07860997	0.37551133	1.39853927	0.268502	0.78832599	0.84651464	grey	0.12375095	0.12545429	GO:0008270,GO:0005515	AT5G49230.1		RING/U-box superfamily protein
Sapur.003G132300.1	0.10205162	-0.23966542	0.81847755	-0.26831	0.78849579	0.84684962	grey	-0.10944839	0.33027365		AT5G60050.1		BTB/POZ domain-containing protein
Sapur.016G121100.2	0.16768529	0.16549714	0.61811063	0.267718	0.78891604	0.84705267	grey	0.21720495	0.0777551		AT4G12480.1	NF-YC11	nuclear transcription factor, subunit C11
Sapur.008G087200.1	1.80047337	0.06845452	0.25570893	0.267626	0.78898538	0.84701086	grey	-0.00616564	0.93892167		AT1G68060.1		Chaperone DnaJ-domain superfamily protein
Sapur.004G138300.1	46.7328326	0.08008245	0.14956506	-0.2675	0.78906931	0.84779128	grey	-0.03631026	0.62153331		AT5G54640.1		early nodulin 93
Sapur.006G167600.1	0.76799988	0.08540457	0.31931132	0.267466	0.78913703	0.84779128	grey	0.05349584	0.49002883		AT3G28430.1		hypothetical protein
Sapur.019G023930.2	0.09317763	-0.32182314	1.20393917	-0.26746	0.78917075	0.84783051	grey	-0.18942985	0.01737284		AT1G70220.1		Outer arm dynein light chain 1, putative
Sapur.003G097700.2	0.14403459	0.22059318	0.82732129	0.266626	0.78974229	0.84775458	grey	0.04883009	0.17715476	GO:0005085,GO:0016020,GO:0006810,GO:0005215	AT1G18120.1	ATDUR3,DUR3	urea active transporter-like protein, solute:sodium symporter%2C putative
Sapur.010G047900.1	0.21614144	0.16550487	0.61919487	-0.2663	0.78982511	0.84781157	grey	-0.09855572	0.68829435		AT5G27540.1		Remorin family protein
Sapur.001G160900.1	0.53666268	0.09726895	0.36759412	0.265913	0.79030226	0.84826981	grey	-0.03209957	0.67892659		AT4G09550.1		ATP-dependent caseinolytic (Clp) protease/crotonase family protein
Sapur.002G058900.1	0.81814941	-0.07074872	0.26464185	-0.2653	0.79060936	0.84832164	grey	-0.04248806	0.69458705	GO:0006355,GO:0003677	AT4G24060.1		Dof zinc finger protein family protein
Sapur.017G002200.4	2.25168217	0.07906575	0.28154984	0.265184	0.79086761	0.84872333	grey	0.01189157	0.88242767	GO:0005515	AT2G44150.1	ASHH3,SDG7	histone-lysine N-methyltransferase ASHH3
Sapur.010G186000.1	44.2314766	0.08318739	0.13211888	0.265068	0.79089168	0.84872333	grey	-0.00935652	0.81217179		AT2G21280.1	PHF1	phosphate transporter traffic facilitator1
Sapur.001G130100.1	0.14310839	-0.19328427	0.72935667	-0.26514	0.79092659	0.84872333	grey	-0.12867664	0.18272891	GO:0005200	AT5G47010.1		transmembrane protein, putative
Sapur.T036100.1	0.73649728	-0.09421663	0.35137933	-0.26485	0.79112682	0.84880413	grey	-0.03922762	0.62747627		AT1G70320.1	ATCIMS,ATXPO1,HIT2,XPO	exportin 1A
Sapur.019G115100.1	3.39166443	0.08018483	0.16315678	-0.2648	0.79134789	0.84880413	grey	-0.02939025	0.76611019		AT1G35120.1		F-box/LRR-protein, putative
Sapur.014G097200.1	0.75410722	-0.09023409	0.34059102	-0.26466	0.79169586	0.84908454	grey	-0.04769286	0.60347337	GO:0007165,GO:0000155,GO:0000160	AT4G27430.1	CKI1	Signal transduction histidine kinase
Sapur.006G214400.3	0.32915706	-0.23182314	1.22093917	-0.26463	0.79191022	0.84914261	grey	0.06347105	0.44494026	GO:0005634,GO:0006355	AT1G52290.1		Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein
Sapur.013G040000.1	0.09761587	0.30008783	1.13544134	0.264293	0.79153328	0.84933154	grey	0.09129725	0.25563061				
Sapur.007G260000.1	0.11409022	0.23156029	0.87517037	-0.2642	0.79176169	0.84946195	grey	-0.06023026	0.45365334	GO:0005114,GO:0016491,GO:0005107	AT5G68320.1	sks17	SKU5 similar 17
Sapur.004G149500.1	783.8185522	0.08051112	0.03128726	0.26372	0.79199155	0.84969846	grey	0.03690963	0.66347859	GO:0016485,GO:0016021	AT3G44330.1		
Sapur.008G128800.1	0.15617473	0.17341163	0.61760526	-0.2636	0.79209283	0.84974856	grey	-0.13662428	0.09706363		AT3G47840.1		hypothetical protein
Sapur.003G249000.2	0.23818449	0.12016377	0.45600158	-0.26336	0.79227689	0.84994643	grey	-0.08735846	0.29702172		AT3G21520.1		Sec14p-like phosphatidylinositol transfer family protein
Sapur.003G079200.1	6.10953984	0.08179222	0.13966463	-0.2633	0.79230623	0.84994643	grey	-0.02439056	0.75808384				
Sapur.014G001500.1	8.11555548	0.07927482	0.30182372	0.262828	0.79283515	0.85032481	grey	0.03370154	0.67519826		AT1G71380.1		TRAF-like family protein
Sapur.009G119100.3	35.3307022	0.02153738	0.08188148	0.262742	0.79279131	0.85035135	grey	-0.04224132	0.59075632		AT5G22790.1	RER1	reticulate-related 1
Sapur.009G057500.1	0.29847751	-0.12681803	0.49391033	0.262771	0.79278	0.85035135	grey	-0.03152722	0.64284043	GO:2001070,GO:0006006,GO:0005524,GO:0003871,GO:0006003,GO:0003824	AT1G07920.2,FKP,FKBP	Fructose-1,6-bisphosphate	fructose-6-phosphate,2-kinase/fructose-2,6-bisphosphate
Sapur.017G074200.3	0.66426827	0.08913717	0.33017091	0.262696	0.79278586	0.85035135	grey	-0.07769256	0.33492866		AT5G39360.1	EDL2	circadian clock coupling factor 2GT
Sapur.017G025500.1	0.12713606	0.25080629	0.78849406	-0.2625	0.79289617	0.85064755	grey	0.11500807	0.15299027	GO:0005515	AT5G27510.1	GTI1,HAC13,HAF01,HAF1,T	HAC13 protein (HAC13)
Sapur.007G049600.1	0.30877579	0.11503608	0.43110187	0.26207	0.79326718	0.85078248	grey	-0.00974384	0.90597774		AT5G62520.1	SRO5	similar to RCD one 5
Sapur.018G028300.1	0.81928376	0.09100145	0.34117421	-0.2617	0.79376139	0.85104195	grey	-0.02023226	0.45365334	GO:0008176,GO:0006400	AT2G48400.1		tRNA (guanine-N(7)-)-methyltransferase
Sapur.019G145500.1	0.05318399	0.43862671	1.67628194	0.261668	0.79357341	0.85126287	grey	0.11334295	0.15811163	GO:0016829,GO:0010333,GO:0080167,GO:0000287	AT7G21175,TPS21		terpene synthase 21
Sapur.003G075500.1	0.15663745	0.17341163	0.61760526	-0.2616	0.79369214	0.85131857	grey	0.06484614	0.81837566	GO:0008233,GO:0006508	AT4G27130.1	BETA-VPE,BETAVPE	beta vacuolar processing enzyme
Sapur.012G029900.1	19.2315299	0.02643745	0.10113888	0.261368	0.79378529	0.85131282	grey	-0.02896689	0.73809136	GO:0043531	AT3G14470.1		NB-ARC domain-containing disease resistance protein
Sapur.006G163800.1	10.5131161	0.02180423	0.10685149	0.261127	0.79398447	0.85136338	grey	-0.00435778	0.95563768	GO:0005515	AT1G65320.1		Calcium-dependent lipid-binding (CaLB domain) family protein
Sapur.011G068200.2	0.05565993	0.31268202	0.93808171	-0.2609	0.79403218	0.85136338	grey	0.08194116	0.31238161		AT1G74810.1		Dna/HsdR protein family protein
Sapur.013G070700.4	0.17851196	0.09437389	0.74654752	-0.26106	0.79404705	0.85136338	grey	-0.4974201	3.42E-11	GO:0006412,GO:0005634,GO:0003723,GO:0000287,GO:0004826	AT1G72550.1		phenylalanyl-tRNA synthetase beta chain, putative
Sapur.003G058100.1	0.30055851	0.12016377	0.45600158	-0.26096	0.79406124	0.85136338	grey	-0.02439056	0.75808384		AT3G23050.1		hypothetical protein
Sapur.002G041800.1	0.15720267	0.21473894	0.82761806	0.260998	0.79409428	0.85136338	grey	0.05447563	0.48809901		AT5G47010.1		hypothetical protein
Sapur.003G025600.1	0.50366717	0.36361659	1.41168819	0.260744	0.79419197	0.85161684	grey	0.04809276	0.54255718	GO:0006464,GO:0009707	AT2G25730.1	HCS1	holocarboxylase synthase 1
Sapur.008G108100.2	1.45353891	-0.06457599	0.2476763	-0.26073	0.79429306	0.85147005	grey	-0.03399476	0.67249147	GO:0005975,GO:0004553	AT2G01630.1		O-Glycosyl hydrolases family 17 protein
Sapur.005G141200.1	4.34463126	0.07460267	0.28507452	0.260242	0.79430103	0.85147005	grey	-0.01498966	0.82218143	GO:0005515	AT1G77440.2		ermadfu/bun-like cytokinin-binding protein / calcium/lipid-binding domain (CaLB) protein
Sapur.010G096800.1	1.11763914	0.07157459	0.27490971	0.260367	0.79458622	0.85175107	grey	-0.02860419	0.71933474	GO:0005515,GO:0043161,GO:0006629,GO:0003684	AT4G20540.1	RAD23-1,RAD23C	Rad23 UV excision repair protein RAD23, putative
Sapur.003G062900.1	1.40368604	0.07160267	0.27490971	0.260213	0.79464948	0.85175107	grey	-0.0316147	0.88353155				
Sapur.017G100000.1	1.08615741	0.07483009	0.28755987	0.260228	0.79482983	0.85181976	grey	-0.01883646	0.88239528	GO:0005085,GO:0016020,GO:0012507,GO:0003138,GO:0006855	AT1G71140.1		MATE efflux family protein
Sapur.012G062800.1	439.2586238	-0.02043547	0.07783748	-0.25983	0.79520633	0.85200264	grey	-0.02331776	0.77191448	GO:0015114,GO:0048038,GO:0003008,GO:0008131,GO:0005507	AT4G22490.1		Copper amine oxidase family protein
Sapur.001G047600.2	4.31955918	0.07487203	0.17254037	-0.25945	0.79529141	0.85210379	grey	0.21884007	0.05832342	GO:0003700,GO:0005634,GO:0006355,GO:0000700	AT2G42460.2	AGL6,SEP3	K-box region and MADS-box transcription factor family protein
Sapur.T050000.1	0.07237187	0.33891757	1.30680821	0.259347	0.79536277	0.85274354	grey	0.11909539	0.13737527	GO:0008270,GO:0003676	AT4G27290.1		
Sapur.003G120900.1	11.5968857	0.06331744	0.16717644	-0.25911	0.79554723	0.85314728	grey	-0.01091966	0.84163368		AT5G56370.1		Ankyrin repeat family protein
Sapur.003G161600.1	254.5714162	-0.02043547	0.07783748	-0.25883	0.79576753	0.85271429	grey	-0.03482348	0.65028489	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G02070.1	BAM3	Leucine-rich receptor-like protein kinase family protein
Sapur.004G146400.1	1.18658624	0.07173474	0.27741481	-0.25856	0.79597024	0.85280191	grey	-0.02671004	0.64787523	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G21261.2	WAK2	wall associated kinase 2
Sapur.T002100.1	0.85207639	0.06416264	0.24830072	0.2584	0.79608042	0.85291662	grey	0.04001508	0.61877975		AT5G61600.1	ATPOB1,POB1	POZ/BTB contain G-protein 1
Sapur.004G147900.1	542.3664647	0.07158386	0.07158386	0.25838	0.79618347	0.85355557	grey	-0.02822563	0.75618463	GO:0005515	AT2G42280.1	GMI1	gamma-irradiation and mitomycin c induced 1
Sapur.T110000.1	0.06019487	0.39944155	1.31725503	0.258076	0.79634832	0.85390842	grey	0.16425718	0.03981901		AT5G06920.1		EAP30/Vps31 family protein
Sapur.017G047400.1	49.5923883	0.02508387	0.09924595	-0.25806	0.79636126	0.85390842	grey	-0.00299766	0.97026328				
Sapur.008G088400.1	115.4696295	0.01805516	0.07005654	0.257903	0.79649159	0.85392441	grey	0.02856926	0.72534263		AT1G60190.1		phosphatidylinositol N-acetylglucosaminyltransferase subunit Y
Sapur.007G061000.1	0.36737341	-0.10062188	0.50694905	-0.25766	0.79668415	0.85456632	grey	-0.04541916	0.57220727	GO:0009733	AT1G23830.1		SAUR-like auxin-responsive protein family
Sapur.T162000.1	42.0355128	0.12338872	0.0866889	0.257664	0.79668625	0.85456632	grey	-0.04703824	0.53802079	GO:0003899,GO:0003677,GO:0032549	AT4G18090.1	NRP/20	nuclear RNA polymerase D2B
Sapur.007G075100.1	2.33700617	-0.05705589	0.22489514	-0.25752	0.79677715	0.85325571	grey	-0.02912876	0.71958863	GO:0043565,GO:0006355,GO:0003700	AT5G68410.1	ATWRKY51,WRKY51	WRKY DNA-binding protein 51
Sapur.001G054500.1	0.06427334	0.38802148	1.16274456	0.257402	0.79688168	0.85336242	grey	0.09988418	0.11238212	GO:0006412,GO:0003824	AT1G51510.1		cinnamoyl-coa reductase-like 1
Sapur.008G070700.1	0.28413935	0.16268686	0.49263687	0.256862	0.79728097	0.85392073	grey	0.02438267	0.76180796		AT5G26550.1		peptidyl-prolyl cis-trans isomerase, putative
Sapur.003G038500.1	0.36447701	0.15210882	1.23293134	0.256228	0.79779302	0.85400355	grey	-0.11402338	0.15121087	GO:0003677	AT2G36270.1	NGA4	AP2/B3-like transcriptional factor family protein
Sapur.001G047900.2	0.39195271	0.11285776	0.40884099	-0.25607	0.79789265	0.85459388	grey	-0.07614923	0.34064073		AT3G24265.3		Protein of unknown function (DUF3664)
Sapur.003G204400.2	0.12974244	0.16268686	0.49263687	0.256178	0.79797172	0.85452331	grey	-0.17817763	0.02238821		AT4G22600.1		ARM repeat superfamily protein
Sapur.013G141700.1	2090.82265	-0.00785799	0.03060349	-0.25593	0.79809481	0.85452331	grey	-1.05285613	0.18947547	GO:0006413,GO:0003743	AT5G20520.1	EIF2 BETA,EMB3401	eukaryotic translation initiation factor 2 beta subunit
Sapur.001G191800.3	0.58897324	0.08569184	0.33602529	0.255911	0.79819588	0.85452331	grey	-0.06058116	0.45025387	GO:0016787	AT5G45280.2		Pectinacetylesterase family protein
Sapur.012G080300.1	73.8682024	0.02107088	0.08238853	-0.25576	0.79819715	0.85454854	grey	-0.41224635	0.07772245	GO:0004854	AT1G19120.1	IMPL1	myo-inositol monophosphatase like 1
Sapur.159G090700.1	565.9270769	0.02185058	0.08681822	0.255538	0.79830726	0.85480497	grey	0.01850138	0.81810283		AT5G50100.1		thiol-disulfide oxidoreductase DCC, putative
Sapur.006G123200.2	0.12725237	0.12338872	0.49263687	-0.25553	0.79833587	0.85480497	grey	0.16819255	0.03676123	GO:0008234	AT4G18480.1	CKI1,CKL1	casein kinase I-like protein
Sapur.006G175400.1	0.57886243	-0.03882988	0.15148833	-0.2554	0.79841079	0.85493764	grey	-0.02482619	0.7526041				
Sapur.004G173900.1	0.10443923	-0.26088498	1.13529425	-0.25534	0.79845156	0.85495985	grey	-0.3087994	1.64E-05	GO:0005515,GO:0006468,GO:0004672	AT2G19150.1		Leucine-rich repeat protein kinase family protein
Sapur.005G068500.1	2.00609815	0.05121837	0.16249487	0.255325	0.79847328	0.85495985	grey	-0.02751201	0.73224052		AT4G08890.1		Protein of unknown function (DUF3511)
Sapur.008G082200.1	1882.470531	0.07746332	0.08842128	-0.25523	0.79854461	0.85502464	grey	-0.01495771	0.85300406	GO:0006412,GO:0003743,GO:0042819	AT5G61410.1	ATRPL4,ATRPL3,PDA1,PD	cytoplasmic ribosomal protein PDA1, putative
Sapur.006G080000.1	1269.04531	0.03617427	0.14187907	-0.25496	0.79875859	0.85519685	grey	-0.01161912	0.88155243	GO:0016747	AT2G21130.1		HXXXD-type acyl-transferase family protein
Sapur.006G089800.3	0.52058887	-0.10042666	0.41088276	-0.25467	0.79878341	0.85530327	grey	-0.21433878	0.03538379	GO:0005114,GO:0016627,GO:0003995,GO:0050660,GO:0008152	AT1G53220.1	ATIVD,IVD,IVDH	isovaleryl-CoA-dehydrogenase
Sapur.015G100000.1	3.77229538	-0.03616633	0.14218028	-0.25436	0.79929406	0.85561451	grey	0.00339699	0.96324881				
Sapur.009G122300.3	4.90384828	0.06285471	0.17860018	0.253557	0.79988313	0.85620064	grey	0.02606215	0.77861267		AT5G22330.1	MED19A	RNA-binding protein, putative
Sapur.019G008300.1	0.07667132	0.26041985	1.14613574	0.253387	0.79999303	0.85626787	grey	0.02214058	0.72608631	GO:0008134,GO:0006886	AT5G44680.1		ARM repeat superfamily protein
Sapur.003G157900.1	0.35281037	0.39301617	1.56074325	0.253335	0.80009361	0.85637953	grey	0.17979871	0.02424203	GO:0006355,GO:0003700,GO:0007275	AT5G51190.1	PLT2	Integrase-type DNA-binding superfamily protein
Sapur.008G135100.1	0.36491499	0.35765461	1.41174264	-0.2526	0.80037163	0.85701124	grey	-0.24892165	0.00289016				
Sapur.016G230100.2	0.14961752	0.18182784	0.71952138	0.252781	0.80047337	0.85780623	grey	0.03829764	0.63925973	GO:0016787	AT5G52620.1	PPX-2,PPX2	protein phosphatase X 2
Sapur.005G042900.1	4.4881152	0.05768721	0.14895685	-0.25274	0.80049495	0.85786859	grey	-0.16015304	2.34E-06	GO:0043565,GO:0006355,GO:0003700	AT4G00730.1	ATWRKY30,WRKY30	WRKY DNA-binding protein 30
Sapur.008G072000.3	0.08423666	0.27185589	1.07437924	-0.25241	0.80073381	0.85801008	grey	-0.03662631	0.9391E-05		AT5G61160.1		Protein of unknown function (DUF315)
Sapur.003G122300.1	0.53483224	0.18185752	0.73078666	-0.25235	0.80073345	0.85798833	grey	-0.20684412	0.00047225		AT5G04870.1		DTW domain-containing protein
Sapur.005G113000.1	601.951896	-0.01064156	0.04219765	-0.2523	0.80081234	0.85798833	grey	-0.27808201	0.7295447		AT4G31190.1	PTB3	polypyrimidine tract-binding protein 3
Sapur.007G121600.1	0.86996581	0.31151192	1.23769735	0.25176	0.80122791	0.85791483	grey	0.06452494	0.4191364	GO:0003677	AT5G59880.1	ATHB52,HB52	homeobox protein 52
Sapur.009G000400.1	0.30884477	0.11238177	0.44714738	-0.25185	0.80139107	0.85768256	grey	-0.05051928	0.51938613		AT1G22460.1		FKBP-like peptidyl-prolyl cis-trans isomerase family protein
Sapur.003G304900.6	0.30700687	-0.09705776	0.39010207	-0.25089	0.80192446	0.85788785	grey	-0.13673029	0.03125948		AT4G03500.1		Ankyrin repeat family protein
Sapur.005G139700.1	0.14228864	0.08683806	0.31428665	0.250625	0.80215239	0.85818281	grey	0.04793821	0.51189897				peroxisomal/mitochondrial protein, putative
Sapur.013G395000.1	0.14281803	0.09174127	0.33186247	-0.25117	0.80168641	0.85781273	grey	-0.13625894	0.08833458	GO:0016747	AT3G48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase
Sapur.003G130600.1	0.38088477	0.11238177	0.44714738	-0.25105	0.80179466	0.85798256	grey	0.07364581	0.3184947	GO:0006386,GO:0003723	AT5G47640.1	TGH	SWAP (Suppressin of white-apricot)-containing protein
Sapur.013G304900.6	0.30700687	-0.09705776	0.39010207	-0.25089	0.80192446	0.85788785	grey	-0.12352872	0.12327803		AT2G47330.2		myosin heavy chain-related
Sapur.006G088300.1	105.1422864	0.01806488	0.03266422	-0.25026	0.80264617	0.85866891	grey	0.02214058	0.72608631		AT5G44680.1		ARM repeat superfamily protein
Sapur.012G156000.1	0.84192109	-0.07265879	0.29119513	-0.25061	0.80211241	0.85815704	grey	-0.08912469	0.26709401	GO:0006872,GO:0000166	AT5G07670.1	ATECA2,ECA2	endomembrane-type Ca-ATPase 4
Sapur.003G095200.1	1.74051337	0.06508364	0.2508	-0.25047	0.80316687	0.85835153	grey	0.03079572	0.91797883				
Sapur.016G228600.1	0.25765586	0.12505114	0.49957602	0.250241	0.80340039	0.85838721	grey	-0.0272171	0.73513737	GO:0006622,GO:0003824,GO:0080019	AT1G51980.1	FAR2,MS2	jojoba acyl CoA reductase-related male sterility protein
Sapur.018G104000.1	0.10004192	0.25207539	1.00975139	-0.25024	0.80340546	0.85838721	grey	-0.18689503	0.03908585		AT1G07030.1	GalAK	galactokinase, putative
Sapur.T003370.1	0.26153357	0.11586128	0.44560723	0.250089	0.80379799	0.85880751	grey	-0.01983016	0.81994808		AT4G16050.1		Aminotransferase, plant mobile domain family protein
Sapur.006G146400.3	0.17609046	-0.16768714	0.70666646	-0.25	0.80356892	0.85852746	grey	-0.12764287	0.11641938		AT2G34180.1		hypothetical protein
Sapur.016G191000.1	0.06328181	0.27849429	1.41004029	0.249668	0.80384229	0.85876953	grey	0.14289748	0.07420988		AT1G68190.1		Zinc knuckle (CCHC-type) family protein
Sapur.153G037900.1	0.16765072	0.28483402	0.74117535	-0.2494	0.80305814	0.85809774	grey	-0.12764093	0.11141996	GO:0008270,GO:0016776			
Sapur.003G093900.1	642.711134	0.00869398	0.03453724	0.248802	0.80349089	0.85853932	grey	0.00017487	0.99972222	GO:0005634	AT2G20340.1		Galactose oxidase/kelch repeat superfamily protein
Sapur.016G239300.1	0.07594235	0.30314088	1.23163531	0.248588	0.80369954	0.85932796	grey	0.15231535	0.05859294	GO:0043565,GO:0006355,GO:0003700	AT5G58120.1	ATB2/BZIP1,BZIP61	Basic-leucine zipper (bZIP) transcription factor family protein
Sapur.011G057700.2	0.85464188	0.08182784	0.33186247	0.247963	0.80383628	0.85940915	grey	-0.03787808	0.62561055		AT3G19290.1		Lysine-rich protein family
Sapur.020G054000.9	0.23416637	0.13231725	0.49619868	0.246342	0.80386903	0.85947673	grey	-0.02439242	0.81892385	GO:0005515	AT5T18301.1	ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1
Sapur.016G241600.1	0.0842965	0.32462152	1.30737247	0.248301	0.80380742	0.85952972	grey	0.07362166	0.3607646		AT5G18620.1		transmembrane protein, putative
Sapur.016G227000.1	6.75491686	0.06577605	0.30806421	0.248269	0.80395450	0.85962197	grey	0.02114202	0.75047584	GO:0006413,GO:0005737,GO:0003743,GO:0003723	AT4G18040.1	AT.EIF4E1,CUM1,EIF4E,eIF4	eukaryotic translation initiation factor 4E
Sapur.T016700.1	0.18647922	0.17237971	0.63419322	0.247934	0.80418519	0.85991749	grey	0.05015076	0.95294944				
Sapur.003G097400.1	909.294724	0.03669501	0.02424643	0.247837	0.80429755	0.85993084	grey	-0.04419314	0.24626021		AT4G04590.1	RTN1,B3	Reticulan like protein B3
Sapur.003G169700.2	0.34516518	0.10470605	0.42292466	0.247728	0.80439529	0.86007118	grey	0.01446387	0.85731752		AT4G02880.2		CUE domain protein, putative
Sapur.003G227000.1	5.3368864	0.05777605	0.20766691	0.247669	0.80451645	0.86018295	grey	0.01017781	0.

Sapur.013G075100.1	63.7840314	3.02059581	0.08875127	2.232063	0.81668921	0.86940328	grey	0.04088278	0.61148412					NA
Sapur.013G041000.1	619.1710395	0.01744887	0.07520908	2.332002	0.81663244	0.8494263	grey	0.01727987	0.82892703	GO:0007165;GO:0000155;GO:0005155;GO:0000160	ATSG06580.1	EIN4	Signal transduction histidine kinase, hybrid-type, ethylene sensor	ethylene receptor
Sapur.006G214000.1	16.48873142	0.28663849	0.08544473	2.33152	0.81609935	0.86700874	grey	0.00724649	0.93873013		ATSG25250.1		SPIN/Band 7/PHB domain-containing membrane-associated protein family	flotillin-like protein
Sapur.004G109800.1	0.07016637	0.30456796	1.30635757	2.331495	0.81603046	0.86970874	grey	0.11399714	0.16258723					NA
Sapur.016G214100.1	0.07024869	0.30456824	1.30635783	2.331495	0.81603108	0.86970874	grey	0.11434161	0.12075029					hypothetical protein
Sapur.005G022200.1	0.06967989	0.30245797	1.30724966	2.33137	0.81702746	0.86976523	grey	0.06557926	0.41448845					NA
Sapur.008G274300.1	17.40682756	-0.02506116	0.10997764	-2.33119	0.81756921	0.86984759	grey	0.00924044	0.98321987		ATSG26580.1			ATP-binding protein, putative
Sapur.010G046600.1	1986.792006	0.00706763	0.03442504	-2.33117	0.81788616	0.86984759	grey	0.02164556	0.78790954	GO:0008152	AHG13430.1	ATLEUCL1L1	isopropyl malate isomerase large subunit 1	3-isopropylmalate dehydratase, large subunit
Sapur.016G226700.1	0.16626782	0.05826884	0.68468848	-2.331108	0.81732125	0.86988395	grey	0.06454046	0.42192916	GO:0055114;GO:0016491	ATSG17020.1	ATSRG1;SRG1	senescence-related gene 1	flavonol synthase/flavanone-3-hydroxylase, putative
Sapur.007G095100.1	0.27866459	0.05658659	0.68045028	-2.331093	0.81724126	0.86988395	grey	0.01752136	0.83839089		ATSG15170.4	MAPKKK/ANP/KK3	mitogen-activated protein kinase kinase kinase 3	MAP kinase kinase kinase
Sapur.T001400.2	14.64864663	0.01828177	0.07886573	-2.330882	0.81704681	0.87004681	grey	0.05561866	0.96407197	GO:0070652;GO:0051225	ATSG07181.1			HAUS augmin-like complex subunit 4
Sapur.010G053700.1	0.91085137	0.08173734	0.13912645	-2.33081	0.81769156	0.87008391	grey	0.02837216	0.73428886		ATSG16610.1		heat shock protein 70 (Hsp 70) family protein	heat shock 70 kDa protein
Sapur.T081900.1	0.27082928	0.09230376	0.40011803	-2.33069	0.81725594	0.87047873	grey	-0.00935754	0.99645695		ATSG28455.1	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.007G037000.1	2.09668619	-0.06304724	0.23283479	-2.3305	0.81730796	0.87047873	grey	0.01310296	0.75449325		ATSG6870.1	AGL11;BC36	AGAMOUS-LIKE 11; bhlc 1	NA
Sapur.001G079000.2	0.07028104	0.26470728	1.14853614	-2.330477	0.81771428	0.87067996	grey	0.05207047	0.23558105	GO:0055085;GO:0016021;GO:0015329;GO:0006812	ATSG41630.1	ATCHX18;CHX18	cation/h+ exchanger 18	cation proton exchanger
Sapur.001G178300.1	0.10455865	0.25826353	0.97258249	-2.330458	0.81810356	0.87107534	grey	0.05857966	0.45251243	GO:0003677	ATSG26780.1	FLS3	AP2/B3-like transcriptional factor family protein	NA
Sapur.019G028500.3	0.0961812	-0.27968913	1.21520752	-2.23016	0.81769385	0.87047586	grey	-0.09541743	0.23454362		ATSG28593.2			costomer protein, putative
Sapur.018G011800.2	0.13803303	-0.37302999	0.75210157	-2.33007	0.81804048	0.87025519	grey	0.01278886	0.87369134	GO:0005515	ATSG02240.1	MEE66	F-box family protein	F-box family protein
Sapur.009G098600.1	1778.3136	0.00277684	0.04602526	-2.33003	0.81823925	0.87069331	grey	0.02102574	0.68350623		AHG13430.1	ATLEUCL1L1	isopropyl malate isomerase large subunit 1	3-isopropylmalate dehydratase, large subunit
Sapur.I59G021500.1	2.40751881	0.04621209	0.19434002	2.3296	0.81840466	0.87028753	grey	0.05490499	0.49462938	GO:0008138;GO:0006470	ATSG23730.3	PHS1	dual specificity protein phosphatase family protein	NA
Sapur.010G171900.4	0.05854873	0.24478371	1.54523656	2.329495	0.81840466	0.87028753	grey	-0.1946114	0.1	GO:0005515;GO:0003700;GO:0007275	ATSG45610.1	AAP2.7;TOE1	related to AP2.7	AP2 transcription factor
Sapur.009G068200.1	0.34036312	0.29235588	0.82313163	2.329488	0.81842001	0.87088128	grey	0.05714521	0.47731471	GO:0006334;GO:0005634;GO:0003677;GO:0000786	ATSG49950.1	ATTBB1;TTBB1	telomere repeat binding factor 1	single myb histone
Sapur.007G026100.1	101.7867569	0.08182276	0.15993384	2.329393	0.81852238	0.87090698	grey	0.02483274	0.76182255	GO:0003824	ATSG7955.1	CAMS1	camello-like 1	beta-amylase
Sapur.006G122500.1	0.06825533	0.36329353	1.15053592	2.329222	0.81869126	0.87105069	grey	0.07600957	0.12532648		ATSG7000.2			hypothetical protein
Sapur.014G029300.3	1.5110115	-0.06304724	0.27621453	-2.3291	0.81875135	0.87180373	grey	0.01310296	0.75449325		ATSG47550.1	SEC3A	exocyst complex component sec3A	exocyst complex component Sec3
Sapur.T051700.2	0.10260287	0.21973479	0.99325207	2.329069	0.81881494	0.87123404	grey	-0.20245789	0.01096253	GO:0016787	ATSG51540.1		N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase
Sapur.010G095500.1	0.06883349	0.32148544	1.40642371	-2.32855	0.81921951	0.87125889	grey	-0.21973777	0.05569045		ATSG20825.1	ULT2	Developmental regulator, ULTRAPETALA	ULT transcription factor, putative
Sapur.016G236405.1	0.07116943	0.25318397	1.14760305	-2.28849	0.81924658	0.87180067	grey	0.06896024	0.38918443		ATSG95181.1			hypothetical protein
Sapur.010G084300.1	0.59437853	-0.07284032	0.31892492	-2.32839	0.81938132	0.87158112	grey	-0.08842854	0.27076595		ATSG26370.3		Protein of unknown function (DUF2741)	DUI4378 domain protein
Sapur.006G164600.1	0.14795686	0.29235588	0.82313163	2.328221	0.81940702	0.87190892	grey	-0.00940342	0.98595238					DUI4378 domain protein
Sapur.009G047900.1	0.13455408	0.17135727	0.75113366	-2.328	0.81964168	0.87183629	grey	-0.06315682	0.43184053		ATSG13170.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.005G071300.1	0.10489384	0.24478371	1.07376164	-2.2797	0.81967424	0.87183629	grey	-0.1946114	0.1	GO:0005515;GO:0003700;GO:0070775	ATSG45610.1	SDE3	P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.015G111900.1	0.38094017	0.09162867	0.40151329	2.327905	0.81973731	0.87183629	grey	-0.03987623	0.61995177	GO:0005515	ATSG14230.1			ankyrin protein
Sapur.008G182000.1	0.82152756	0.29988564	1.31663078	-2.327	0.81984866	0.87187636	grey	0.08684895	0.23878336		ATSG24180.1		hydroxyproline-rich glycoprotein family protein; putative	hydroxyproline-rich glycoprotein family protein, putative
Sapur.005G190800.1	64.7368749	0.01618741	0.07107164	2.327769	0.81982564	0.87186281	grey	0.00281371	0.97210785		ATSG50430.1			lines amino-terminus protein
Sapur.006G075400.2	1.78244649	0.07284032	0.31892492	-2.32703	0.81992647	0.87222159	grey	0.05497274	0.48802334	GO:0055114;GO:0016491;GO:0006633;GO:0005506	ATSG26370.3	CER3;LPI;WAX2;YRE	Fatty acid hydroxylase superfamily	ecdysoneless protein
Sapur.016G152600.2	0.26761266	-0.01766045	0.4468035	-2.27714	0.82034192	0.87229729	grey	0.07381849	0.35796211		ATSG08020.1		Ring/FYVE/PHD zinc finger protein, putative	RING/FYVE/PHD zinc finger protein, putative
Sapur.010G087900.1	0.86935995	0.34115167	1.50542984	2.326614	0.82072819	0.87267583	grey	0.16524997	0.03898956	GO:0007165;GO:0005515	ATSG29001.1		Toll-interleukin-resistance (TIR) domain family protein	transmembrane receptor, putative
Sapur.013G082100.1	0.13791484	0.16461256	0.73647326	2.326604	0.82072819	0.87267583	grey	-0.00302412	0.97001632		ATSG56010.1		Pyridoxal phosphate (PLP)-dependent enzyme superfamily protein	cysteine desulfurase
Sapur.007G087800.1	0.22009794	0.12763025	0.56423561	2.3262	0.82104524	0.87263413	grey	0.09638016	0.90646211	GO:0003677;GO:0043565;GO:0006355;GO:0003700	ATSG22430.1	ATHB6;HB6	homeobox protein 6	homeobox leucine zipper protein
Sapur.006G264600.1	0.31944724	0.19235588	0.62709185	2.32609	0.82131649	0.87326494	grey	-0.00479447	0.91506264	GO:0003723	ATSG21461.1		RNA binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.I32G045800.1	3.36405387	-0.0969855	0.42916685	-2.32589	0.82132671	0.87208457	grey	-0.02846079	0.72762761					NA
Sapur.017G048800.1	0.13800127	-0.08488248	0.81668713	-2.3259	0.82132016	0.87208457	grey	0.09325245	0.83672015		ATSG47382.1		SAUR-like auxin-responsive protein family	SAUR family protein
Sapur.004G047700.1	0.56185114	0.09492409	0.41986318	2.325858	0.82132134	0.87334187	grey	0.20397669	0.03039295		ATSG29680.1	CAD1	MAC/Perforin domain-containing protein	MAC/perforin domain protein
Sapur.005G347200.1	0.05931	0.31907086	1.41408816	-2.32567	0.82142166	0.87232514	grey	-0.26402234	0.00832861	GO:0006508;GO:0004185	ATSG42461.1	scpl42	serine carboxypeptidase	serine carboxypeptidase
Sapur.004G128300.1	0.15490052	0.15988336	0.70861287	2.325636	0.82144728	0.87261527	grey	0.03080879	0.62692089	GO:0009055	ATSG26330.1		Cupredoxin superfamily protein	NA
Sapur.016G258800.1	13.1704852	0.02491941	0.10734217	2.325339	0.82171593	0.87406744	grey	-0.08855992	0.91243391	GO:0005515	ATSG47890.1	ARIP7;RLP7	receptor-like protein 7	NA
Sapur.019G057300.1	0.06661163	0.25155164	1.40351703	2.325194	0.82187986	0.87414118	grey	0.13831523	0.08032215		ATSG40760.1		DNAse I-like superfamily protein	NA
Sapur.T087700.2	3.28344784	0.03535656	0.14898922	2.325088	0.82193985	0.87354629	grey	0.03769267	0.63925766	GO:0003824;GO:0042127;GO:0018140;GO:0005965	ATSG42080.1	ATFTR;FRA1;WIG	Prenylhydrazinase family protein	protein farnesyltransferase subunit beta
Sapur.005G012200.1	104.4898812	0.01618741	0.07107164	2.324962	0.82227247	0.87402268	grey	-0.01577945	0.84498063	GO:0004648;GO:0006470;GO:0005524	ATSG28330.1		AGC (cyAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	Serine/Threonine kinase family protein
Sapur.003G049700.1	2.68947665	-0.06200947	0.18727342	-2.32449	0.82237248	0.87380517	grey	-0.01458607	0.85613889		ATSG42780.1		Protein of unknown function (DUF1000)	PITH domain plant protein
Sapur.008G095100.1	186.4837957	0.00255164	0.0064655	-2.32424	0.82259551	0.87416164	grey	-0.02700787	0.73068345					hypothetical protein
Sapur.014G073700.1	0.19207848	0.14231041	0.63501691	2.323947	0.82278204	0.87436161	grey	0.0624251	0.43734709		ATSG41761.1			NA
Sapur.016G056400.1	0.19003027	0.07486394	0.42466173	2.323932	0.82280874	0.87436161	grey	0.09325245	0.83672015					hypothetical protein
Sapur.I59G066300.1	0.26431839	-0.11144531	0.49798815	-2.2379	0.82393853	0.87446938	grey	-0.0847446	0.93587636	GO:0006281;GO:0003678;GO:0000723	ATSG28780.1		PIF1 helicase	NA
Sapur.006G231300.1	10.20738864	0.02491941	0.10734217	2.323878	0.82393718	0.87461866	grey	0.01457702	0.85636218					NA
Sapur.009G040600.1	2617.706831	0.01021459	0.04578718	2.323288	0.82331182	0.87496278	grey	-0.01127491	0.98741657	GO:0055085;GO:0016021	ATSG12860.1	DIT1	dicarboxylate transporter 1	2-oxoglutarate/malate translocator
Sapur.005G241000.1	33.51420941	0.05081995	0.25086227	-2.32327	0.82325227	0.87496278	grey	0.02948369	0.71397371	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATSG27510.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.008G156300.1	2.37556861	0.09234154	0.23317848	-2.323	0.82329115	0.87501867	grey	-0.03249115	0.67931657		ATSG29100.1	DER1	DERLIN-1	derlin protein
Sapur.002G161000.1	0.0554871	0.34117297	1.53049349	2.322916	0.82380571	0.87532614	grey	0.13227394	0.01584146	GO:0016787;GO:0005741;GO:0042721;GO:0003883	ATSG02120.1		CTP synthase family protein	CTP synthase
Sapur.I19G028300.2	0.10954623	0.07486394	0.42466173	2.322608	0.82410974	0.87532614	grey	0.05497274	0.48802334		ATSG26330.1	JAI1;JAZ3;TIFY6B	jasmonate-zim-domain protein 3	jasmonate ZIM-domain protein, putative
Sapur.003G144400.1	0.11302107	0.24191941	0.10734217	2.321339	0.82573593	0.87436744	grey	-0.08855992	0.91243391	GO:0005515	ATSG47890.1	ARIP7;RLP7	sulfotransferase 28	flavonol 4'-sulfotransferase, putative
Sapur.019G027300.1	0.06661163	0.25155164	1.40351703	2.321194	0.82587986	0.87514118	grey	0.13831523	0.08032215		ATSG40760.1		DNAse I-like superfamily protein	NA
Sapur.T087700.2	3.28344784	0.03535656	0.14898922	2.320588	0.82193985	0.87354629	grey	0.03769267	0.63925766	GO:0003824;GO:0042127;GO:0018140;GO:0005965	ATSG42080.1	ATFTR;FRA1;WIG	Prenylhydrazinase family protein	protein farnesyltransferase subunit beta
Sapur.006G012200.1	104.4898812	0.01618741	0.08008842	-2.32462	0.82227247	0.87402268	grey	-0.01577945	0.84498063	GO:0004648;GO:0006470;GO:0005524	ATSG28330.1		AGC (cyAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	Serine/Threonine kinase family protein
Sapur.003G049700.1	2.68947665	-0.06200947	0.18727342	-2.32449	0.82237248	0.87380517	grey	-0.01458607	0.85613889		ATSG42780.1		Protein of unknown function (DUF1000)	PITH domain plant protein
Sapur.008G095100.1	186.4837957	0.00255164	0.0064655	-2.32424	0.82259551	0.87416164	grey	-0.02700787	0.73068345					hypothetical protein
Sapur.014G073700.1	0.19207848	0.14231041	0.63501691	2.323947	0.82278204	0.87436161	grey	0.0624251	0.43734709		ATSG41761.1			NA
Sapur.016G056400.1	0.19003027	0.07486394	0.42466173	2.323932	0.82280874	0.87436161	grey	0.09325245	0.83672015					hypothetical protein
Sapur.I59G066300.1	0.26431839	-0.11144531	0.49798815	-2.2379	0.82393853	0.87446938	grey	-0.0847446	0.93587636	GO:0006281;GO:0003678;GO:0000723	ATSG28780.1		PIF1 helicase	NA
Sapur.006G231300.1	10.20738864	0.02491941	0.10734217	2.323878	0.82393718	0.87461866	grey	0.01457702	0.85636218					NA
Sapur.009G040600.1	2617.706831	0.01021459	0.04578718	2.323288	0.82331182	0.87496278	grey	-0.01127491	0.98741657	GO:0055085;GO:0016021	ATSG12860.1	DIT1	dicarboxylate transporter 1	2-oxoglutarate/malate translocator
Sapur.005G241000.1	33.51420941	0.05081995	0.25086227	-2.32327	0.82325227	0.87496278	grey	0.02948369	0.71397371	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATSG27510.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.008G156300.1	2.37556861	0.09234154	0.23317848	-2.323	0.82329115	0.87501867	grey	-0.03249115	0.67931657		ATSG29100.1	DER1	DERLIN-1	derlin protein
Sapur.002G161000.1	0.0554871	0.34117297	1.53049349	2.322916	0.82380571	0.87532614	grey	0.13227394	0.01584146	GO:0016787;GO:0005741;GO:0042721;GO:0003883	ATSG02120.1		CTP synthase family protein	CTP synthase
Sapur.I19G028300.2	0.10954623	0.07486394	0.42466173	2.322608	0.82410974	0.87532614	grey	0.05497274	0.48802334		ATSG26330.1	JAI1;JAZ3;TIFY6B	jasmonate-zim-domain protein 3	jasmonate ZIM-domain protein, putative
Sapur.003G144400.1	0.11302107	0.24191941	0.10734217	2.321339	0.82573593	0.87436744	grey	-0.08855992	0.91243391	GO:0005515	ATSG47890.1	ARIP7;RLP7	sulfotransferase 28	flavonol 4'-sulfotransferase, putative
Sapur.019G057300.1	0.06661163	0.25155164	1.40351703	2.321194	0.82587986	0.87514118	grey	0.13831523	0.08032215		ATSG40760.1		DNAse I-like superfamily protein	NA
Sapur.008G095200.4	0.10021626	0.22478314	1.01356522	2.321766	0.82446342	0.87571781	grey	0.0614954	0.95851804		ATSG25500.1		Plasma-membrane choline transporter family protein	plasma-membrane choline transporter-like protein
Sapur.008G245400.1	6.18653688	0.08750763	0.32217692	2.321703	0.82454599	0.87595762	grey	0.02464598	0.67285687					NA
Sapur.I59G013300.1	2.66775403	0.08369089	0.37613922	2.32165	0.82458994	0.87591982	grey	-0.03203363	0.67973394	GO:0005515;GO:0006488;GO:0005524;GO:0004672	ATSG47060.1		Leucine-rich repeat protein kinase family protein	Leucine-rich repeat protein kinase family protein
Sapur.016G063000.2	1.05382601	0.07486394	0.42466136	2.3604762	0.82462136	0.87591118	grey	0.03182343	0.88088716	GO:0016567;GO:0006842	ATSG26330.1		RING/U-box superfamily protein	zinc finger protein, putative
Sapur.019G208400.1	0.09081235	-0.25240464	1.13931042	-2.32154	0.82467083	0.87592118	grey	-0.12321597	0.12414481		ATSG04470.1		Ankyrin repeat family protein	ankyrin repeat protein 13C-B
Sapur.006G022700.1	0.82069388	-0.06108898	0.27538708	-2.32154	0.82467522	0.87592118	grey	-0.0869742	0.38385212	GO:0005515	ATSG40320.1		WW domain-containing protein	polyglutamine tract-binding protein, putative
Sapur.017G088300.1	0.06023813	-0.07938932	1.29138119	-2.2142	0.82473293	0.87585911	grey	-0.18931117	0.07154828	GO:0005634;GO:0003677;GO:0006260	ATSG39241.1		Ribosomal protein S5 family protein	40S ribosomal protein S8
Sapur.010G134600.1	104.31734	-0.05233086	0.23638288	-2.32138	0.82475263	0.87592274	grey	-0.04192503	0.60427619	GO:0009505;GO:0003824	ATSG02860.1		Phenazine biosynthesis PhzC/PhzF protein	phenazine biosynthesis protein, PhzF family protein
Sapur.005G085500.1	1.04889904	0.05696498	0.27139717	-2.32112	0.82505145	0.87616164	grey	0.06624708	0.45973884		ATSG17710.1			hypothetical protein
Sapur.003G056000.2	0.14846654	0.15840563	0.74278647	2.321204	0.82501535	0.8761658	grey	0.04860236	0.54515269	GO:0016021	ATSG12400.1	TOM20A	tobamovirus multiplication 2A	tetraspanin family protein
Sapur.003G111600.1	0.06051247	0.26208697	1.12127685	2.321005	0.82528218	0.87621007	grey	0.11831417	0.13898121		ATSG20180.1		PLATZ transcription factor	PLATZ transcription factor
Sapur.006G145700.1	0.13991094	0.17486256	0.79228418	-2.32069	0.82534678	0.87642684	grey	-0.13161537	0.10036472	GO:0005515;GO:0006488;GO:0004672	ATSG23950.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.010G101500.1	0.08335163	0.17486394	0.79228684	2.320215	0.82535917	0.87642684	grey	-0.01658858	0.84454245	GO:0005515	ATSG45120.1		Protein interaction domain-containing protein	NA
Sapur.018G102000.4	0.19908863	0.12579422	0.57100344	2.320208	0.82539279	0.87676996	grey	-0.0209152	0.79682855	GO:0007165	ATSG35430.1	ATSDS2;CIPK24;SNRK2.11.5	Protein kinase superfamily protein	CBL-interacting kinase
Sapur.018G191000.1	87.6594883	0.01875087	0.08516527	-2.32017	0.82540099	0.87676996	grey	-0.0323806	0.78079017	GO:0003824;GO:0006470;GO:0004722	ATSG28400.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.009G090500.1	20.60287699	0.05157681	0.15455418	-2.32013	0.82544939	0.87676996	grey	-0.03365705	0.67747731		ATSG49310.1			transmembrane protein, putative
Sapur.013G101300.3	101.1847231	-0.01260882	0.05751762	-2.32007	0.82549128	0.87676533	grey	0.04988627	0.23666209		ATSG2130.1	PerI-like family protein		PERI-DL1 protein
Sapur.005G138000.1	41.1663252	0.01880233	0.08548956	-2.32001	0.82559099	0.87680524	grey	-0.06794913	0.23767243					hypothetical protein
Sapur.010G074200.2	0.0805852	-0.25233824	1.13914207	-2.31961	0.82602231	0.87692115	grey	-0.15065234	0.05996314		ATSG44430.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR domain protein
Sapur.012G070200.1	0.08887777	-0.25053796	1.1395627	-2.31958	0.82605245	0.87692115	grey	-0.06413616	0.93561079	GO:0055114;GO:0016616;GO:0006694;GO:0003854;GO:0019752	ATSG22461.1	mMDH1	Lactate/malate dehydrogenase family protein	malate dehydrogenase
Sapur.010G047500.1	0.47769267	-0.08373201	0.38153729	-2.31656	0.82631984	0.8720282	grey	-0.04018913	0.61281946		ATSG29200.2		O-fucosyltransferase family protein	growth regulator, putative
Sapur.010G125100.1	0.08028897	0.36482965	1.20628615	-2.31557	0.82652303	0.87702202	grey	-0.14817248	0.03129178	GO:0016020;GO:0008378;GO:0006486	ATSG20170.1		Galactosyltransferase family protein	beta-1(3/2)-galactosyltransferase
Sapur.010G169100.1	0.11187622	-0.21808238	0.93138623	-2.31949	0.82628154	0.87702202	grey	-0.15430176	0.05368137		ATSG36370.1			membrane-associated kinase regulator 4, putative
Sapur.I19G047300.2	0.12388919	0.06501579	0.27035756	-2.31943	0.82633512	0.87704691	grey	-0.11831838	0.08872388	GO:0005085;GO:0016020;GO:0051297;GO:0015238;GO:0006855	ATSG08040.1	ATFRD1;FRD3;MAN1	MATE efflux family protein	MATE efflux family protein
Sapur.011G102000.1	0.09008663	0.63526209	2.90476587	2.318684	0.82689611	0.87703674	grey	0.09646065	0.23857106					NA
Sapur.019G054200.1	7.35089949	0.03805704	0.12856216	2.318203	0.82727557	0.87746705	grey	0.04101601	0.63032394	GO:0055085;GO:0016021	ATSG17010.3		Major facilitator superfamily protein	NA
Sapur.004G184400.1	2.44480587	0.02486167	0.11197698	2.318311	0.82736675	0.87769278	grey	-0.01965456	0.83939852					hypothetical protein
Sapur.017G111100.1	4.47364338	-0.05012267	0.22683996	-2.31808	0.82738616	0.87809476	grey	-0.04015758	0.61579437	GO:0016788	ATSG40990.1	GLIP1	GDSL lipase 1	GDSL lipase 1
Sapur.I19G026700.1	0.13475515	0.16127823	0.72866024	2.317818	0.82740519	0.87817216	grey	-0.12384046	0.12017828	GO:0016887;GO:0005524	ATSG26270.1		ABC-2 type transporter family protein	ABC-2 type transporter family protein
Sapur.005G017500.1	0.0594869	0.33106026	1.52268574	2.317442	0.82786301	0.87846128	grey	-0.17281784	0.03041963		ATSG27820.1		Ribosomal L18p/L5e family protein	NA
Sapur.017G048300.1	0.06804414	0.28482425	1.30862386	-2.31706	0.82816349	0.87925289	grey	-0.22116169	0.05375281					NA
Sapur.019G089600.2	0.08710607	0.27910005	1.28675918	2.31684	0.82825544	0.87820716	grey	0.10939862	0.17281389	GO:0055114;GO:0016702	ATSG15120.1		Protein of unknown function (DUF1637)	2-aminoethanethiol dioxygenase
Sapur.I59G027500.1	67.65027576	-0.01122002	0.23640182	-2.31682	0.82826138	0.87880518	grey	-0.01670236	0.85646766	GO:0005515;GO:0006488;GO:0004672	ATSG47570.1		Leucine-rich repeat protein kinase family protein	Leucine-rich repeat protein kinase family protein
Sapur.006G060700.1	0.06854859	0.30413204	1.4041208	-2.3166	0.82852397	0.87899011	grey	-0.23928837	0.00157545	GO:0005515	ATSG57180.2	CIA2	chloroplast import apparatus 2	import apparatus 2 protein, putative
Sapur.005G127400.1	0.07518744	0.36483443	1.12018958	2.316292	0.82853762	0.87920088	grey	0.10479486	0.19499043		ATSG49320.1		Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein	acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein, putative
Sapur.014G136600.1	39.2184634	0.01651353	0.07630822	2.316409	0.82868286	0.87909061	grey	0.00242858	0.97591253		ATSG04480.1			transmembrane protein, putative
Sapur.010G023700.1	255.8513843	0.01658501	0.07627189	2.315907	0.82900408	0.87949114	grey	-0.04829706	0.54805943		ATSG12700.1		ATP binding;nucleic acid binding;helicases	NA
Sapur.017G092600.1	0.10945412	-0.16592573	0.78539064	-2.31586	0.82920708	0.87963721	grey	-0.09339814	0.83238603		ATSG28700.1			hypothetical protein
Sapur.I19G107300.1	0.38754847	0.27969743	1.29648885	2.315735	0.82939464	0.87933563	grey	-0.09184878	0.25557617	GO:0016758;GO:0008152	ATSG22400.1	ATUGT83A1;UGT83A1	UDP-Glycosyltransferase superfamily protein	UDP-glycosyltransferase family protein
Sapur.003G089800.1	1930.270166	0.00437829	0.43968354	2.315702	0.82942017	0.87933563	grey	0.03584447	0.63883214		ATSG04340.1	ATOAM34;OSA54	osmotin 34	thaumatin-like protein
Sapur.018G090600.1	0.10814651	-0.21707562	1.00818761	-2.31532	0.82961422	0.87961993	grey	-0.15341526	0.05502781					NA
Sapur.005G042900.1	40.95500721	0.05182512	0.16095664	2.315144	0.82966924	0.87980224	grey	0.01548833	0.87831662		ATSG27310.1		F-box family protein	F-box GID2-like protein
Sapur.006G147100.3	0.28414261	0.10402183	0.48374638	2.315027	0.82974263	0.87994254	grey	0.07698908	0.33792008		ATSG12230.1	MEDI19A		hypothetical protein
Sapur.010G158800.1	0.06055693	0.30203743	1.41207435	2.31498	0.83076916	0.87984554	grey	0.14243424	0.05747878					NA
Sapur.003G102400.2	0.66498625	-0.06519444	0.30940477	-2.31499	0.82976373	0.87994254	grey	0.02071806	0.79674626		AHG23820.1		Pectin lyase-like superfamily protein	glycoside hydrolase family 28 protein
Sapur.003G137800.1	20.06987882	0.02202088	0.10802079	2.314967	0.82979232	0.87994254	grey	0.02482255	0.78164603	GO:0003677	AHG48870.1	NGA1	AP2/B3-like transcriptional factor family protein	B3 domain transcription factor NGA1, putative
Sapur.017G085000.1	45.56191719	0.05157977	0.16464885	2.314691	0.82983398	0.87995115	grey	0.02439716	0.78945218					NA
Sapur.016G215200.2	0.06483138	0.30187368	1.40460824	2.314854	0.82987697	0.87995105	grey	0.10439535	0.19343783	GO:0004803	ATSG19540.2	ATCYS6;ATCYS8;CYS8	cystatin 8	cysteine protease inhibitor
Sapur.006G183500.1	222.5472362	0.01618741	0.07107164	2.314767	0.82988166	0.88007191	grey	0.01330856	0.85865445	GO:0055114;GO:0020037;GO:0004879;GO:0046601	ATSG7165.1		Peroxidase superfamily protein	NA
Sapur.002G046500.1	215.9606199	0.01493188

Sapur.01G027000.1	0.06237489	-0.26665683	1.40238217	-0.18908	0.85009332	0.89660591	grey	-0.23943404	0.00253109	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT4G31940.1	CYP82C4	cytochrome P450, family 82, subfamily C, polypeptide 4	NA	
Sapur.009G017500.1	1.99775508	0.03577001	0.189186146	0.189073	0.85005538	0.89660591	grey	-0.01451665	0.83727242		AT3G44280.1		Major facilitator superfamily protein	plant/T2D9-50 protein	
Sapur.011G013030.2	0.09217718	0.20349585	1.07271183	0.18693	0.85009660	0.89668904	grey	0.00522056	0.70433656	GO:0005515	AT3G61144.1	AMSH3	associated molecule with the SH3 domain of STAM 3	Mov34/MPN/PAD-1 family protein	
Sapur.018G082000.1	2513.092794	0.00898279	0.04757834	0.188821	0.85033142	0.89671703	grey	0.00123216	0.98783838	GO:0006508;GO:0005622;GO:0004177	AT4G30920.1		Cytosol aminopeptidase family protein	leucine aminopeptidase	
Sapur.007G070000.1	7.0671376	0.02631631	1.04904174	0.188803	0.85024839	0.89671703	grey	-0.00181953	0.98183027	GO:0003700;GO:0003700	AB81		Integrase-type DNA-binding superfamily protein	AP2/EBP domain transcription factor	
Sapur.017G044300.2	3.32466945	-0.06064723	0.32163201	-0.18856	0.85047523	0.89689106	grey	0.03328184	0.96741049	GO:0016787	AT3G07130.1	ATPAP15,PAP15	purple acid phosphatase 15	purple acid phosphatase	
Sapur.004G027200.1	0.86146203	0.06320564	1.41237295	0.188421	0.85054691	0.89697626	grey	0.08680048	0.27938971		AT5G25760.1	ATGDU2,GDU2	glutamine dumper 2	transmembrane protein, putative	
Sapur.T047000.1	0.07352388	-0.38380584	1.50723946	-0.18805	0.85058736	0.89700263	grey	-0.15692747	0.04968807	GO:0043142;GO:0003527;GO:0017038	AT5G08840.2	emb2411	DNA replication helicase, putative	DNA replication helicase Dna2, putative	
Sapur.013G125200.1	3.86421868	-0.04715773	0.22197677	-0.1881	0.85078204	0.89718359	grey	-0.01975408	0.8056232		AT4G14400.1	ACD6	ankyrin repeat family protein	NA	
Sapur.UNG001700.2	1.76302274	0.17008276	0.22057826	-0.18682	0.85082432	0.89718359	grey	0.01918153	0.8156664		AT5G23810.2			hypothetical protein	
Sapur.010G038400.1	0.12007368	-0.15163638	0.82784958	-0.18791	0.85094491	0.89726357	grey	-0.12272084	0.12572657	GO:0051260	AT5G55000.2	FIP2	potassium channel tetramerisation domain-containing protein / pentapeptide repeat-containing protein	potassium channel tetramerisation domain-containing protein	
Sapur.019G044400.1	1.66.094204	0.08153188	0.07628581	-0.18769	0.85098397	0.89726357	grey	0.01908018	0.81267513	GO:0005515	AT5G27240.1	IQD24	IQ-domain 24	IQ calmodulin-binding motif protein	
Sapur.005G179800.3	0.0973022	-0.17976913	0.95697659	-0.18783	0.85100457	0.89736757	grey	0.07854831	0.32814487	GO:0016567;GO:0006402;GO:0005515	AT3G54790.1		ARM repeat superfamily protein	ubiquitin-protein ligase, PUB2	
Sapur.009G056000.1	0.05861835	0.36417237	0.41706527	-0.18483	0.85108369	0.89736757	grey	0.00600806	0.28197529		AT4G09020.1			hypothetical protein	
Sapur.001G076400.1	0.10760253	0.16115941	0.86135238	-0.18758	0.85125444	0.89765473	grey	0.03735969	0.64226103	GO:0050662;GO:0008824	AT4G27250.1		NAD(P)-binding Rossmann-fold superfamily protein	dihydrofolinoyl-4-reductase	
Sapur.016G131200.1	258.5678941	-0.08407231	0.04219438	-0.18666	0.85135408	0.89887453	grey	-0.02609051	0.61746229	GO:0008324;GO:0006470;GO:0004722	AT2G38880.1	PLL4	pectinesterase 4	protein phosphatase 2C, putative	
Sapur.008G065600.1	11.71852254	-0.01544304	0.08328463	-0.18664	0.85194036	0.89891061	grey	-0.05722964	0.48821118		AT1G79480.1		Carbohydrate-binding X8 domain superfamily protein	carbohydrate-binding module family 43 protein	
Sapur.006G172600.1	0.07624714	0.26632123	1.21614917	0.18646	0.85208760	0.89922228	grey	0.08505813	0.28955431	GO:0005515	AT3G62310.1		SAUR-like auxin-responsive protein family	auxin responsive SAUR protein	
Sapur.T047900.1	0.05266476	0.08208268	1.42733438	0.18645	0.85219715	0.89930029	grey	0.08415372	0.29869067	GO:0017126;GO:0005575;GO:0032957;GO:0005622;GO:0005524;GO:0003028	AT4G28170.1	emb2411	Helicase, Sf3 superfamily, putative SF3 helicase family protein	Inositol 1,3,4-trisphosphate 5/6-kinase family protein	
Sapur.001G160000.2	1.18685154	-0.05342397	0.28707841	-0.1861	0.85238953	0.89846702	grey	-0.03158335	0.69458809		AT5G52230.1			cysteinobactetial aminoacyl-tRNA synthetase CAND domain protein	
Sapur.001G155000.1	0.06351555	0.36859164	1.14264647	0.18608	0.85245149	0.89852504	grey	0.16098188	0.15157653		AT5G25461.1		Mov34/MPN/PAD-1 family protein	26S proteasome non-ATPase regulatory subunit	
Sapur.008G155100.1	17.92352059	0.01553183	0.08389808	-0.18581	0.85260707	0.89911069	grey	-0.11112083	0.16589761	GO:0008168;GO:0003723;GO:0008033;GO:0006364;GO:0003723	AT2G42470.1	ATFBR1,ATFBR1,FBR1,FIB1,5	fibrillarin 1,ATFBR1,ATFBR1,FBR1,FIB1,5	fibrillarin 1	rRNA 2'-O-methyltransferase fibrillarin 2
Sapur.T046100.1	6.76614244	0.04550163	0.35106602	-0.18492	0.85329	0.89927512	grey	-0.04641798	0.52182715					hypothetical protein	
Sapur.017G030800.1	9.53811398	-0.07181858	0.38550185	-0.18485	0.85348619	0.89931541	grey	-0.02369281	0.76919689	GO:0008168	AT5G15125.1		5-adenosyl-L-methionine-dependent methyltransferases superfluorin protein	NA	
Sapur.003G036300.3	0.31691766	0.06455227	0.34175247	0.3675297	0.85348699	0.89931541	grey	0.07564831	0.3184467	GO:0016491;GO:0005975	ATPH52,PH52		alpha-glucan phosphorylase, H	alpha-glucan phosphorylase, H	
Sapur.014G141700.1	0.06018372	0.24316397	1.1418756	0.18466	0.85398611	0.89937768	grey	0.35697009	4.84E-06	GO:0006414;GO:0005622;GO:0003746	AT4G11120.1		translation elongation factor Ts (EF-Ts), putative	elongation factor Ts protein	
Sapur.016G139200.2	33.4567999	0.05182552	0.08576492	-0.18425	0.85384032	0.89969134	grey	-0.00399804	0.98347823		AT1G08830.2	2-ISO,2-ISO1,1-2-ISO1,2	15-cis-zeta-carotene isomerase	15-cis-zeta-carotene isomerase	
Sapur.005G160600.1	0.06397992	0.21394068	1.64695744	0.184128	0.85393137	0.89969014	grey	0.02950075	0.71240709		AT2G29030.1		PLATZ transcription factor family protein	NA	
Sapur.013G076000.1	105.3577531	0.02162387	0.11748799	0.184058	0.85398156	0.89974223	grey	0.02545084	0.75168139					NA	
Sapur.011G027900.1	260.5918821	0.00684832	0.03725482	0.183969	0.85408078	0.89979259	grey	0.00492249	0.95577477	GO:0031683;GO:0010601;GO:0007186;GO:0004871;GO:0003924	AT5G33930.1	XLG3	extra-large GTP-binding protein 3	NA	
Sapur.003G123800.5	0.06918218	0.25930106	1.40950266	0.183961	0.85404665	0.89979259	grey	0.0994552	0.21505672	GO:0006355;GO:0005634;GO:0003700;GO:0046983;GO:0003677	AT4G35660.1	AGL30,ATSOC1,SOC1	AGAMOUS-like 20	MADS-box transcription factor	
Sapur.U016G025700.1	0.06051559	0.26859164	1.34265614	0.183946	0.85405147	0.89979259	grey	0.06744474	0.40153221	GO:0005515;GO:0006468;GO:0005622;GO:0004672	AT5G47570.1		Leucine-rich repeat protein kinase family protein	NA	
Sapur.013G100500.1	0.10750676	-0.16570273	0.91107786	-0.18386	0.85410582	0.89975717	grey	-0.13467113	0.0926465	GO:0006468;GO:0005524;GO:0004672;GO:0005515	AT4G11110.1	SPA1	SPA1-related 2	ubiquitin ligase cullin1, putative	
Sapur.009G029900.1	0.06419442	0.30276796	1.61130306	0.183368	0.85450920	0.90022237	grey	0.08749458	0.27872688					NA	
Sapur.005G027900.1	0.05738588	0.30378681	1.65885916	0.183132	0.85469467	0.90028951	grey	0.11804584	0.14171277		AT5G45920.2			hypothetical protein	
Sapur.010G028300.1	0.05266256	0.19560581	1.05365254	0.183063	0.85476602	0.90031767	grey	0.17324741	0.03003684	GO:0008270;GO:0004089	AT3G45160.1	ATGCA1,ATSABP3,CA1,SABP	carbonic anhydrase 1	NA	
Sapur.019G055500.1	0.45335808	0.08679512	0.47829519	0.182883	0.85489144	0.90048351	grey	-0.0887627	0.18451138		AT5G16320.1		Fasciclin-like arabinogalactan family protein	NA	
Sapur.016G239600.1	416.0000551	-0.01555682	0.10593576	-0.18272	0.85527365	0.9005203	grey	-0.02123869	0.79191665	GO:0016020	AT5G38360.1	ERD4	Early-responsive to dehydration stress protein (ERD4)	early-responsive to dehydration protein	
Sapur.005G186005.1	0.05087084	0.18309762	1.83206213	0.182713	0.85532599	0.9005203	grey	0.13181658	0.65474109		AT5G61610.1			hypothetical protein	
Sapur.009G078200.1	4334.200349	0.00780364	0.04782704	0.182334	0.85532829	0.90085028	grey	-0.02679864	0.73901243	GO0008171	AT4G34050.1	CCoAOMT1	5-adenosyl-L-methionine-dependent methyltransferases superfamily protein	caffeoyl-CoA 3-O-methyltransferase	
Sapur.006G117700.1	3.32326153	0.07684833	0.22441827	0.181913	0.85545172	0.90086694	grey	0.02787123	0.73892895		AT5G08190.1	PSF1	partner of SLK1 protein 1	DNA replication complex GINS protein PSF1	
Sapur.016G149500.1	0.35267104	0.30376568	1.6701234	0.181901	0.85560577	0.9097687	grey	0.10621264	0.18518328	GO:0006614;GO:0005199				NA	
Sapur.009G017900.1	46.7088127	-0.01756422	0.05188009	-0.18168	0.85574569	0.90259517	grey	0.08243723	0.91825222	GO:0005515	AT3G56880.1	ATMBF1B,MBF1B	multiprotein bridging factor 1B	multiprotein bridging factor 1	
Sapur.005G064200.1	0.05718109	0.30378884	1.67398896	0.181483	0.85588561	0.90364757	grey	-0.10457195	0.10241036	GO:0006468;GO:0004672;GO:0006474	AT5G58910.1		Protein kinase superfamily protein	tyrosine kinase family protein	
Sapur.006G282300.1	0.30070514	0.02738267	0.19205219	0.18142	0.85604060	0.90406213	grey	-0.0267	0.83708088	GO:0006468;GO:0006470	AME3		Protein kinase superfamily protein	Serine/Threonine kinase 61	
Sapur.005G132500.1	0.2884888	-0.08160466	0.45270385	-0.18112	0.85627031	0.90160327	grey	-0.05997718	0.45555501	GO0005515	AT5G20040.1		Galactose oxidase/kelch repeat superfamily protein	kelch repeat F-box protein	
Sapur.009G018200.1	0.59718566	0.05187402	0.39907674	0.181067	0.85632582	0.90160362	grey	0.05256458	0.57165527	GO0005515;GO0005634	AT2G37710.1		RmlC-like cupins superfamily protein	nutient reservoir protein, putative	
Sapur.005G145800.2	0.06560175	0.25672728	1.42235826	0.180587	0.85675721	0.90192104	grey	0.0938356	0.24246239	GO0005515	AT5G77005.2	ATSPP2,SPP2B	RNI-like superfamily protein	F-box protein SKP2A	
Sapur.002G141100.2	0.61252964	-0.06332761	0.39250789	-0.18045	0.85680501	0.90192104	grey	-0.04479241	0.57498882	GO:0004648;GO:0006470;GO:0005524	AT5G60170.1	emb1220	pre-mRNA processing ribonucleoprotein binding region-containing protein	U4/U6.snRNP nuclear ribonucleoprotein Prp31	
Sapur.001G232500.1	0.32193785	0.15729381	0.69717868	-0.18044	0.85685453	0.90205664	grey	-0.14099236	0.07938329		AT5G66610.1		Domain of unknown function (DUF642)	DUF313 domain protein	
Sapur.016G176300.1	0.1617849	0.14598234	0.67407688	0.179763	0.85738336	0.90240023	grey	-0.37428347	1.33E-06		AT4G09880.1			DUF546 family protein	
Sapur.007G050000.1	0.30018917	0.07984864	0.54514562	0.179	0.85756257	0.90261871	grey	-0.02383025	0.79262419	GO0005524	AT5G55240.1	BCS1	cytochrome b-c1	AAA family ATPase	
Sapur.013G112400.2	3.88511177	0.02609723	0.15036382	0.179366	0.85765563	0.90286528	grey	0.00644518	0.93615641	GO0007264;GO0005525	AT5G45970.1	ARAC2,ATRAC2,ATROP7,RA	RAC-like 2	Ras small GTPase family Ras protein	
Sapur.004G017900.1	0.33328024	0.07609164	0.21683541	-0.17924	0.85776549	0.90291168	grey	0.00803174	0.94041314	GO0016491	AT3G21330.1	DYT1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	helix loop helix DNA-binding protein	
Sapur.014G108400.7	0.06839912	-0.05388897	0.30831668	-0.17917	0.85780184	0.90278154	grey	0.00430222	0.99573265		AT4G37920.1		Kinase interacting (KIP1-like) family protein	KIP1-like protein	
Sapur.005G058900.1	0.34017543	0.07528399	0.51441446	0.178328	0.85823798	0.90320434	grey	-0.13658896	0.08804763	GO0008080	AT4G37570.2	NAGS2	N-acetyl-L-glutamate synthase	N-acetyl-glutamate synthase	
Sapur.003G082000.2	1.43967899	-0.03482642	0.19509673	-0.17851	0.85832168	0.90317585	grey	-0.01484194	0.86004636		AT4G16790.1		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative	
Sapur.003G022200.1	15.16766175	-0.07975233	0.15988296	-0.17807	0.85863843	0.90351183	grey	-0.00453026	0.95294669	GO0006334;GO0005634	AT3G19480.3	NAP1;2,NFA02,NFA2	nucleosome assembly protein 1,2	nucleosome assembly protein	
Sapur.011G058200.3	0.10660356	0.17600887	1.00954611	-0.1779	0.85879610	0.90362572	grey	-0.18809624	0.01832548		AT1G50130.1			transmembrane protein, putative	
Sapur.009G161100.4	0.06645264	-0.24822498	1.20047021	-0.17762	0.85902695	0.90379842	grey	-0.15372527	0.05457433	GO0004648;GO0004672;GO0005524	AT5G38350.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein	
Sapur.001G067800.4	0.12593388	0.3427887	0.82640494	0.17707	0.85907	0.90379842	grey	-0.02920438	0.75469945	GO0005515;GO0003700	AT3G26661.1		Mediator complex, subunit Med10	nutient reservoir protein, putative	
Sapur.013G131000.1	20.24339212	-0.09236429	0.10941694	-0.17715	0.85907726	0.90379842	grey	-0.32029274	4.33E-05	GO0005515	AT2G02680.1	ATNB51,NB51	nyingeen breakage syndrome 1	Mph-like DNA-binding domain protein	
Sapur.009G161200.1	0.06664247	0.17969051	1.01182279	-0.1775	0.85916399	0.90379842	grey	-0.13608827	0.08293136		AT5G41020.1		myb family transcription factor	NA	
Sapur.013G143400.3	0.23957082	0.09173625	0.51639207	0.177465	0.85919505	0.90379842	grey	-0.06079369	0.44951273	GO0004648;GO0005524;GO0004672	AT5G13670.1		Protein kinase family protein	casein kinase, putative	
Sapur.003G094100.1	1.38446024	0.09628148	0.51001	0.176944	0.85931032	0.90379842	grey	-0.01237004	0.87074883	GO0016491;GO0005515	AT4G12010.1		Flavoprotein monooxygenase (TR-NAB1-LRR class) family	NA	
Sapur.009G067000.1	19.94201483	0.01808104	0.10214139	0.177067	0.85942572	0.90409313	grey	-0.00896416	0.91127163		AT5G66310.1			hypothetical protein	
Sapur.009G132700.1	0.05585518	0.12443805	0.68507306	-0.1774	0.85947554	0.90409313	grey	-0.07843016	0.33462017	GO0005515;GO0045531	AT4G27120.1		NB-ARC domain-containing disease resistance protein	NA	
Sapur.006G022300.1	0.07025822	-0.24835957	1.40468004	-0.17684	0.85963846	0.90422464	grey	-0.18071767	0.02351504		AT3G56590.1		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative	
Sapur.016G097500.1	2.36558162	0.05585201	0.02888408	0.176713	0.85973377	0.90427185	grey	-0.01902784	0.81268089		AT5G03670.1		ankyrin repeat family protein	NA	
Sapur.013G078000.1	0.17549917	0.06035616	0.51307845	0.175602	0.85989204	0.90447295	grey	-0.04085217	0.61598611	GO0008270	AT3G60910.1		DHHC type zinc finger family protein	palmitoyltransferase ZDHHC15, putative	
Sapur.009G057900.1	0.11062301	0.17894362	1.01423908	0.176431	0.85995429	0.90449767	grey	-0.00785136	0.92188901	GO0046459;GO0016579	AT2G46840.1	UBP19	ubiquitin-specific protease 19	NA	
Sapur.006G161500.1	144.4952467	0.00350136	0.04423863	0.174221	0.85998169	0.90450788	grey	-0.02763634	0.75113493					NA	
Sapur.U019G076800.1	0.31995885	-0.07596198	0.43157586	-0.17063	0.86026537	0.90736151	grey	-0.07293388	0.36403901					NA	
Sapur.007G044000.2	0.06759434	0.26321916	1.51276818	0.170077	0.86031784	0.90756151	grey	0.08270326	0.29279041		AT1G07350.1			RWD-like protein, putative	
Sapur.005G076900.1	0.0779049	0.23283634	1.29796797	0.175941	0.86034026	0.90473273	grey	0.09643834	0.21668631	GO0008270;GO0003676;GO0004657;GO0003755;GO0000413	AT1G07320.1	ATCYP59,CYP59	cyclophilin 59	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein	
Sapur.U016G025400.1	5891.770025	-0.06602197	0.03017446	-0.17585	0.86042531	0.90476089	grey	0.04660582	0.52140805	GO0008312;GO0008324	AT5G44260.1		Transketolase	transketolase	
Sapur.005G069400.4	0.39406601	0.01615466	0.14873888	0.17585	0.86043175	0.90476089	grey	-0.0291008	0.71555262		AT5G08520.1		Duplicated homeodomain-like superfamily protein	MYB8 domain class transcription factor	
Sapur.019G042500.1	0.18449073	0.09237498	0.52587654	-0.17566	0.86058183	0.90487989	grey	-0.15102453	0.05801826	GO0007165;GO0005515;GO0043531	AT5G38930.1		Disease resistance protein (TIR-NBS-LRR class) family	NA	
Sapur.005G129900.1	0.07759944	0.22819877	1.32181193	0.17549	0.86069458	0.90492495	grey	0.08893055	0.27304225		AT5G19620.1			hypothetical protein	
Sapur.016G099800.2	2.76637475	-0.02815269	0.16250569	-0.17547	0.86070815	0.90492495	grey	0.22685667	0.00429743	GO0004648;GO0005524;GO0004672	AT5G06510.1		Protein kinase superfamily protein	tyrosine kinase domain protein	
Sapur.003G070000.1	0.03105049	-0.08082321	0.45468369	-0.17521	0.86083419	0.90518797	grey	-0.06717852	0.23267968					NA	
Sapur.004G009600.1	5.34074174	0.05301264	0.30261074	0.175169	0.86094077	0.90516454	grey	0.01575182	0.82709768	GO0005885;GO0016020;GO0005515	AT3G61690.1		MATE efflux family protein	MATE efflux family protein	
Sapur.U016G021100.2	29.77743334	0.01050387	0.05997927	0.175127	0.86097846	0.90522132	grey	0.00551650	0.94698612	GO0016020;GO0006486;GO0004376	AT3G46130.1	STT3B	oligosaccharyltransferase sensitive 3-like b	dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit STT3	
Sapur.006G204700.2	0.24617056	-0.09260713	0.53160422	-0.17474	0.86128854	0.90536447	grey	-0.07007068	0.18012724	GO0015136;GO0005515	AT4G32580.4		2Fe-2S ferredoxin-like superfamily protein	electron carrier/electron transporter/iron-ion binding protein, putative	
Sapur.U016G008700.1	0.21260034	0.07594747	0.53268071	-0.17464	0.86132146	0.90540124	grey	-0.37132214	1.66E-06	GO0005515	AT1G77210.1		PHD-finger family protein	PHD-Finger protein	
Sapur.017G028000.2	0.0542203	0.26765888	1.52427025	0.174603	0.86139383	0.90541403	grey	-0.03720124	0.64350742	GO0037723	AT5G17340.1	APO4	Arabidopsis thaliana protein of unknown function (DUF704)	APO RNA-binding protein	
Sapur.006G167000.1	1.76669466	0.06123869	0.33689571	-0.17444	0.86150315	0.90557498	grey	0.04653043	0.63428773	GO0016021	AT2G41530.1		Endomembrane protein 70 protein family	endomembrane family protein	
Sapur.019G088100.1	0.08717338	0.18709469	1.07057545	0.174356	0.86158353	0.9055572	grey	0.06960044	0.18639524		AT1G01240.1	ATVOZ1,VOZ1	vascular plant one zinc finger protein 1	transcription factor VOZ2	
Sapur.003G011000.2	1.53269119	0.03970645	0.23819408	-0.17409	0.86159757	0.90575887	grey	0.01978589	0.85751636		AT5G26690.1		Protein of unknown function (DUF841)	plant/NBC17-8 protein	
Sapur.009G283600.1	0.05195545	0.26765972	1.51962347	0.174024	0.86185439	0.90592375	grey	0.04431045	0.24008312		AT4G08801.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein, putative	
Sapur.T047000.1	1.05325908	-0.03947263	0.22737883	-0.1736	0.86218315	0.90607075	grey	-0.03055379	0.79450703					NA	
Sapur.U016G006001.1	711.0585351	0.00961129	0.05718807	0.173311	0.86246929	0.90618797	grey	-0.01889425	0.82553577	GO0005509	AT5G12330.1		Calcium-binding EF-hand family protein	calcium-binding protein CML7, putative	
Sapur.014G121100.2	0.15617626	0.12640938	0.72957426	0.173258	0.86244796	0.90624423	grey	-0.19188206	0.01063189	GO0007010;GO0005524;GO0003777;GO0005871	AT5G23670.1	KINESIN-12B,PAKRP1L	phragmoplast-associated kinesin-related protein, putative	kinesin-like protein	
Sapur.T048300.1	0.07168814	-0.21180856	1.21088526	-0.17303	0.86263482	0.90636123	grey	-0.12222602	0.02357522		AT1G69270.1		PLATZ transcription factor family protein	NA	
Sapur.013G108800.1	0.29100245	0.08144728	0.47072357	0.172939	0.86269665	0.90641535	grey	-0.05784557	0.45701385	GO0016567;GO0004842;GO0006468;GO0004672	AT4G09060.1		U-box domain-containing protein kinase family protein	tyrosine kinase family protein	
Sapur.T048400.1	37.46613468	0.01153000	0.07466254	0.172887	0.86272326	0.90647057	grey	-0.01408536	0.83326556	GO0004372;GO0003743	AT1G75350.1		eukaryotic translation initiation factor 5A1 family protein	NA	
Sapur.15WG048500.1	0.05688753	0.26791297	1.55085832	0.172754	0.86284609	0.90647253	grey	0.06937424	0.18609368	GO0016491;GO0009058	AT4T6000.1	SS3	stricticidine synthase 3	NA	
Sapur.T000200.1	0.96324603	0.04228304	0.34484181	0.17272	0.86287788	0.90652394	grey	0.07144054	0.37092938					endomembrane family protein	
Sapur.T100700.1	0.09742866	0.17984882	1.03916995	0.172719	0.86287939	0.90647253	grey	0.00410107	0.95925267	GO0005515;GO0046468;GO0005524;GO0004672	AT4G37530.1		Leucine-rich repeat protein kinase family protein	Leucine-rich repeat protein kinase family protein	
Sapur.005G037400.4	0.09978715	0.16547459	0.95861765	-0.17362	0.86295196	0.90652873	grey	-0.07136255	0.3746587		AT5G09440.1	ATCYSD1,CYSD1	cysteine synthase D1	cysteine synthase	
Sapur.U016J018000.2	0.10347721	0.25585653	1.48585566	-0.17306	0.86339412	0.90683757	grey	0.36891798	2.11E-06	GO0038324;GO0006470;GO0004722	AT5G48040.1		Protein phosphatase 2C family protein	protein phosphatase 2C	
Sapur.009G017500.9	3.80873953	0.03931256	0.23877948	-0.17262	0.86362430	0.90752446	grey	-0.16685781	0.03931343		AT3G22160.1		Cysteine proteinases superfamily protein	OTU-like cysteine protease	
Sapur.U016J008000.1	0.08159388	0.24326715	1.41790785	-0.17153	0.86380732	0.90774253	grey	0.08933926	0.24128607	GO0043565;GO0006355;GO0003700	AT4WRKY11,WRKY13		WRKY DNA-binding protein 11	WRKY transcription factor	
Sapur.010G045800.1	0.06296801	0.34155809	1.99156892	-0.17151	0.86386577	0.90770425	grey	-0.44287024	6.32E-09		AT5G45120.1	PDLP2	plasmodesmata-located protein 2	cysteine-rich repeat secretory	
Sapur.015G147000.1	0.28608526	0.06480454	0.55027921	-0.17118	0.86392429	0.90785285	grey	-0.01060604	0.86438449	GO0005634	AT4G24040.1	JMJ14,JMJD4TB	JUMONJI 14	lysine-specific demethylase 5A	
Sapur.018G025000.5	0.15376748	0.11795811	0.66434476	0.171316	0.86397595	0.90788718	grey	-0.04937562	0.58380243	GO0006355;GO0003700	AT5G11260.1	HYL1,ED 5	Basic-leucine zipper (bZIP) transcription family protein	bZIP transcription factor	
Sapur.U016G030001.1	0.16544843	0.07594747	0.5758451	-0.17108	0.86398279	0.90788718	grey	-0.10409269	0.18449628	GO0051114;GO0016491;GO0008270	AT5G42620.1		Gro/ES-like zinc-binding alcohol dehydrogenase family protein	2o-dependent alcohol dehydrogenase, class III	
Sapur.012G087400.1	12.32049898	-0.04125740	0.24115621	-0.17111	0.86413635	0.90791808	grey	-0.0326572	0.89472624		AT5G45160.1		Root hair defective 3 GTP-binding protein (RHD3)	ROOT HAIR defective-like protein	
Sapur.U016G084000.2	0.14318355	-0.13388627	0.78177452	-0.17102	0.86428849	0.90796352	grey	-0.02679491	0.79148169	GO0003676	AT4G35170.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in RNA-binding protein 34 (RBM34)-like protein	
Sapur.U016J008000.1	7.7972554	-0.00257686	0.10516802	-0.17086	0.86437037	0.90796854	grey	0.00151495	0.88461889	GO0005515	AT5G61160.1	SKIP8	STILAM 6+ ouvarol family protein	NA	
Sapur.008G067000.2	0.11971374	0.14882628	0.86768734	0.170647	0.86450	0.90785061	grey	-0.02208059	0.78249749	GO0020037	AT2G27110.2	IRS3	FARS-related sequence 3	FARS-related sequence protein	
Sapur.015G097600.1	22.51370965	0.01208864	0.12488863	0.170017	0.86456103	0.90814096	grey	0.00703079	0.93234002		AT4T4J5,IN5		formin-like 2 domain protein	formin-like 2 domain protein	
Sapur.017G010000.1	8.66379831	0.06904896	0.40874513	0.17051	0.86480921	0.90764352	grey	0.02367021	0.76815411				5-adenosyl-L-methionine-dependent methyltransferases superfluorin protein	NA	
Sapur.U016J025000.1	7.31247488	-0.01656169	0.10888693	0.170472	0.86488869	0.90784364	grey	0.00151495	0.88461889	GO0005515	AT5G61160.2	SKIP8	Transmembrane 4 L6 family protein	transmembrane fragile-X-F protein	
Sapur.007G001000.1	45.71624635	0.01434706	0.08108787	0.170075	0.86495157	0.90811088	grey	-0.01004584	0.90024166	GO0008236;GO0006508;GO0070008;GO0004252	AT5G03380.1		Prolyl oligopeptidase family protein	SIA prolyl oligopeptidase family, amino-terminal beta-propeller domain protein	
Sapur.T187000.1	0.18055333	0.08882377	0.62184	0.169963	0.86497463	0.90816487	grey	0.00702974	0.95234002		AT5G62460.1	CLE25	CLAVATA3/ESR-RELATED 25	peptide hormone	
Sapur.U016J14000.3	7.99270607	0.02763089	0.16259634	0.169826	0.86514695	0.90824887	grey	0.02806158	0.72718936	GO0016272;GO0006457	AT5G49510.2	PFD3	prefoldin subunit 3	prefoldin subunit 3	
Sapur.U016J004700.2	0.11650882	0.18128313	1.05747385	0.169661	0.86532468	0.90824887	grey	-0.00496463	0.95908341		AT2G27900.1			DUF3420 family protein	
Sapur.017G125100.1	1.26646675	-0.04519826	0.26198542	-0.1698	0.86556692	0.90824887	grey	-0.03288727	0.68717643					NA	
Sapur.U016J023000.1	65.71882088	0.00908994	0.05861829	-0.16956	0.86535968	0.90836429	grey	-0.02757775	0.73179707		AT4G25225.1			DUF4536 domain protein	
Sapur.U016J18500.1	0.1124642	-0.01136043	0.89607604	-0.16852	0.86569	0.90874023	grey	-0.05

Sapur.019G053300.1	2509.032194	-0.00656599	0.042497596	-0.1545	0.87721344	0.916650971	grey	-0.028830762	0.720016929	GO:0045454,GO:0015035,GO:0006662	AT5G16400.1	ATF2,TRXF2	thioredoxin F2	thioredoxin F-type protein
Sapur.010G017200.1	10.79771912	-0.015745018	0.101930013	-0.15447	0.877240023	0.916650971	grey	-0.007951258	0.921269765	GO:0000166,GO:0005525	AT5G18570.1	ATOBGC,CPSAR1,EMB269	GTP1/OBG family protein	Obg family GTPase CgtA
Sapur.011G023600.1	11.1293924	-0.022465734	0.145478206	-0.15443	0.87727322	0.916652619	grey	-0.030940757	0.700474022	GO:0004674,GO:0006468,GO:0004672	AT4G21380.1	ARK3,RK3	receptor kinase 3	NA
Sapur.T032700.1	0.076174499	0.189818082	1.229686125	0.154363	0.877323498	0.916652619	grey	0.027746816	0.730128353	GO:0005509	AT4G13440.1		Calcium-binding EF-hand family protein	EF-hand pair protein
Sapur.008G146700.3	0.129923194	0.124179832	0.804637944	0.15433	0.877349487	0.916652619	grey	-0.031544803	0.694914616		AT1G67720.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.016G198900.4	0.192282745	-0.093191876	0.603862566	-0.15433	0.877352461	0.916652619	grey	-0.069214362	0.389041595	GO:0016747	AT5G41130.1		Esterase/lipase/thioesterase family protein	esterase/lipase/thioesterase family protein
Sapur.013G056200.2	0.178637109	-0.103412207	0.671548049	-0.15399	0.877617006	0.91690049	grey	0.051451501	0.522200047	GO:0030955,GO:0006096,GO:0004743,GO:0000287	AT5G56350.1		Pyruvate kinase family protein	NA
Sapur.002G058300.2	1.204783802	0.035886185	0.233302549	0.153818	0.877753061	0.917001616	grey	0.028243291	0.725491169	GO:0006470,GO:0004722	AT1G43900.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.009G102300.1	1038.926847	-0.010800244	0.070223948	-0.1538	0.877769673	0.917001616	grey	-0.043376957	0.589595394	GO:0016020,GO:0006810,GO:0005215	AT4G23400.1	PIP1;5,PIP1D	plasma membrane intrinsic protein 1;5	aquaporin, MIP family%2C PIP subfamily protein
Sapur.005G120300.1	0.207289783	0.062750122	0.409050692	0.153404	0.878079479	0.917296294	grey	-0.051721181	0.520018708					NA
Sapur.013G036500.1	0.08437171	-0.250060162	1.630976196	-0.15332	0.878146465	0.917337298	grey	0.039745692	0.621145312		AT5G28150.1		Plant protein of unknown function (DUF868)	plant/T9J14-19 protein
Sapur.001G175800.1	0.06791949	0.234098719	1.527247835	0.153281	0.878176351	0.917339544	grey	0.108483446	0.176238969					hypothetical protein
Sapur.016G090500.1	0.200686237	-0.086852968	0.56714101	-0.15314	0.878286491	0.91742562	grey	-0.096959351	0.227032893	GO:0006468,GO:0004672	AT1G07570.2	APK1,APK1A	Protein kinase superfamily protein	tyrosine kinase
Sapur.15WG007600.1	4.505295542	0.020267454	0.132424344	0.153049	0.878359395	0.917452778	grey	0.045031824	0.575464166		AT3G26100.2		Regulator of chromosome condensation (RCC1) family protein	RCC1 and BTB domain protein, putative
Sapur.006G100200.2	0.093051759	0.163934317	1.07374602	0.152675	0.878654471	0.917669329	grey	-0.059940754	0.455833796		AT1G08080.1	ACA7,ATACA7	alpha carbonic anhydrase 7	carbonic anhydrase, putative
Sapur.002G170600.7	0.242448988	-0.084128537	0.551048309	-0.15267	0.878658532	0.917669329	grey	-0.030348275	0.705942485		AT3G07660.1		Kinase-related protein of unknown function (DUF1296)	DUF1296 family protein
Sapur.15WG049800.1	0.117276665	-0.131915211	0.86455997	-0.15258	0.878728904	0.917713846	grey	-0.105040123	0.190447483	GO:0005515	AT3G47570.1		Leucine-rich repeat protein kinase family protein	receptor kinase-like protein, putative
Sapur.005G135100.1	0.260962783	-0.067295926	0.442212534	-0.15218	0.879044928	0.918014902	grey	-0.0702818	0.381751601		AT1G43770.2		RING/FYVE/PHD zinc finger superfamily protein	hypothetical protein
Sapur.004G002300.2	0.753824644	-0.045831017	0.301252393	-0.15213	0.8790805	0.918023064	grey	0.018980694	0.813472895	GO:0016887,GO:0005524	AT4G04180.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	AAA family ATPase
Sapur.010G202900.1	2.135995348	0.030520003	0.201090471	0.151772	0.879366373	0.918292606	grey	0.007831296	0.922453842					NA
Sapur.016G298900.3	0.113783093	-0.145555521	0.959369751	-0.15172	0.87940783	0.918306904	grey	-0.11711816	0.144072627	GO:0008168,GO:0008152,GO:0006480	AT5G44450.1		methyltransferases	alpha amino-terminal protein methyltransferase
Sapur.016G258400.3	11.3498194	-0.015934328	0.10510842	-0.1516	0.879503246	0.918377544	grey	0.000128282	0.998727758		AT3G15355.1	PFU1,UBC25	ubiquitin-conjugating enzyme 25	ubiquitin-conjugating enzyme
Sapur.003G162400.4	0.174227068	-0.093063319	0.614324631	-0.15149	0.879590122	0.918439264	grey	-0.05705149	0.477878402		AT5G13000.1	ATGSL12,gsl12	glucan synthase-like 12	callose synthase
Sapur.011G091200.1	0.111225452	0.163335558	1.078476994	0.15145	0.879620591	0.918442083	grey	0.031411304	0.696141903	GO:0008270,GO:0003676				NA
Sapur.008G016000.3	0.431865001	0.064412877	0.425437899	0.151404	0.879657263	0.918451378	grey	0.039392739	0.624250317		AT3G52870.1		IQ calmodulin-binding motif family protein	calmodulin-binding family protein, putative
Sapur.010G079000.1	0.135483386	-0.133447058	0.883748107	-0.151	0.87997474	0.918724851	grey	-0.126257842	0.115100368	GO:0006468,GO:0004672	AT2G02800.2	APK2B	protein kinase 2B	tyrosine kinase domain protein
Sapur.001G133300.1	0.066128328	0.228744443	1.517757875	0.150712	0.880202845	0.918875983	grey	0.052899341	0.510543887		AT1G54070.1		Dormancy/auxin associated family protein	dormancy/auxin associated protein
Sapur.018G009300.1	4.333262844	0.022220353	0.147521343	0.150625	0.880271802	0.918918966	grey	0.015662575	0.84563159	GO:0016020,GO:0004970	AT2G29110.1	ATGLR2.8,GLR2.8	glutamate receptor 2.8	glutamate receptor
Sapur.003G090000.1	19.62278707	0.021345645	0.141911725	0.150415	0.880437245	0.919014666	grey	0.004940916	0.951028586		AT3G14260.1		Protein of unknown function (DUF567)	tubby C 2 protein
Sapur.008G102400.4	4.359857078	-0.023118124	0.153708073	-0.1504	0.880446838	0.919014666	grey	-0.015282777	0.849329893	GO:0055114,GO:0016972	AT2G01270.1	AtQSOX2,QSOX2	quiescin-sulfhydryl oxidase 2	protein disulfide-isomerase
Sapur.003G003700.1	0.139422744	-0.12712062	0.847100561	-0.15007	0.880712891	0.919263363	grey	-0.140911779	0.078356222	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G37370.1	CYP81D8	cytochrome P450, family 81, subfamily D, polypeptide 8	cytochrome P450 family protein
Sapur.001G095900.2	0.054344789	0.230095337	1.535025438	0.149897	0.880846069	0.919373356	grey	0.053966257	0.502041459		AT4G22740.2		glycine-rich protein	NA
Sapur.010G200700.1	0.115203242	-0.161979933	1.081510615	-0.14977	0.880944555	0.91941812	grey	-0.134208821	0.093780561		AT2G43870.1		Pectin lyase-like superfamily protein	endo-polygalacturonase
Sapur.008G016200.1	30.88461635	0.026962326	0.180172396	0.149647	0.881042828	0.919476112	grey	-0.174636725	0.028702792	GO:0033926	AT5G22510.1	At-A/N-InvE,INV-E	alkaline/neutral invertase	alkaline/neutral invertase
Sapur.006G002900.4	0.357230501	0.059968024	0.401695893	0.149287	0.881327076	0.919701259	grey	-0.032491901	0.686230593		AT5G47730.1		Sec14p-like phosphatidylinositol transfer family protein	SEC14 cytosolic factor, putative
Sapur.001G097700.2	0.188435264	0.090883073	0.609959111	0.148999	0.881554713	0.919870391	grey	-0.040612683	0.613546603		AT4G22670.1	AtHip1,HIP1	HSP70-interacting protein 1	Hsc70-interacting protein, putative
Sapur.004G146100.1	2.897234826	0.038151014	0.256069221	0.148987	0.881563801	0.919870391	grey	0.033701859	0.675195929	GO:0030247,GO:0006468,GO:0005524,GO:0004672	AT1G16120.1	WAKL1	wall associated kinase-like 1	NA
Sapur.006G017400.1	0.061203696	-0.210874093	1.415490577	-0.14898	0.881572588	0.919870391	grey	-0.187410723	0.018755823	GO:0016758,GO:0008152	AT3G22250.1		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase family protein
Sapur.004G103000.1	0.062127037	-0.196170428	1.319429983	-0.14868	0.881807592	0.920083667	grey	-0.165722411	0.038054455	GO:0006260,GO:0005524,GO:0003677	AT5G46280.1	MCM3	Minichromosome maintenance (MCM2/3/5) family protein	DNA replication licensing factor MCM3-like protein
Sapur.010G148200.1	0.060579467	0.245013574	1.648297574	0.148646	0.881832623	0.920083667	grey	0.129011484	0.107326155	GO:0006457,GO:0003755,GO:0000413	AT3G55920.1		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase
Sapur.016G036500.1	0.524291911	0.052974515	0.356677507	0.148522	0.881930696	0.920091448	grey	-0.021334092	0.790848119	GO:0008168,GO:0008152	AT2G41380.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosylmethionine-dependent methyltransferase, putative
Sapur.008G051800.1	81.13883596	0.01257352	0.084672457	0.148496	0.881951357	0.920091448	grey	-0.155789065	0.051373655	GO:0005515	AT5G05780.1	AE3,ATHMOV34,RPN8A	RP non-ATPase subunit 8A	26S proteasome regulatory particle non-ATPase subunit
Sapur.003G009700.1	0.212157762	-0.098451954	0.663184104	-0.14845	0.881984937	0.920096929	grey	-0.056317392	0.483570016		AT1G20600.1		AP2/B3-like transcriptional factor family protein	NA
Sapur.019G064200.1	0.240069263	0.073047534	0.492171645	0.148419	0.882012249	0.920096929	grey	-0.012260934	0.878865844		AT2G40810.2	ATATG18C,ATG18C	homolog of yeast autophagy 18C	autophagy-related protein 18c
Sapur.001G095500.1	1.415111391	-0.037103556	0.250085594	-0.14836	0.882055961	0.920099534	grey	-0.035137623	0.66219124	GO:0016192,GO:0006904	AT1G12360.1	KEU	Sec1/munc18-like (SM) proteins superfamily	SNARE-interacting protein KEULE protein
Sapur.001G069800.2	0.397254446	-0.060595455	0.408476143	-0.14835	0.882070385	0.920099534	grey	-0.046279146	0.564918908	GO:0006355,GO:0003677	AT4G24060.1		Dof-type zinc finger DNA-binding family protein	Dof zinc finger protein
Sapur.003G068900.1	18.60069187	0.019745058	0.133386979	0.148028	0.882320376	0.920331276	grey	0.011038624	0.890862865	GO:0005515	AT3G17380.1		TRAF-like family protein	ubiquitin carboxyl-terminal hydrolase, putative
Sapur.014G028000.1	0.062676889	0.266394494	1.800777653	0.147933	0.882395621	0.920351975	grey	0.073158445	0.362522838					NA
Sapur.002G170500.3	1.581389084	0.032126959	0.217293808	0.14785	0.882460896	0.920351975	grey	0.15702507	0.049530429		AT4G25330.1			hypothetical protein
Sapur.016G192100.2	2.464784458	-0.024706657	0.167115368	-0.14784	0.882467522	0.920351975	grey	-0.051095554	0.52508628	GO:0008270	AT1G04860.1	ATUBP2,UBP2	ubiquitin-specific protease 2	ubiquitin carboxyl-terminal hydrolase
Sapur.002G167600.1	25.17772797	-0.010608395	0.071762261	-0.14783	0.882479355	0.920351975	grey	-0.295204807	0.00017449		AT1G10660.3			transmembrane protein, putative
Sapur.019G025300.1	0.152664672	0.10700426	0.725270692	0.147537	0.88270818	0.920561592	grey	-0.033176447	0.679979295					NA
Sapur.017G067700.1	4.202238038	-0.021263931	0.144457319	-0.1472	0.88297518	0.920787431	grey	0.290717844	0.000221033	GO:0003676	AT1G14340.1		RNA-binding (RRM/RBD/RNP motifs) family protein	nucleic acid-binding protein
Sapur.008G025200.2	0.082408499	0.19069134	1.295527188	0.147192	0.882980413	0.920787431	grey	0.045376485	0.5725411	GO:0016192,GO:0006904	AT3G54860.1	ATVPS33,VPS33	Sec1/munc18-like (SM) proteins superfamily	vacuolar protein sorting-associated-like protein
Sapur.004G171800.1	116.274862	0.010864405	0.073885164	0.147044	0.883096914	0.920855949	grey	0.015483005	0.847379742		AT5G01910.1			hypothetical protein
Sapur.005G150800.1	0.094077538	0.16659413	1.133252015	0.147005	0.883127783	0.920855949	grey	0.001495839	0.985165757	GO:0006893,GO:0000145	AT1G21170.1	SEC5B	Exocyst complex component SEC5	NA
Sapur.004G049000.1	0.353681819	-0.054215919	0.368808226	-0.147	0.883129644	0.920855949	grey	-0.02362076	0.7690306		AT5G53280.1	PDV1	plastid division1	NA
Sapur.010G200300.1	0.060532364	0.20918307	1.425176821	0.146777	0.8833081	0.920983957	grey	0.049637514	0.536992758					transmembrane protein, putative
Sapur.010G163800.1	21.15133815	-0.01797608	0.122621836	-0.1466	0.883449561	0.921053655	grey	0.136972042	0.087152764		AT3G12590.1			hypothetical protein
Sapur.004G148600.1	0.072688996	-0.35852828	2.445693155	-0.1466	0.88345109	0.921053655	grey	-0.136899281	0.087322356	GO:0016579,GO:0004843	AT2G27350.1		OTU-like cysteine protease family protein	rice genome annotation project, cysteine-type peptidase%2C putative
Sapur.004G141000.1	0.056360252	0.207494122	1.418296941	0.146298	0.88368608	0.921257738	grey	0.065798718	0.412926194					NA
Sapur.T043500.1	0.151381293	-0.087049484	0.595137555	-0.14627	0.883709954	0.921257738	grey	-0.109600861	0.171800621		AT3G28455.1	CLE25	CLAVATA3/ESR-RELATED 25	NA
Sapur.016G020700.1	0.07121294	0.1910543	1.307455439	0.146127	0.883821278	0.921344752	grey	0.031834068	0.692258051		AT4G14965.1	AtMAPR4,MAPR4	membrane-associated progesterone binding protein 4	fiber protein Fb38
Sapur.008G037000.9	0.052158454	0.207496151	1.426178828	0.145491	0.884323239	0.921838969	grey	0.067022784	0.404269417	GO:0046540,GO:0000398	AT1G28060.1		Pre-mRNA-splicing factor 3	U4/U6 small nuclear ribonucleoprotein PRP3, putative
Sapur.009G042700.2	0.061529465	0.205731347	1.414939698	0.145399	0.884395558	0.9218853	grey	0.066734994	0.406294979	GO:0006508,GO:0004185	AT3G63470.1	scpl40	serine carboxypeptidase-like 40	serine carboxypeptidase
Sapur.006G127000.1	95.14481681	-0.009937134	0.068656165	-0.14474	0.884917985	0.922339449	grey	-0.00079745	0.992091357		AT5G19740.1		Peptidase M28 family protein	M28 Zn-peptidase family protein
Sapur.012G086600.1	0.061426563	0.191070932	1.32040532	0.144706	0.884942787	0.922339449	grey	0.046326129	0.564523506		AT5G45160.1		Root hair defective 3 GTP-binding protein (RHD3)	NA
Sapur.005G167200.4	0.093042613	0.125978237	0.873032067	0.1443	0.885263841	0.922636566	grey	0.020917798	0.794838123		AT3G22550.1		Protein of unknown function (DUF581)	senescence-associated protein SAG102
Sapur.014G121100.5	0.075518238	-0.175474121	1.218313767	-0.14403	0.885476528	0.922779427	grey	-0.028402029	0.724010612	GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT3G23670.1	KINESIN-12B,PAKRP1L	phragmoplast-associated kinesin-related protein, putative	kinesin-like protein
Sapur.003G012600.3	0.170676099	-0.084291825	0.585817348	-0.14389	0.885589265	0.922867835	grey	-0.081608864	0.309590942		AT1G11400.2	PYM	partner of Y14-MAGO	partner of Y14-mago protein, putative
Sapur.001G062300.5	0.197769769	-0.07334426	0.50991348	-0.14384	0.885629441	0.922880624	grey	-0.15003422	0.060719679					NA
Sapur.T128100.1	0.125278552	-0.111922446	0.780842385	-0.14334	0.886025208	0.923263949	grey	-0.147676252	0.064932181					NA
Sapur.018G090600.2	0.109299675	-0.143936957	1.007886557	-0.14281	0.886439708	0.923666769	grey	-0.027545072	0.732015487	GO:0031515,GO:0030488,GO:0016429	AT5G14600.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	tRNA (adenine-N(1))-methyltransferase catalytic subunit TRMT61A
Sapur.013G058300.1	7.285287709	-0.026734388	0.187316266	-0.14272	0.886508745	0.923668864	grey	-0.033463422	0.677365067		AT5G39160.1		RmlC-like cupins superfamily protein	NA
Sapur.003G095100.1	20.80895727	0.038062416	0.266775729	0.142676	0.886546301	0.923668864	grey	0.012695399	0.874608034					NA
Sapur.012G015500.1	0.156492081	-0.118239896	0.828784205	-0.14267	0.886553429	0.923668864	grey	-0.043232892	0.590833054	GO:0003677	AT2G33860.1	ARF3,ETT	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related	B3 DNA-binding domain protein
Sapur.012G032400.7	0.101645486	0.152097865	1.066748271	0.142581	0.88662123	0.92368131	grey	0.038825014	0.629258596	GO:0006468,GO:0004672	AT1G73660.1		protein tyrosine kinase family protein	tyrosine kinase domain protein
Sapur.019G093500.1	0.059942852	-0.283676416	1.995147173	-0.14218	0.886935299	0.923979403	grey	-0.134515975	0.093024617					NA
Sapur.007G119000.1	0.4994225	0.054803391	0.386454354	0.141811	0.887229474	0.924207827	grey	0.022396557	0.780689619		AT2G28580.1		Plant protein of unknown function (DUF247)	NA
Sapur.T106200.1	0.074623504	0.15301179	1.079138187	0.141791	0.887245307	0.924207827	grey	-0.013601827	0.865736634		AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO	exportin 1A	NA
Sapur.009G123700.1	3.3870603	0.022283809	0.157413803	0.141562	0.887426001	0.924345024	grey	-0.143628852	0.072717511	GO:0008270,GO:0006355	AT2G27110.2	FRS3	FAR1-related sequence 3	FAR1-related sequence protein
Sapur.017G054800.1	15.59186259	-0.019349722	0.136816621	-0.14143	0.887531716	0.924426024	grey	-0.01075328	0.893667194					hypothetical protein
Sapur.005G144100.1	0.462394506	0.079218405	0.560547443	0.141323	0.887614557	0.924483195	grey	-0.020228873	0.801452834	GO:0005509	AT1G21550.1		Calcium-binding EF-hand family protein	calcium-binding protein, putative
Sapur.003G062000.2	3.012632462	-0.029919306	0.21201195	-0.14112	0.887774473	0.924591521	grey	0.1363922	0.08851159	GO:0043565,GO:0006355,GO:0005634,GO:0003700	AT1G32330.1	ATHSFA1D,HSFA1D	heat shock transcription factor A1D	heat shock transcription factor 1
Sapur.011G015400.1	0.132514666	-0.187994109	1.33351633	-0.14098	0.887888718	0.924644976	grey	-0.105507915	0.188469607	GO:0055114,GO:0016491	AT4G21200.1	ATGA2OX8,GA2OX8	gibberellin 2-oxidase 8	gibberellin 2-beta-dioxygenase
Sapur.15WG001200.1	1142.958366	-0.004689887	0.033273478	-0.14095	0.88790967	0.924644976	grey	-0.034536365	0.66762525	GO:0016020	AT4G27585.1		SPFH/Band 7/PHB domain-containing membrane-associated protein family	band 7 family protein
Sapur.010G196400.2	0.096309721	-0.14212949	1.0091012	-0.14085	0.887990333	0.92469986	grey	-0.125498303	0.117320131		AT5G04840.1		bZIP protein	BZIP protein
Sapur.009G011700.2	0.077710719	-0.160958607	1.14405931	-0.14069	0.888114222	0.924794631	grey	-0.173296056	0.029969656	GO:0007165,GO:0006468,GO:0004672	AT2G26980.4	CIPK3,SnRK3.17	CBL-interacting protein kinase 3	CBL-interacting Serine/Threonine-kinase
Sapur.019G006400.1	0.103276215	-0.134867867	0.958810686	-0.14066	0.888137264	0.924794631	grey	-0.127831382	0.110605884					NA
Sapur.009G065400.1	0.099932205	0.151074305	1.074343976	0.14062	0.888170107	0.924799714	grey	-0.008955192	0.911367519		AT1G50060.1		CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein	pathogenesis-related protein
Sapur.001G180600.2	0.269149566	0.064585739	0.459953942	0.140418	0.888329864	0.924936941	grey	-0.076691145	0.339747028	GO:0005524,GO:0003676,GO:0004386	AT1G58060.1		RNA helicase family protein	RNA helicase
Sapur.013G033600.2	0.078395063	-0.21080855	1.50186725	-0.14036	0.888372161	0.924951862	grey	0.289100708	0.000240466	GO:0005515	AT3G05090.2	LRS1	Transducin/WD40 repeat-like superfamily protein	salt-induced WD protein
Sapur.001G139900.1	0.139758336	0.099754468	0.712981379	0.139912	0.888729722	0.925215736	grey	0.007835298	0.922414338		AT4G17330.1	ATG2484-1,G2484-1	G2484-1 protein	agenet domain protein
Sapur.014G042200.1	1922.317544	-0.052331804	0.374060697	-0.1399	0.888737495	0.925215736	grey	-0.012279334	0.878685444	GO:0005515	AT3G17380.1		TRAF-like family protein	NA
Sapur.004G054000.3	0.135973993	-0.101150568	0.723358333	-0.13983	0.888790626	0.925240392	grey	-0.076529886	0.340766465		AT5G02520.1			NA
Sapur.013G080200.1	64.13251356	0.018425427	0.13179742	0.139801	0.88881713	0.925240392	grey	0.008940673	0.911510631	GO:0055085,GO:0016020	AT5G12080.3	ATMSL10,MSL10	mechanosensitive channel of small conductance-like 10	NA
Sapur.008G051200.1	623.9391991	-0.00712612	0.051151004	-0.13932	0.889200964	0.925581692	grey	-0.035650801	0.657567152	GO:0016021,GO:0008233,GO:0006465,GO:0005787	AT2G39960.1		Microsomal signal peptidase 25 kDa subunit (SPC25)	NA
Sapur.007G006600.1	0.100433516	0.126269288	0.907594096	0.139125	0.889351147	0.925708361	grey	0.029483443	0.713951676		AT2G22795.1			transmembrane protein, putative
Sapur.T136000.1	906.6974555	-0.008322553	0.059835522	-0.13909	0.889378632	0.925708361	grey	-0.01936261	0.80979025	GO:0008536,GO:0006886	AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO	exportin 1A	NA
Sapur.009G085100.1	0.058261177	0.230175697	1.657930408	0.138833	0.889582	0.925861761	grey	0.07270458	0.365516097	GO:0035091	AT2G15900.1		Phox-associated domain;Phox-like;Sorting nexin, C-terminal	sorting nexin-16 protein
Sapur.002G036500.1	0.077894017	-0.170167123	1.22843496	-0.13852	0.88982669	0.926058148	grey	-0.16455996	0.039444886					NA
Sapur.013G077500.1	0.111411464	0.108802383	0.786043255	0.138418	0.889910225	0.926115943	grey	-0.033078369	0.680873624					NA
Sapur.017G000300.1	1.499080552	0.034159826	0.246858396	0.138378	0.889941507	0.926119356	grey	0.022899955	0.775889295	GO:0005515	AT2G44130.1		Galactose oxidase/kelch repeat superfamily protein	NA
Sapur.006G180900.3	0.061235325	-0.210789798	1.529786948	-0.13779	0.890406153	0.926518159	grey	-0.315001412	5.86E-05	GO:0044237	AT2G05830.1		NagB/RpiA/CoA transferase-like superfamily protein	methylthioribose-1-phosphate isomerase
Sapur.T071200.1	27.84497016	-0.034582032	0.250981844	-0.13779	0.890408771	0.926518159	grey	-0.001993517	0.980231154		AT3G18670.1		Ankyrin repeat family protein	inversin, putative
Sapur.008G049200.2	0.052601278	0.230183559	1.671686944	0.137695	0.890481175	0.926554762	grey	0.060769995	0.449613105		AT5G05930.1	ATGC1,GC1	guanylyl cyclase 1	guanylyl cyclase
Sapur.004G061900.1	0.070951327	0.192506041	1.398298999	0.137672	0.890499976	0.926554762	grey	0.052743758	0.511789951		AT5G16620.1	ATTIC40,PDE120,TIC40	hydroxyproline-rich glycoprotein family protein	translocon Tic40 protein
Sapur.008G134700.1	0.119892002	-0.131794489	0.957701214	-0.13762	0.89054434	0.926571772	grey	-0.067570836	0.400428628	GO:0006355,GO:0003700	AT3G23230.1		Integrase-type DNA-binding superfamily protein	NA
Sapur.007G103400.2	0.1007687	0.124823218	0.907357839	0.137568	0.890582008	0.926581816	grey	-0.012724567	0.87432231		AT4G33625.1			COPI associated protein
Sapur.010G062400.1	171.6815845	0.006426364	0.046767549	0.137411	0.890706131	0.926681805	grey	0.008627397	0.914599276		AT4G14820.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.007G089600.1	0.122613178	0.124122459	0.903992212	0.137305	0.890789886	0.92673979	grey	0.002615405	0.974066056	GO:0008270	AT5G08750.2		RING/FYVE/PHD zinc finger superfamily protein	zinc finger protein
Sapur.006G094400.2	0.262397014	0.058359258	0.425391839	0.137189	0.890881077	0.926805509	grey	-0.114472054	0.153416821	GO:0043169,GO:0005975,GO:0003824,GO:0004553	AT5G03650.1	SBE2.2	starch branching enzyme 2.2	starch branching enzyme II
Sapur.018G027200.1	0.067346507	-0.244418347	1.782835148	-0.1371	0.890955455	0.926853733	grey	-0.21214367	0.007645385					hypothetical protein
Sapur.018G022600.1	0.683771583	0.055083107	0.402050708	0.137005	0.891026549	0.926898537	grey	0.045874089	0.568333286		AT4G32272.1		Nucleotide/sugar transporter family protein	NA
Sapur.005G182200.2	0.058272973	-0.20893267	1.526943286	-0.13683	0.891164642	0.926987095	grey	-0.196918836	0.013438882		AT1G75250.1	ATRL6,RL6,RSM3	RAD-like 6	Myb transcription factor
Sapur.008G000400.1	0.249816181	0.062635582	0.45791028	0.136786	0.89120018	0.926987095	grey	-0.028145562	0.726403202		AT5G52552.1	CPuORF14	conserved peptide upstream open reading frame 14	NA
Sapur.009G027500.1	0.204240831	0.107034668	0.783990928	0.136525	0.891405954	0.927118255	grey	0.028737389	0.720886068					hypothetical protein
Sapur.002G167400.2	0.072689784	0.191163852	1.401038002	0.136444	0.891469941	0.927142975	grey	0.021466767	0.789577615	GO:0003824,GO:0006470,GO:0004722	AT3G62260.2		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.018G111900.1	0.062681537	0.168187749	1.232827485	0.136424	0.891485786	0.927142975	grey	0.03159833	0.694422751		AT5G12060.1		Plant self-incompatibility protein S1 family	NA
Sapur.002G009400.1	0.214545339	0.071943093	0.52823937	0.136194	0.891667828	0.927231162	grey	0.34858212	7.68E-06	GO:0008236,GO:0006508,GO:0070008,GO:0004252	AT1G76140.1		Prolyl oligopeptidase family protein	prolyl oligopeptidase
Sapur.016G040300.2	0.104716801	0.147519222	1.08319942	0.136188	0.891672326	0.927231162	grey	0.003729058	0.963029904		AT4G20990.1	ACA4,ATACA4	alpha carbonic anhydrase 4	carbonic anhydrase, putative
Sapur.018G103900.2	0.104045196	0.153279907	1.125607483	0.136175	0.891682722	0.927231162	grey	0.081392944	0.310877053	GO:0009058,GO:0003824	AT2G38670.1	PECT1	phosphorylethanolamine cytidylyltransferase 1	ethanolamine-phosphate cytidylyltransferase
Sapur.001G108900.1	0.060503727	-0.246264549	1.809987708	-0.13606	0.891774888	0.927279564	grey	0.313262826	6.47E-05	GO:0006355,GO:0005634,GO:0005524,GO:0032502,GO:0006351	AT4G37740.1	AtGRF2,GRF2	growth-regulating factor 2	growth-regulating factor, putative
Sapur.003G083700.1	0.19335615	-0.077842522	0.572323305	-0.13601	0.89181223	0.927279564	grey	-0.057988153	0.470669253	GO:0055114,GO:0004616,GO:0051287,GO:0016616,GO:0008152	AT1G12550.1		D-isomer specific 2-hydroxyacid dehydrogenase family protein	D-isomer specific 2-hydroxyacid dehydrogenase family protein, putative
Sapur.008G132400.1	0.059537785	0.192522719	1.415504176	0.13601	0.891813378	0.927279564	grey	0.035684429	0.657264587					transmembrane protein, putative
Sapur.019G036000.1	6.370412871	-0.028969558	0.213102857	-0.13594	0.891867394	0.92728309	grey	-0.025767901	0.748707587		AT5G45520.1		Leucine-rich repeat (LRR) family protein	hypothetical protein
Sapur.007G105900.1	0.144183246	0.098775026	0.726780757	0.135908	0.89189433	0.92728309	grey	-0.047719903	0.552854062	GO:0003677				B3 DNA-binding domain protein
Sapur.013G073300.2	1.575886708	-0.026784604	0.19713844	-0.13587	0.891926443	0.92728309	grey	-0.017543272	0.827369298		AT5G17690.1	LHP1,TFL2	like heterochromatin protein (LHP1)	chromo domain protein
Sapur.T051000.1	0.058021556	0.207519224	1.527405762	0.135864	0.891928916	0.92728309	grey	0.092148256	0.251038056		AT1G04080.1	PRP39	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.019G025600.1	0.052218851	-0.208924547	1.539710985	-0.13569	0.892065756	0.92730876	grey	-0.201584911	0.011350688					NA
Sapur.005G105100.1	0.065312163	0.205760752	1.520298288	0.135342	0.892341198	0.927539428	grey	0.077560049	0.334287419		AT2G23620.1	ATMES1,MES1	methyl esterase 1	alpha/beta hydrolase fold protein
Sapur.T181300.1	1.045011664	-0.032348348	0.23901696	-0.13534	0.892343746	0.927539428	grey	-0.038903536	0.628564893		AT3G28455.1	CLE25	CLAVATA3/ESR-RELATED 25	NA
Sapur.T024000.1	0.564516707	0.047480336	0.351197137	0.135196	0.892457162	0.927606234	grey	-0.015517497	0.847043899		AT3G60470.1		Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.013G095400.1	0.147875585	0.116771514	0.863778373	0.135187	0.89246411	0.927606234	grey	0.015383182	0.848351871					NA
Sapur.006G124100.2	0.169570454	0.083508187	0.618009146	0.135125	0.892513427	0.927628341	grey	-0.007983266	0.920953854	GO:0006468,GO:0004672	AT3G13690.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	somatic embryogenesis receptor kinase
Sapur.002G152300.1	0.167365005	-0.094556701	0.703794497	-0.13435	0.893123671	0.928180678	grey	-0.096026057	0.231558081		AT2G47940.1	DEGP2	DEGP protease 2	NA
Sapur.006G151000.2	0.10607287	-0.143785105	1.070260331	-0.13435	0.893129046	0.928180678	grey	-0.095733524	0.232989434	GO:0008725,GO:0006284	AT5G57970.2		DNA glycosylase superfamily protein	DNA-3-methyladenine glycosylase, putative
Sapur.15WG057900.1	0.053652387	-0.244404312	1.819946575	-0.13429	0.893171659	0.928195797	grey	-0.188205323	0.018250533		AT1G73890.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/LTP family protein
Sapur.004G005000.2	0.113839548	0.116701827	0.869961052	0.134146	0.893287097	0.928280916	grey	-0.013274875	0.868934707	GO:0006629,GO:0006508,GO:0004190	AT1G62290.1		Saposin-like aspartyl protease family protein	aspartic proteinase oryzasin protein
Sapur.013G109100.1	11.62023868	-0.015591938	0.116255844	-0.13412	0.893309699	0.928280916	grey	0.191756583	0.016133866	GO:0006887,GO:0000145	AT1G71820.1	SEC6	SEC6	exocyst complex subunit SEC6, putative
Sapur.013G043800.2	0.079895015	0.153145917	1.142448867	0.134051	0.89336259	0.928306711	grey	0.124602684	0.11998018		AT1G10095.1		Protein prenylyltransferase superfamily protein	protein prenyltransferase, alpha subunit
Sapur.008G170300.1	3.160512872	0.032581082	0.243354105	0.133883	0.893494753	0.928342471	grey	0.013597415	0.865779774					NA
Sapur.013G107400.1	0.051317971	-0.244402198	1.825746184	-0.13386	0.893509897	0.928342471	grey	-0.196317103	0.013731266	GO:0016788	AT1G29670.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.013G074200.1	0.136260825	0.11028916	0.824199505	0.133814	0.893549917	0.928342471	grey	-0.000162602	0.998387382	GO:0051082,GO:0015631,GO:0007021	AT2G30410.2	KIS,TFCA	tubulin folding cofactor A (KIESEL)	tubulin folding cofactor A
Sapur.018G105200.1	0.519489036	0.04346901	0.32486921	0.133805	0.893557053	0.928342471	grey	0.003594483	0.964363187					NA
Sapur.003G150400.2	0.463546465	-0.046858623	0.350229446	-0.13379	0.893565416	0.928342471	grey	-0.034468374	0.668240827	GO:0008270	AT3G15140.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	exonuclease
Sapur.019G007300.1	0.610540316	0.050849718	0.380247384	0.133728	0.893617673	0.9283676	grey	-0.025315303	0.752977666		AT1G14870.1	PCR2	PLANT CADMIUM RESISTANCE 2	NA
Sapur.001G092300.1	0.106708847	0.127542948	0.954325505	0.133647	0.893681545	0.928399245	grey	0.029853838	0.710517579		AT1G12560.1	ATEXP7.ATEXPA7.ATHEXP A	expansin A7	expansin-A7 protein
Sapur.001G123200.1	1290.617381	0.006133823	0.045912565	0.133598	0.893720538	0.928399245	grey	0.034229444	0.670405808	GO:0005524,GO:0006508,GO:0004176,GO:0004252,GO:0030163	AT5G47040.1	LON2	lon protease 2	Lon protease-like, peroxisomal protein
Sapur.004G102100.2	4.853018937	-0.022974702	0.171988245	-0.13358	0.893732344	0.928399245	grey	-0.01983057	0.805283613	GO:0005975,GO:0004553	AT1G30080.1		Glycosyl hydrolase superfamily protein	glycoside hydrolase family 17 protein
Sapur.005G155600.1	12.68736361	0.014206367	0.106448893	0.133457	0.893831846	0.928473444	grey	0.016919555	0.8334161		AT1G71740.1			transmembrane protein, putative
Sapur.017G066700.1	0.080078088	0.128505698	0.963901052	0.133318	0.893941616	0.928558305	grey	0.024930284	0.756616075					NA
Sapur.007G056900.1	0.070971694	-0.173509171	1.302228856	-0.13324	0.894003457	0.928593378	grey	-0.180770968	0.023472678		AT4G35730.1		Regulator of Vps4 activity in the MVB pathway protein	NA
Sapur.013G084500.1	0.212016576	-0.081617534	0.61331998	-0.13307	0.894134096	0.928699905	grey	0.009629394	0.904725115					NA
Sapur.T046500.2	5.461772817	0.016099087	0.121146662	0.132889	0.894280981	0.928794133	grey	0.04927192	0.539999163	GO:0030259,GO:0016758,GO:0005975,GO:0008152	AT3G07020.1		UDP-Glycosyltransferase superfamily protein	UDP-glucose:sterol glucosyltransferase
Sapur.003G035800.2	3.446553264	-0.020374293	0.15357157	-0.13267	0.894454613	0.928945295	grey	-0.04373921	0.586488526		AT1G17455.2	ELF4-L4	ELF4-like 4	ELF4-like protein
Sapur.016G257700.2	0.092253849	0.142218108	1.072614799	0.13259	0.894517559	0.928959057	grey	-0.13785077	0.085125349	GO:0006468,GO:0005524,GO:0004672,GO:0005515	AT3G15354.1	SPA3	SPA1-related 3	ubiquitin ligase cop1, putative
Sapur.011G067000.1	0.167543269	-0.087855016	0.663285069	-0.13245	0.8946249	0.929034631	grey	-0.100584707	0.210048236		AT1G43760.1		DNAse I-like superfamily protein	NA
Sapur.005G094300.1	0.10295143	-0.10867619	0.821663668	-0.13226	0.894775802	0.929162162	grey	-0.128852775	0.107762746	GO:0005515	AT3G54350.3	emb1967	Forkhead-associated (FHA) domain-containing protein	micro-spherule protein, amino-terminal domain protein
Sapur.T104200.1	0.151728661	0.081200094	0.614321884	0.132178	0.894843172	0.929200712	grey	-0.027257783	0.734705598		AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO	exportin 1A	NA
Sapur.15WG049300.1	0.095599758	0.13231455	1.001278377	0.132146	0.894869114	0.929200712	grey	-0.042002874	0.60144794	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT3G47570.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.006G045200.1	0.10742785	0.116442166	0.882273732	0.13198	0.895000399	0.929307858	grey	-0.005617533	0.944332506	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G42250.1	CYP712A1	cytochrome P450, family 712, subfamily A, polypeptide 1	cytochrome P450 family protein
Sapur.005G107400.1	581.4781756	0.003713306	0.028167347	0.13183	0.895118614	0.929385273	grey	0.02588421	0.747611478		AT4G37040.1	MAP1D	methionine aminopeptidase 1D	methionine aminopeptidase
Sapur.009G094800.1	590.0908168	-0.032445148	0.246142812	-0.13181	0.895131156	0.929385273	grey	-0.054066961	0.501242776	GO:0043565,GO:0006355,GO:0003700	AT1G75390.1	AtbZIP44,bZIP44	basic leucine-zipper 44	BZIP transcription factor
Sapur.003G014000.1	484.6865058	0.004550795	0.034579536	0.131604	0.895297747	0.929529059	grey	0.024649342	0.759274343	GO:0071805,GO:0016020,GO:0015079	AT5G09400.1	KUP7	K+ uptake permease 7	potassium transporter
Sapur.016G273100.3	0.082856798	0.14221347	1.081144987	0.13154	0.895348396	0.92955162	grey	-0.025496716	0.7512652	GO:0008168,GO:0008152	AT3G20650.1		mRNA capping enzyme family protein	methyltransferase domain protein
Sapur.016G162600.1	1.853849553	-0.025325236	0.192728515	-0.1314	0.89545598	0.929605797	grey	-0.030895399	0.700892126		AT1G07170.1		PHF5-like protein	NA
Sapur.002G123700.3	0.129403552	0.10764958	0.820119693	0.131261	0.895568988	0.929664753	grey	0.017097772	0.83168731	GO:0016757,GO:0047262	AT3G61130.1	GAUT1,LGT1	galacturonosyltransferase 1	alpha-1%2C4-galacturonosyltransferase
Sapur.007G037600.3	1.022472746	0.031571583	0.240712616	0.131159	0.895649669	0.929719326	grey	0.014460573	0.857347312	GO:0006629	AT2G26560.1	PLA IIA,PLA2A,PLP2	phospholipase A 2A	patatin-like phospholipase
Sapur.003G090700.1	4929.569104	0.004597622	0.035138251	0.130844	0.895898873	0.929919637	grey	-0.016944876	0.833170418	GO:0055114,GO:0016491,GO:0016209,GO:0006979,GO:0004602	AT4G11600.1	ATGPX6.GPX6.LSC803.PHGP	glutathione peroxidase 6	NA
Sapur.018G099700.1	0.083846127	-0.140114844	1.071825731	-0.13073	0.895992541	0.929987676	grey	-0.156280065	0.050634742		AT5G52580.1		RabGAP/TBC domain-containing protein	RabGAP/TBC domain protein
Sapur.002G115500.1	0.143142481	-0.097799764	0.748637691	-0.13064	0.89606249	0.930031093	grey	-0.066966868	0.404662505		AT2G44950.1	HUB1,RDO4	histone mono-ubiquitination 1	histone ubiquitination protein group protein
Sapur.002G129700.2	0.079671283	-0.140108523	1.074866651	-0.13035	0.896289777	0.930206336	grey	-0.15507035	0.052471358	GO:0016161,GO:0000272	AT2G45880.1	BAM7,BMY4	beta-amylase 7	beta-amylase
Sapur.T166800.1	0.0768094	-0.196139608	1.505012173	-0.13032	0.896309882	0.930206336	grey	0.186777442	0.019167164		AT1G21080.3		DNAJ heat shock N-terminal domain-containing protein	DnaJ heat shock amino-terminal domain protein
Sapur.004G145200.2	0.122080264	0.11165743	0.86382043	0.12926	0.89715192	0.930957318	grey	-0.016737197	0.835185881	GO:0006468,GO:0005524,GO:0004672	AT1G21230.1	WAK5	wall associated kinase 5	tyrosine kinase domain protein
Sapur.006G102600.1	4.29244158	-0.021769122	0.168644029	-0.12908	0.897291765	0.93105359	grey	-0.157925051	0.048223153		AT5G65560.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.012G093900.1	16.77629025	-0.014449698	0.111951028	-0.12907	0.897300997	0.93105359	grey	-0.007082475	0.929848775	GO:0055114,GO:0032542	AT1G31170.4	ATSRX,SRX	sulfiredoxin	sulfiredoxin, putative
Sapur.004G074300.1	28.85966983	0.008040613	0.062326652	0.129008	0.897351615	0.931076902	grey	-0.009985808	0.901216272		AT5G38880.1			NA
Sapur.011G045300.1	20.57452514	-0.043758889	0.339697804	-0.12882	0.897502367	0.931117506	grey	-0.017032492	0.832320464		AT5G45900.1	APG7.ATAPG7.ATATG7.ATG	ThiF family protein	hypothetical protein
Sapur.007G039300.1	0.068431202	0.194034751	1.506295561	0.128816	0.897503359	0.931117506	grey	0.08946225	0.26517756	GO:0008146	AT3G50620.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	sulfotransferase domain protein
Sapur.011G097700.1	0.116901037	0.111680163	0.867584791	0.128725	0.897574969	0.93116259	grey	0.155937296	0.051149644		AT5G54660.1		HSP20-like chaperones superfamily protein	small heat-shock protein, putative
Sapur.010G143900.1	1.428353735	0.030496281	0.237007966	0.128672	0.897617218	0.931177212	grey	0.059604738	0.458368063	GO:0033925,GO:0005737	AT5G05460.1		Glycosyl hydrolase family 85	endo-beta-N-acetylglucosaminidase
Sapur.014G034200.1	0.115055311	-0.096313263	0.750741364	-0.12829	0.897918789	0.931382233	grey	-0.177867412	0.025836224		AT3G60410.3		Protein of unknown function (DUF1639)	DUF1639 family protein
Sapur.001G104200.2	0.190471883	0.088076515	0.687666198	0.12808	0.898085401	0.931516811	grey	-0.00341163	0.966174949	GO:0003723,GO:0003676,GO:0045131,GO:0000398	AT5G51300.1		splicing factor-related	zinc finger protein, putative
Sapur.010G098500.2	0.121451856	0.109654327	0.858353464	0.12775	0.898347122	0.931759054	grey	0.012357112	0.877922981		AT1G25500.2		Plasma-membrane choline transporter family protein	plasma-membrane choline transporter-like protein
Sapur.013G020200.1	0.129185622	-0.109892018	0.862134892	-0.12746	0.898572379	0.931963463	grey	-0.122001156	0.127972463					NA
Sapur.005G123300.2	0.152024876	-0.097833607	0.769496247	-0.12714	0.898829743	0.932201158	grey	-0.096286656	0.230288199	GO:0016567,GO:0004842,GO:0005515	AT2G23140.1		RING/U-box superfamily protein with ARM repeat domain	U-box protein
Sapur.012G065400.1	0.056041014	0.194051064	1.528749461	0.126935	0.898992232	0.932340444	grey	0.015438054	0.847817472		AT5G63050.1	EMB2759	embryo defective 2759	embryo defective 2759 protein
Sapur.005G091400.1	26.23228161	0.027093655	0.21351973	0.126891	0.899026954	0.932340895	grey	0.021210599	0.792031186		AT1G71950.1		Proteinase inhibitor, propeptide	NA
Sapur.008G032300.1	0.1285666	-0.108501359	0.855265848	-0.12686	0.899049046	0.932340895	grey	-0.060494037	0.45167794	GO:0005515	AT2G34900.1	GTE01,GTE1,IMB1	Transcription factor GTE6	global transcription factor group protein, putative
Sapur.013G054800.2	0.086484032	0.12856078	1.015118299	0.126646	0.899220503	0.932484382	grey	-0.133246263	0.096181173	GO:0005515,GO:0016568,GO:0005634	AT1G54390.4	ING2	PHD finger protein-related	PHD-finger protein
Sapur.T151100.1	0.0688206	0.154818486	1.22273377	0.126617	0.899243797	0.932484382	grey	-0.053936962	0.502273921					NA
Sapur.003G103200.3	0.068088409	0.154819784	1.223590456	0.126529	0.899313126	0.932527035	grey	0.053755403	0.503715886	GO:0008270	AT4G23860.2		PHD finger protein-related	E3 ubiquitin-protein ligase UBR7, related protein%2C putative
Sapur.003G116600.2	0.059646458	-0.208859968	1.65469142	-0.12622	0.899555476	0.932749093	grey	-0.374264507	1.37E-06	GO:0006221,GO:0003883	AT1G30820.1		CTP synthase family protein	CTP synthase
Sapur.004G175700.2	0.07794168	0.153452874	1.219056913	0.125878	0.89982822	0.932973402	grey	0.055266468	0.491781053		AT3G23590.1	MED33A,RFR1	REF4-related 1	hypothetical protein
Sapur.002G140400.1	168.2472943	0.045525051	0.36202227	0.125752	0.89992818	0.933047794	grey	0.026199703	0.744640799		AT2G02560.2	ATCAND1.CAND1.ETA2.HVE	cullin-associated and neddylation dissociated	NA
Sapur.15WG131500.2	0.077748174	-0.175278809	1.395907936	-0.12557	0.900075346	0.933171123	grey	-0.150478738	0.059951238		AT1G10180.1			plant/F14N23-6 protein, putative
Sapur.006G052700.1	0.221802234	-0.059497889	0.475461253	-0.12514	0.900414935	0.933464676	grey	-0.072847911	0.36456918		AT3G53270.1		Small nuclear RNA activating complex (SNAPc), subunit SNAP43 protein	small nuclear RNA activating complex (SNAPc), subunit SNAP43
Sapur.009G017100.1	0.071944688	0.143876945	1.152207686	0.124871	0.900625939	0.93365416	grey	0.003198926	0.96828269		AT3G58000.1		VQ motif-containing protein	NA
Sapur.007G027800.2	13.11377074	-0.009754459	0.078240697	-0.12467	0.900782878	0.933758318	grey	-0.098912037	0.217767908		AT4G36800.1	RCE1	RUB1 conjugating enzyme 1	ubiquitin-conjugating enzyme
Sapur.006G176300.7	3.508609882	0.018191403	0.146000455	0.124598	0.900841607	0.933771135	grey	0.078548531	0.32814497	GO:0008270,GO:0003676	AT3G53500.2	RSZ32	RNA-binding (RRM/RBD/RNP motifs) family protein with retrovirus zinc finger-like domain	RNA recognition motif, a.k.a. RRM%2C RBD protein
Sapur.005G180200.3	0.222653163	-0.062898819	0.504864677	-0.12459	0.900851708	0.933771135	grey	-0.057769536	0.472346531		AT2G20495.1			Serine/Threonine-kinase, putative
Sapur.004G034600.1	0.10969772	0.112985496	0.907975198	0.124437	0.900969466	0.933853063	grey	-0.109146007	0.173597188		AT1G28540.1			transmembrane protein, putative
Sapur.006G173400.1	0.150787269	-0.085799991	0.689631028	-0.12441	0.900987218	0.933853063	grey	-0.08725729	0.277183597	GO:0006310,GO:0006281,GO:0006260,GO:0005634,GO:0003677	AT3G52630.2		Nucleic acid-binding, OB-fold-like protein	replication protein A 14 kDa subunit A
Sapur.005G204900.1	5.009809036	0.016447311	0.132371707	0.124251	0.901116576	0.933957872	grey	-0.01608297	0.841541895	GO:0055085,GO:0022857,GO:0016021	AT1G76430.1	PHT1;9	phosphate transporter 1;9	inorganic phosphate transporter, putative
Sapur.014G057600.1	97.71146521	-0.01058115	0.085209553	-0.12418	0.901174361	0.933988494	grey	-0.016451657	0.837958706	GO:0055085	AT1G12600.1		UDP-N-acetylglucosamine (UAA) transporter family	adenosine 3'-phospho 5'-phosphosulfate transporter 2
Sapur.008G008300.1	48.76550408	0.012742393	0.10291039	0.12382	0.901457579	0.934223474	grey	0.007117214	0.929505576		AT5G04890.1	RTM2	HSP20-like chaperones superfamily protein	HSP20/alpha crystallin family protein
Sapur.009G029000.1	21.50980113	0.012167995	0.098888539	0.123048	0.902069423	0.934798975	grey	0.004598018	0.954423387	GO:0016758,GO:0008152	AT5G59590.1	UGT76E2	UDP-glucosyl transferase 76E2	UDP-glycosyltransferase
Sapur.007G099300.3	0.225689095	-0.064692135	0.526862408	-0.12279	0.902275347	0.934983075	grey	-0.060210833	0.453802501	GO:0005515	AT5G24320.1		Transducin/WD40 repeat-like superfamily protein	WD40 domain protein
Sapur.010G061000.1	362.8558408	0.005492961	0.044847899	0.12248	0.902519049	0.93520631	grey	-0.273763894	0.000521698	GO:0004424,GO:0000105	AT4G14910.1	HISN5B	HISTIDINE BIOSYNTHESIS 5B	imidazoleglycerol-phosphate dehydratase
Sapur.006G107800.1	210.503956	-0.009483471	0.077615345	-0.12219	0.902752095	0.935389185	grey	-0.04826506	0.548321796	GO:0016020,GO:0015018	AT2G37090.1	IRX9	Nucleotide-diphospho-sugar transferases superfamily protein	secondary cell wall-related glycosyltransferase family 43 protein
Sapur.001G131700.1	0.053990166	-0.244347096	2.000708112	-0.12213	0.90279582	0.935405186	grey	-0.18403155	0.021042331		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.013G107000.1	0.182075048	0.075390288	0.618334976	0.121925	0.902958677	0.935544618	grey	-0.016992842	0.832705081	GO:0006470,GO:0004725	AT1G71860.3	ATPTP1,PTP1	protein tyrosine phosphatase 1	tyrosine phosphatase
Sapur.016G305100.2	0.136412461	0.086445262	0.713047902	0.121233	0.903506125	0.936082498	grey	0.001541393	0.984714046		AT4G26555.1		FKBP-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase
Sapur.15WG076300.1	0.082427175	0.168250771	1.389741216	0.121066	0.903638553	0.936176801	grey	0.051844212	0.519025106	GO:0009733	AT3G12830.1		SAUR-like auxin-responsive protein family	NA
Sapur.011G034600.1	262.9070055	0.005219009	0.043175509	0.120879	0.903786944	0.936256127	grey	0.005121923	0.949236912		AT5G53750.1		CBS domain-containing protein	CBS domain protein CBSX5
Sapur.008G093500.1	1.330986673	-0.031193585	0.258380495	-0.12073	0.903907017	0.936351187	grey	-0.023513911	0.770046191		AT1G68820.1		Transmembrane Fragile-X-F-associated protein	transmembrane fragile-X-F protein
Sapur.008G042400.5	0.066549455	0.130628232	1.086458703	0.120233	0.904298546	0.93672743	grey	-0.024494692	0.760738842	GO:0003824	AT2G39550.1	ATGGT-IB,GGB,PGGT-I	Prenyltransferase family protein	geranylgeranyltransferase type I beta subunit
Sapur.007G044100.1	67.57500351	0.009006115	0.074996875	0.120087	0.904414596	0.936818301	grey	-0.033305249	0.678805487					NA
Sapur.T131500.1	0.121036989	-0.108291807	0.90243975	-0.12	0.904483994	0.936860844	grey	-0.180138956	0.023970687					NA
Sapur.018G036600.3	3.614148407	0.017495551	0.145880993	0.11993	0.904538366	0.936887821	grey	0.026117156	0.745417707		AT1G74530.1			transmembrane protein, putative
Sapur.004G076500.5	3.551952815	0.018394506	0.15359508	0.11976	0.90467348	0.936998424	grey	0.031560037	0.694774618		AT5G11390.1	WIT1	WPP domain-interacting protein 1	WPP domain interacting tail-anchored protein, putative
Sapur.004G013700.1	0.083045641	0.129074917	1.078149667	0.119719	0.90470581	0.937002566	grey	-0.003295181	0.967328843					NA
Sapur.011G047700.5	0.110785468	-0.10827489	0.906641243	-0.11942	0.904939303	0.937185699	grey	0.078548531	0.32814497	GO:0006468,GO:0004672	AT4G18710.1	ATSK21.BIN2.DWF12.SK21.U	Protein kinase superfamily protein	shaggy-related kinase
Sapur.008G002400.1	14.24157792	0.013769373	0.115633872	0.119077	0.905214087	0.937382219	grey	0.021010507	0.79394908	GO:0005515	AT3G17380.1		TRAF-like family protein	nucleic acid-binding protein, putative
Sapur.012G086800.1	0.092650596	0.153558878	1.290249585	0.119015	0.90526358	0.937404122	grey	0.167872258	0.035591641	GO:0005525	AT5G45160.1		Root hair defective 3 GTP-binding protein (RHD3)	ROOT HAIR defective-like protein
Sapur.003G053900.2	0.075702971	-0.212512746	1.790176395	-0.11871	0.905504713	0.937565754	grey	-0.089569897	0.264600646	GO:0006508,GO:0004176,GO:0005524,GO:0004252,GO:0030163	AT5G47040.1	LON2	lon protease 2	Lon protease-like, peroxisomal protein
Sapur.003G039200.1	0.070394374	0.15493152	1.305700457	0.118658	0.905546485	0.937579654	grey	0.00213249	0.978853328					NA
Sapur.002G168400.1	1096.151077	-0.006739396	0.056987532	-0.11826	0.905860946	0.937875879	grey	-0.153481418	0.054967175	GO:0006556,GO:0004478,GO:0005524	AT1G02500.1	AtSAM1.MAT1.SAM-1.SAM1	S-adenosylmethionine synthetase 1	S-adenosylmethionine synthase
Sapur.010G099000.3	5.061137893	-0.014450543	0.12225474	-0.1182	0.905908977	0.937896247	grey	-0.018584662	0.817295958		AT1G25540.2	PFT1	phytochrome and flowering time regulatory protein (PFT1)	mediator complex subunit 25 von willebrand factor type A protein
Sapur.012G055100.1	0.10561003	0.113211891	0.958988212	0.118053	0.906025287	0.937987303	grey	-0.028592307	0.72223723	GO:0005515,GO:0030117,GO:0016192,GO:0006886,GO:0005198,GO:0030126	AT1G62020.1		Coatomer, alpha subunit	coatomer alpha subunit, putative
Sapur.008G009000.1	22.84994023	-0.013251159	0.112299687	-0.118	0.9060691	0.9380033	grey	-0.005921713	0.941323449					NA
Sapur.018G116500.1	0.22981852	0.059955204	0.508734868	0.117852	0.906185266	0.938094197	grey	0.001604676	0.984086554					NA
Sapur.009G004800.1	0.056701824	0.194131678	1.657523033	0.117122	0.906763727	0.938634269	grey	0.14818544	0.064002863		AT5G60760.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	2-phosphoglycerate kinase
Sapur.019G035300.1	0.180634972	0.068536402	0.58586683	0.116983	0.906873603	0.938718627	grey	-0.020125545	0.80244617	GO:0006355,GO:0003700	AT5G19790.1	RAP2.11	related to AP2 11	AP2/ERF domain transcription factor
Sapur.017G012000.1	0.090163778	0.152241219	1.303521481	0.116792	0.907024678	0.938845623	grey	0.013212307	0.869546958	GO:0004842	AT4G38600.1	KAK,UPL3	HEAT repeat ;HECT-domain (ubiquitin-transferase)	NA
Sapur.15WG053400.1	0.216615081	-0.056882056	0.48750871	-0.11668	0.907114388	0.938889433	grey	-0.034409364	0.668775273	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT3G47570.1		Leucine-rich repeat protein kinase family protein	NA

Sapur.T113100.1	1.026583313	-0.026867926	0.230355729	-0.11664	0.907148716	0.938889433	grey	0.00198235	0.980341865			PLATZ transcription factor family protein	NA
Sapur.003G005900.1	0.351488637	0.235158335	2.00218122	0.116631	0.907152166	0.938889433	grey	0.137999075	0.084786932				hypothetical protein
Sapur.005G185100.2	1.005352043	0.034034867	0.292060202	-0.11652	0.907240869	0.938911857	grey	0.011707412	0.151232031	GO:0008270;GO:0006355		FAR1-related sequence 11	FAR1-related sequence protein
Sapur.015WG128600.3	4.884715485	0.019330246	0.165166455	0.116429	0.907312221	0.938895316	grey	0.0108807	0.892414576	GO:0055114;GO:0016491;GO:0006520		GDH2	glutamate dehydrogenase 2
Sapur.006G219000.5	0.104001581	0.11863235	1.120320851	0.116341	0.907308336	0.938895316	grey	0.051127824	0.524834287	GO:0008270		Ankyrin-repeat family protein with DHHC zinc finger domain	DHHC zinc finger protein
Sapur.010G248900.1	0.115751565	-0.096119732	0.826239697	-0.11634	0.907387676	0.938895316	grey	-0.114997711	0.115157582				hypothetical protein
Sapur.003G248300.1	535.8502332	-0.004732631	0.004094154	-0.1163	0.907416717	0.938896938	grey	-0.075983419	0.344745212	GO:0005585;		Leucine-rich repeat (LRR) family protein	LRR receptor-like kinase
Sapur.010G138200.1	0.074705262	-0.175308856	1.508037665	-0.1167	0.907516698	0.93905946	grey	-0.142115737	0.075815637	GO:0005515		ubiquitin-specific protease 12	ubiquitin carboxyl-terminal hydrolase
Sapur.T003000.1	1.662640871	0.024555162	0.215520605	0.115794	0.907816103	0.93911053	grey	0.00246158	0.975590867				NA
Sapur.015G268900.1	25.96028575	0.017755331	0.125843112	0.11669	0.907882498	0.93947661	grey	0.004384085	0.938482933				NA
Sapur.010G087700.2	0.358808374	-0.208793491	1.806641434	-0.11557	0.907934091	0.93436724	grey	-0.17595854	0.027485519	GO:0005975;GO:0004553		O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-d(glucosidase, putative
Sapur.T000400.1	0.834400004	0.011455134	0.286463311	-0.11522	0.908192621	0.93961369	grey	-0.016115983	0.653045702			Kinase-related protein of unknown function (DUF1296)	hypothetical protein
Sapur.007G015300.3	0.151912244	0.079057577	0.692503226	0.115055	0.908456167	0.93980278	grey	-0.025047471	0.7552815			FG-GAP repeat-containing protein	aldehyde dehydrogenase, putative
Sapur.003G197600.3	0.088173082	0.117771381	1.034172184	-0.11483	0.908569772	0.93980127	grey	-0.042612174	0.608063684			LRR domain-containing protein	Fas-associated factor Fic1
Sapur.006G208000.3	0.070093157	-0.173101533	1.508469341	-0.1149	0.908521418	0.93981658	grey	0.078548531	0.32814697	GO:0008270		Ran BP2/NZF zinc finger-containing protein family	Zn-finger in Ran-binding protein family
Sapur.003G180600.2	0.035610008	-0.029481769	0.146215889	0.114498	0.908508026	0.94040603	grey	-0.012477428	0.857161338			Protein of unknown function (DUF1664)	B-cell translocation factor, putative
Sapur.001G053300.2	0.062867715	-0.173232169	1.52092263	-0.11396	0.909270116	0.94062345	grey	-0.117638006	0.142288779	GO:0006457		PEBP-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase
Sapur.012G196400.1	0.861602825	-0.072321628	1.523247739	-0.11378	0.909408881	0.94057461	grey	-0.174786751	0.028561908			Protein of unknown function, DUF538	DUF538 family protein
Sapur.005G139300.2	8.842807662	0.012905663	0.115153927	0.113602	0.909481693	0.94090494	grey	0.020324455	0.761808979			Nucleotide-diphospho-sugar transferases superfamily protein	glycosyltransferase, putative
Sapur.15WG085400.4	1.521598601	-0.026688727	0.230251547	-0.11348	0.90861269	0.94073782	grey	-0.092932246	0.247161872			Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.009G097200.1	0.073144176	0.13863287	1.120320851	0.113267	0.908711276	0.94076053	grey	0.078548531	0.32814697	GO:0003723		RNA-binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.002G190300.2	0.190572543	-0.058896425	0.521605568	-0.1131	0.909649719	0.94096087	grey	-0.08840626	0.370882433	GO:0008270;GO:0005515		RING/U-box superfamily family protein	uso-RING finger protein
Sapur.004G269600.1	0.054818849	0.163813131	1.427096442	0.112942	0.910076214	0.94105937	grey	0.012861657	0.872976624				NA
Sapur.019G060900.3	0.280685526	-0.069469408	0.615243752	-0.11291	0.910090027	0.94105937	grey	-0.123058686	4.14E-05			Acyl-CoA N-acyltransferases (NAT) superfamily protein	GNAT family acetyltransferase
Sapur.004G206200.1	188.7508807	0.011772381	0.124368184	0.112627	0.910232353	0.94106089	grey	-0.048828114	0.548873476				transcription factor Rcc1
Sapur.001G165900.3	0.266565638	0.054409747	0.483606805	0.112508	0.910420442	0.94124448	grey	-0.018861987	0.804981282	GO:0005515		BTB/POZ domain-containing protein family	BTB/POZ domain plant protein
Sapur.15WG027700.1	0.068391773	0.202569771	1.800449481	0.1125	0.910427219	0.94124448	grey	-0.064948001	0.43005128			RNA-directed DNA polymerase (reverse transcriptase)-related family protein	NA
Sapur.010G236000.1	0.163715148	0.088449661	0.872083683	0.112468	0.910439275	0.94125233	grey	-0.041429025	0.857653233	GO:0055114;GO:0016491	ATSRG1;SRG1	senescence-related gene 1	flavonol synthase/flavanone 3-hydroxylase, putative
Sapur.004G151900.5	5.038942685	-0.012461138	0.112468731	-0.1124	0.910588705	0.94171703	grey	-0.010790212	0.893313979	GO:0003676		RNA-binding (RRM/RBD/RNP motifs) family protein	nucleolar phosphoprotein, putative
Sapur.010G207300.3	0.060238924	-0.11945096	1.152607024	0.11363	0.910535371	0.94127153	grey	-0.018457404	0.819721502	GO:0006817	SGR2	short gravitropism 2 (SGR2)	SEC23-interacting protein
Sapur.002G202200.5	0.096173059	-0.127894889	1.139372501	-0.11225	0.910624499	0.94136925	grey	-0.49973976	2.68E-11	GO:0006810;GO:0005622		Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain	Ras GTPase-activating protein-binding protein
Sapur.T002900.1	1.733465717	0.011339515	0.190334317	0.113111	0.910720167	0.94141991	grey	-0.058441815	0.497199665				NA
Sapur.006G014100.2	23.67619493	-0.013860096	0.164126276	-0.11187	0.910903973	0.94154555	grey	-0.013358346	0.868118034	GO:0046872;GO:0000001		Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.004G184200.1	0.277112268	0.064756647	0.510202212	0.111829	0.910904346	0.94154555	grey	0.006724253	0.933369475		AtCHX4;CHX4	cation/H+ exchanger 4	cation exchanger 4
Sapur.015G050900.1	0.053849766	-0.171456066	1.533407021	-0.11181	0.910970383	0.94154555	grey	-0.47970879	2.06E-10	GO:0004888;GO:0006672	ERF1	receptor-like kinase in flowers 1	receptor-like kinase, putative
Sapur.004G000300.1	50.75792389	0.011339515	0.130507031	0.111165	0.911067763	0.94156053	grey	0.014737768	0.836235544				NA
Sapur.T176600.1	0.212842556	0.061983965	0.559601597	0.11146	0.911255488	0.94170325	grey	-0.022887249	0.776010355				NA
Sapur.012G082000.2	0.063980556	0.054078887	1.405563958	0.111328	0.911356217	0.94185312	grey	0.042099633	0.591979923	GO:0006296;GO:0005622	ATRTI;ZRT;ZT	RWhe TnHER-like protein 2	ribonuclease-III-like protein
Sapur.019G284000.3	0.304713924	0.074571559	0.671507584	0.111084	0.911454638	0.94202577	grey	-0.136153123	0.088081234	GO:0055114;GO:0050181;GO:0004733		FMN binding	NA
Sapur.013G139800.1	260.5165565	0.007292819	0.065745273	0.110925	0.911675562	0.94212657	grey	-0.034827513	0.664991749			Methyltransferase-related protein	transmembrane protein, putative
Sapur.002G186200.1	0.056179658	0.154189944	1.417907276	0.11267	0.911716457	0.94215254	grey	0.10587073	0.264378861	TTL	TTL	transferrin-like protein	5-hydroxytryptamide lipoyltase
Sapur.001G085500.1	0.056149469	0.154490613	1.418652105	0.110309	0.911264331	0.94215669	grey	-0.008223053	0.918489008	GO:0004688;GO:0006672		Protein kinase protein with tetratricopeptide repeat domain	kinase domain protein
Sapur.I10G046585.1	64.45600043	0.012259852	0.120037111	0.11028	0.911469692	0.94215669	grey	-0.006106945	0.938820101	GO:0005634	NDF1		NA
Sapur.003G117700.1	0.065448867	0.155043695	1.408606719	0.110063	0.911503773	0.94268259	grey	-0.017472231	0.828057513				hypothetical protein
Sapur.006G213800.1	60.79406543	0.012259852	0.120037111	0.110025	0.911540401	0.94284124	grey	0.015340401	0.819271139	GO:0008017;GO:0007010	ATMAP70-5;MAP70-5	microtubule-associated proteins 70-5	myosin II heavy chain like protein
Sapur.008G285200.2	0.092796487	-0.143402012	1.308388279	-0.1096	0.911275007	0.94296186	grey	-0.081423614	0.310694156				serine/threonine protein phosphatase 4 regulatory subunit
Sapur.006G202500.1	18.19621372	0.011523491	0.105305635	0.109429	0.912862239	0.94320653	grey	-0.006827063	0.932372482				NA
Sapur.009G085700.2	5.625454581	0.011523491	0.105305635	0.112638944	0.913093543	0.94318252	grey	-0.015775058	0.457908115				transmembrane protein, putative
Sapur.006G140400.1	0.823695253	0.012082471	0.204752972	0.108845	0.913225207	0.94340453	grey	-0.066379956	0.438832107				NA
Sapur.016G275500.1	4.403496571	0.011523491	0.345673188	0.108795	0.913384554	0.94340453	grey	-0.027230268	0.73497493				NA
Sapur.T002100.1	1.036155643	0.029463303	0.229232621	0.108783	0.913397954	0.94340453	grey	0.068945581	0.194026316				NA
Sapur.011G008200.4	0.724161827	-0.013348842	0.112864756	-0.1063	0.913409969	0.94351724	grey	-0.102036925	0.103492607	GO:0016020		ERD (early-responsive to dehydration stress) family protein	early-responsive to dehydration-like protein
Sapur.014G065600.3	0.13623811	0.083052066	0.755432089	0.108616	0.913570012	0.94351923	grey	-0.134197146	0.09383939	GO:0004688;GO:0005634;GO:0004672		U-box domain-containing protein kinase family protein	tyrosine kinase family protein
Sapur.003G058000.6	0.058459802	0.121539006	1.806886515	0.108062	0.913620102	0.94314664	grey	0.064419179	0.518838841		ATMYB72;MYB72	myb-like DNA-binding protein family	Myb-like DNA-binding protein family
Sapur.006G121800.2	0.165020861	0.072237153	0.667860605	0.108162	0.913867177	0.94383097	grey	-0.005500013	0.995041113	GO:0016705;GO:0016117	LUT2	Lycopene beta/epsilon cyclase protein	lycopene epsilon cyclase
Sapur.015G045100.2	0.854224213	-0.014342715	0.132642173	0.107969	0.914025499	0.94383832	grey	-0.176704778	0.028838238				hypothetical protein
Sapur.015G105500.1	28.32852276	-0.021031742	0.194812344	-0.10796	0.914028323	0.94383832	grey	-0.003650488	0.963808313				NA
Sapur.012G192600.4	0.052326202	0.195802497	1.812728787	0.107845	0.914018549	0.94402151	grey	-0.009385817	0.907124158	GO:0055114;GO:0016491		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate(Fe(II)-dependent dioxygenase, putative
Sapur.003G165600.1	1.066093163	-0.025323342	0.234971251	-0.10777	0.914076486	0.94402506	grey	-0.008351128	0.912787685	GO:0055085;GO:0016567;GO:0006482		Armadillo/beta-catenin-like repeat family protein	NA
Sapur.004G069600.1	1504.545857	0.005000949	0.054962127	0.107364	0.914500286	0.94407613	grey	-0.003181727	0.988280551	GO:0045454;GO:0008152;GO:0003824	APR3;ATAPR3;PRH-26;PRH2	APS reductase 3	5'-adenylylsulfate reductase, thioredoxin-independent protein
Sapur.T113000.1	1.299619153	0.011523491	0.359732079	0.107167	0.914647264	0.94417194	grey	-0.002183014	0.978872917			PLATZ transcription factor family protein	NA
Sapur.T055700.1	0.064334814	-0.123482426	1.153439755	-0.10697	0.914815125	0.9445123	grey	-0.122712974	0.125769588				NA
Sapur.003G175200.3	0.142588403	0.011524185	1.124754893	0.106917	0.914838824	0.9445123	grey	0.0818476	0.956160887			Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.016G233800.1	276.5128313	0.005849593	0.054875971	0.106578	0.915134567	0.94475149	grey	-0.048636617	0.545242345	GO:0005515		ARM repeat superfamily protein	NA
Sapur.004G344800.2	1.438843409	0.011524185	0.215563813	0.106401	0.915401128	0.94490266	grey	-0.002183014	0.978872917		ATVAM2;ATVPS41;VAM2;VP	vacuolar protein sorting-associated-like protein	vacuolar protein sorting-associated protein
Sapur.002G018100.7	0.182424371	0.079043229	0.751332096	0.10639	0.915729	0.94491826	grey	-0.320536332	4.26E-05	GO:0004527;GO:0006176	AtXRN3;XRN3	5'-3' exoribonuclease 3	5'-3' exoribonuclease
Sapur.003G050200.1	0.152280443	0.011524185	0.118204751	0.106273491	0.915888574	0.94491673	grey	-0.078836237	0.334897416			1H Family of FUS-like bogenesis protein 3	succinate dehydrogenase assembly factor-like protein
Sapur.016G033800.1	0.078557742	-0.139757937	1.163778516	-0.10614	0.915474248	0.94486656	grey	-0.15261927	0.05636191	GO:0006412;GO:0005840;GO:0003735		Ribosomal protein S5 domain 2-like superfamily protein	NA
Sapur.014G082000.2	0.027248372	-0.172264488	1.633005821	-0.10609	0.915100106	0.94486656	grey	-0.152484778	0.055630202	GO:0046872;GO:0000166		ER-type Ca2+-ATPase 2	endoplasmic reticulum-type calcium-transporting ATPase
Sapur.003G161200.5	0.089847413	0.118843201	1.072126125	0.10605	0.915179863	0.94486656	grey	-0.01875026	0.815261385				NA
Sapur.017G026700.1	14.27684772	-0.010437681	0.098749388	-0.1057	0.915281422	0.94510659	grey	-0.037801884	0.638329953			Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.016G186100.1	0.120658892	0.088496561	0.829319765	0.105529	0.915529	0.94525463	grey	-0.015147258	0.850773813			Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	LEA hydroxyproline-rich glycoprotein family
Sapur.010G125600.2	0.098047746	0.083257153	0.780868605	0.10502	0.915692792	0.94535271	grey	-0.15210149	0.055838479	GO:0046873;GO:0030001;GO:0016020	MGT3;MRS2-5	magnesium transporter MRS2-5	magnesium transporter MRS2-5
Sapur.005G154100.2	0.066055754	-0.171788629	1.610678919	-0.1052	0.916231318	0.94547407	grey	-0.115238832	0.052167471			S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	16S rRNA (guanine(527)-N(7))-methyltransferase
Sapur.019G064100.1	0.094097353	-0.106449906	1.013342196	-0.10505	0.916374558	0.94556097	grey	-0.13615833	0.147410817				NA
Sapur.004G032900.1	0.054322904	-0.137886491	1.313505565	-0.10487	0.916469253	0.94561661	grey	-0.146691253	0.058763184	GO:0007275;GO:0006511;GO:0005634		seven in absentia of Arabidopsis 2	E3 ubiquitin-protein ligase SINA2
Sapur.013G130400.2	0.468267503	-0.033328342	0.319719891	-0.10487	0.916480403	0.94561695	grey	-0.033755616	0.674707246	GO:0016787		Cytidine/deoxycytidine deaminase family protein	nucleoside phosphatase family protein
Sapur.011G230700.4	0.291801671	0.055408821	0.515888341	0.10477	0.916585582	0.94563165	grey	-0.008028195	0.919729587	GO:0031981;GO:0006886		SNARE-associated protein-related	snapin/pallidin protein
Sapur.005G021700.1	2.137032749	-0.017674895	0.25498591	-0.10452	0.916691911	0.94583765	grey	-0.025372316	0.752490701	GO:0007165;GO:0005515		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.003G169800.2	0.305485139	-0.053793503	0.571047513	-0.10403	0.917146929	0.94603782	grey	0.01402768	0.86157585			Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.T051900.3	0.00827524	0.066087821	1.088718275	0.103999	0.917170519	0.94603782	grey	-0.12470676	3.23E-05	GO:0007062;GO:0051225			HAUS augmin-like complex subunit
Sapur.015G079400.1	26.59702591	-0.014104473	0.134952499	-0.104	0.917172821	0.94603782	grey	0.002409142	0.976110066	GO:0015763	ALMT9;AtALMT9	aluminum-activated malate transporter 9	aluminum activated malate transporter
Sapur.015G179400.1	0.010448827	0.208727692	2.010244385	-0.10392	0.917302752	0.94613131	grey	0.018008206	0.837092246				HMG (high mobility group) family protein
Sapur.T161800.1	0.767697886	0.028525168	0.275271146	0.103725	0.917387538	0.94626259	grey	-0.040047702	0.618493755		CLE25	CLAVATA/ESR-RELATED 25	2OG-Fe(II) oxygenase family oxidoreductase
Sapur.T187700.2	0.067660164	0.028675527	1.640225256	0.103684	0.917432323	0.94630568	grey	0.068998018	0.494697211	GO:0055114;GO:0016491		2-oxoglutarate(2OG) and Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate(Fe(II)-dependent dioxygenase, putative
Sapur.008G064600.1	0.309936301	-0.043165252	0.416639396	-0.10559	0.917493311	0.94218509	grey	-0.064283592	0.423780613	GO:0055114;GO:0016620		glyceraldehyde-3-phosphate dehydrogenase of plastid 2	glyceraldehyde-3-phosphate dehydrogenase
Sapur.006G135300.2	0.300254468	0.080081937	0.587206415	0.103568	0.917495	0.94218509	grey	-0.046691252	0.85051052	GO:0055114;GO:0016491;GO:0016616;GO:0016615;GO:0006108		Lactate/malate dehydrogenase family protein	malate dehydrogenase
Sapur.003G178000.3	0.418434398	0.036070508	0.370717804	0.103554	0.917535457	0.94218509	grey	-0.023237272	0.752770221				transglutaminase family protein
Sapur.012G077500.1	0.064911781	0.056583231	1.514886794	0.10338	0.917616103	0.94302347	grey	0.055075081	0.530391364				NA
Sapur.005G122301.5	0.054667212	0.172614337	1.669349862	0.103379	0.917626206	0.94302347	grey	0.063032826	0.431883897	GO:0016021;GO:0005215		Transmembrane protein family protein	ion-pore-phosphate transporter family protein
Sapur.005G008000.1	0.083593892	0.171995219	1.136141459	0.103131	0.917850624	0.94469681	grey	0.014027868	0.861572585			Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.T051900.3	0.00827524	0.066087821	1.088718275	0.103999	0.917570519	0.94603782	grey	-0.12470676	3.23E-05	GO:0007062;GO:0051225			HAUS augmin-like complex subunit
Sapur.013G190900.1	0.082247886	0.117201165	1.13743311	0.10304	0.917931186	0.94691333	grey	0.011562442	0.885938308			Protein of unknown function (DUF688)	DUF688 family protein
Sapur.006G051100.1	7.434806856	0.014069683	0.136374606	0.102729	0.918177734	0.94686524	grey	0.022163474	0.772457129	GO:0016020;GO:0015990;GO:0006678;GO:0006427	AtVAP27-2;VAP27-2	Inositol phosphosphingolipid phosphatase family protein	phosphosphingolipid membrane protein pump protein
Sapur.005G197700.1	0.145149831	-0.076092336	0.749752459	-0.10269	0.918208739	0.94688982	grey	-0.090994616	0.257025855	GO:0006876		Splicing factor, CC1-like	CC1-like splicing factor
Sapur.002G072000.4	0.051161013	0.177139522	1.670895892	-0.10257	0.918268282	0.94716127	grey	-0.174089003	0.028746227		AtIDOS;IDOS	Jacalin-related lectin 3 protein	jacalin-related lectin
Sapur.010G002000.2	0.4787778	0.038329862	0.373725902	0.102559	0.918312969	0.94716127	grey	-0.04622667	0.56545283			hydroxyproline-rich glycoprotein family protein	CHLP1
Sapur.006G182000.1	0.051248225	-0.171379294	1.671195387	-0.10255	0.918330943	0.94716127	grey	-0.186409368	0.015254118		AMP1;CPD2;HPT;MPOL;PT	Peptidase M28 family protein	glutamate carboxypeptidase, putative
Sapur.018G064700.2	0.080932136	0.132511523	1.293120124	0.102474	0.918380326	0.94716127	grey	-0.065773653	0.413111703	GO:0015450;GO:0006886;GO:0005744	ATTIM17-2;TIM17;TIM17-2	translocase inner membrane subunit 17-2	import inner membrane translocase subunit Tim17
Sapur.019G047100.1	461.452863	-0.010027338	0.103736077	-0.10245	0.918402732	0.94716127	grey	-0.01481563	0.857834472		AtCHE18;CHE18	carboxylesterase 18	arylacetamide deacetylase, putative
Sapur.006G075916	0.086759516	0.11318247	1.13395109	0.10143	0.918464496	0.94801082	grey	0.012814347	0.874692386				NA
Sapur.012G214000.2	0.14672236	0.068783892	0.673723837	0.102094	0.918602252	0.94815158	grey	-0.01188411	0.882561518	GO:0008270;GO:0005515		RING/U-box superfamily family protein	zinc-finger protein
Sapur.004G078900.1	0.004486464	0.156000276	0.911717164	0.10168	0.918715279	0.94860931	grey	-0.113418712	0.056377652	GO:0008118;GO:0006470;GO:0004484;GO:0006397;GO:0006370		miRNA capping enzyme family protein	ATP-dependent DNA ligase domain protein
Sapur.010G051200.1	0.053517096	0.156584283	1.536284252	0.101888	0.918854508	0.94860931	grey	0.020276392	0.80096128				transmembrane protein, putative
Sapur.006G099700.1	0.053329216	0.156584277	1.537244734	0.101861	0.918872173	0.94860931	grey	0.004704604	0.952968068				nicotinamide adenine dinucleotide transporter
Sapur.010G153800.1	2.060713937	-0.024694489	0.242463316	-0.10185	0.918875733	0.94860931	grey	-0.025371236	0.76942811				hypothetical protein
Sapur.003G071100.3	1.065809009	0.011523491	0.688502003	0.101807	0.918901881	0.94860931	grey	-0.046037668	0.561663157	GO:0005524	ATGTA41;BTAF1;CHR18;CHR	DNA binding;ATP binding;nucleic acid binding;binding;helicases;ATP binding;DNA binding;helicases	TATA-binding protein associated factor
Sapur.016G073200.1	0.10763997	0.088496927	0.86963875	0.101763	0.918984906	0.94897566	grey	-0.023272941	0.772338017	GO:0005515		F-box family protein	transcription regulation protein, putative
Sapur.008G246900.2	0.746635541	0.011523491	0.109437846	0.101618	0.919059627	0.94785204	grey	-0.186409368	0.015254118			Peptidase M28 family protein	glutamate carboxypeptidase, putative
Sapur.018G064700.2	0.080932136	0.132511523	1.293120124	0.101474	0.918380326	0.94716127	grey	-0.065773653	0.413111703	GO:0015450;GO:0006886;GO:0005744	ATTIM17-2;TIM17;TIM17-2	translocase inner membrane subunit 17-2	import inner membrane translocase subunit Tim17
Sapur.019G047100.1	461.452863	-0.010027338	0.103736077	-0.10245	0.918402732	0.94716127	grey	-0.01481563	0.857834472		AtCHE18;CHE18	carboxylesterase 18	arylacetamide deacetylase, putative
Sapur.015G330300.1	0.06675916	0.11318247	1.13395109	0.10143	0.918464496	0.94801082	grey	0.012814347	0.874692386				NA
Sapur.012G214000.2	0.14672236	0.068783892	0.673723837	0.102094	0.918602252	0.94815158	grey	-0.01188411	0.882561518	GO:0008270;GO:0005515		RING/U-box superfamily family protein	zinc-finger protein
Sapur.004G078900.1	0.004486464	0.156000276	0.911717164	0.10168	0.918715279	0.94860931	grey	-0.113418712	0.056377652	GO:0008118;GO:0006470;GO:0004484;GO:0006397;GO:0006370		miRNA capping enzyme family protein	ATP-dependent DNA ligase domain protein
Sapur.010G051200.1	0.053517096	0.156584283	1.536284252	0.101888	0.918854508	0.94860931	grey	0.020276392	0.80096128				transmembrane protein, putative
Sapur.006G099700.1	0.053329216	0.156584277	1.537244734	0.101861	0.918872173	0.94860931	grey	0.004704604	0.952968068				nicotinamide adenine dinucleotide transporter
Sapur.010G153800.1	2.060713937	-0.024694489	0.242463316	-0.10185	0.918875733	0.94860931	grey	-0.025371236	0.76942811				hypothetical protein
Sapur.003G071100.3	1.065809009	0.011523491	0.688502003	0.101807	0.918901881	0.94860931	grey	-0.046037668	0.561663157	GO:0005524	ATGTA41;BTAF1;CHR18;CHR	DNA binding;ATP binding;nucleic acid binding;binding;helicases;ATP binding;DNA binding;helicases	TATA-binding protein associated factor
Sapur.016G073200.1	0.10763997	0.088496927	0.86963875	0.101763	0.918984906	0.94897566	grey	-0.023272941	0.772338017	GO:0005515		F-box family protein	transcription regulation protein, putative
Sapur.008G246900.2	0.746635541	0.011523491	0.109437846	0.101618	0.919059627	0.94785204	grey	-0.186409368	0.015254118			Peptidase M28 family protein	glutamate carboxypeptidase, putative
Sapur.015G250500.3	4.018335707	-0.011523491	0.115153927	-0.1016	0.919195315	0.94915204	grey	-0.044847936	0.58009322			O-fucosyltransferase family protein	GDP-fucose protein O-fucosyltransferase
Sapur.003G158800.1	27.47119957	-0.016099258	0.167669848	-0.10139	0.919246825	0.94738495	grey	-0.10487511	0.191487775	GO:0006412;GO:0005840;GO:0005622;GO:0003735		Ribosomal protein L18e/L15 superfamily protein	60S ribosomal protein L18
Sapur.T054900.1	0.450037147	0.011523491	0.117061413	0.101063	0.919306613	0.94738495	grey	-0.043638127	0.587423861	GO:0005515	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.017G014900.1	65.32917661	-0.016081903	0.138449322	-0.1008	0.919564571	0.94760796	grey	-0.02402064	0.765233279		PHT4;1	phosphate transporter 3;1	NA
Sapur.T013270.1	0.174976416	0.058262253	0.581758253	0.100602	0.919861592	0.94760889	grey	-0.058980249	0.452015	GO:0003676	AtGRP8;CCR1;GR-RBP8;GR	cold, circadian rhythm, RNA binding 1	chloroplast RNA binding
Sapur.013G170300.1	0.063888578	0.141683154	1.408468339	-0.1003	0.919827709	0.94760889	grey	0.011343016	0.164696424	GO:0055515		Phototropic-responsive NPH3 family protein	phototropic-responsive NPH3 family protein
Sapur.T082900.1	0.357218157	0.011523491	0.147662494	0.100042	0.919912294	0.94762148	grey	0.012814347	0.874692386			ATBTF3C domain-containing protein family protein	NA
Sapur.017G118500.2	0.059813579	0.152026000	1.320100179	0.100387	0.920037325	0.9476363	grey	0.042340987	0.598521586	GO:0006886;GO:0005622;GO:0005801		SNARE-like superfamily protein	trafficking protein particle complex subunit 1
Sapur.006G123300.1	0.059573667	0.152026000	1.320100179	-0.1008	0.920089019	0.9476363	grey	-0.074410608	0.334343311		MED19A	RNA binding protein, putative	RNA binding protein, putative
Sapur.006G158000.2	0.059573667	0.152026000	1.320100179	0.100378	0.920064422	0.9476363	grey	-0.006837035	0.931446842		AtR2B	ankyrin repeat-containing 2B	TG81K interacting protein
Sapur.006G168100.1	0.078867425	0.029314284	0.292284812	0.100294	0.920111138	0.94767504	grey	0.31594014	5.56E-05				hypothetical protein
Sapur.001G085100.5	0.394439807	0.011523491	0.087497384	0.098215216	-0.10013	0.947503197	grey	-0.064616149	0.421040006	GO:0055515;GO:0016020		Cornichon family protein	cornichon protein
Sapur.005G098700.1	0.10768483	0.096764217	0.966047332	0.100072	0.920287276	0.94768375	grey	-0.029889319	0.746621359			Sec14p-like phosphatidylinositol transfer family protein	transporter, putative
Sapur.014G099600.1	1.8381783	0.011523491	0.207684897	0.099859	0.920480819	0.94800819	grey	-0.047122747	0.537831049				hypothetical protein
Sapur.T144300.1	0.160558178	-0.07707782	0.710365158	-0.09964	0.920633425	0.94804652	grey	-0.061809836	0.447513344			NB-ARC domain-containing disease resistance protein	NB-ARC domain-containing protein
Sapur.T002800.1	1847.114764	0.000368294

Sapur.007G038500.1	0.072363029	-0.137461892	1.633057921	-0.08428	0.932830128	0.95404176	grey	-0.103840181	0.195590097	AT3G50630.1	NA
Sapur.010G258100.1	81.58867815	-0.027794277	0.331477302	-0.08385	0.931315682	0.95636277	grey	-0.044213078	0.582275557	GO:0010151,GO:0008025,GO:0005758,GO:0005507	AT1G15152.1	ATCOX17,COX17	cytochrome c oxidase 17	cytochrome C oxidase copper chaperone
Sapur.010G137300.1	0.135974988	0.069091448	0.858364128	-0.08367	0.933339112	0.95468633	grey	-0.010056222	0.852830789		AT2G30140.2		Protein of unknown function (DUF674)	NA
Sapur.005G097600.1	128.1588239	0.013635754	0.163404945	0.083448	0.933495623	0.95659796	grey	-0.023864308	0.76671712		AT5G25250.1	ATRAD,RAD,RSM3	RAD-like 6	MFB transcription factor
Sapur.005G200400.1	0.072336224	-0.135788849	1.627746554	-0.0834	0.933517473	0.95639786	grey	-0.132245991	0.096181858		AT3G46530.1		Essential protein Yae1, N-terminal	essential protein Yae1, amino-terminal protein
Sapur.007G001100.1	0.123452405	0.075502359	0.935802569	0.083354	0.933569991	0.95662173	grey	-0.00053696	0.994682623	GO:0008168,GO:0006479	AT3G30030.1	ATPRMT6,PRMT6	protein arginine methyltransferase 6	NA
Sapur.012G008500.6	0.146212796	-0.063206324	0.759255572	-0.08325	0.933654539	0.95679169	grey	-0.065936853	0.385245964	GO:0003676	AT5G49430.2	SR34a	SER/ARG-rich protein 34A	RNA recognition motif 2 in serine/arginine-rich splicing factor 1 (SRSF1)-like protein
Sapur.008H400.1	0.053139044	0.118971182	1.428605477	0.083211	0.933680649	0.95659758	grey	-0.283017313	0.000019784	GO:0046912	AT2G42790.1	CSY3	citrate synthase 3	citrate synthase
Sapur.006G072200.4	0.40062886	-0.031638392	0.380709483	-0.0831	0.933769331	0.95673284	grey	0.02005252	0.900041098	GO:0003824	AT3G39930.1	ATISA1,ISA1	isoamylase 1	isoamylase
Sapur.005G171700.1	205.1668878	0.078688278	0.083302708	0.083192	0.933852296	0.95685351	grey	0.017877498	0.618431321					hypothetical protein
Sapur.002H470100.6	0.124869693	0.062080103	0.748609209	0.083829	0.933867522	0.95689061	grey	0.00601165	0.910796102		AT1G29350.1		Kinase-related protein of unknown function (DUF296)	hypothetical protein
Sapur.010G198300.1	0.011760074	-0.077281659	0.837756127	-0.08279	0.934018505	0.95698063	grey	0.204119671	0.010233164	GO:0016021,GO:0005783	AT4G14520.1		translocon-associated protein subunit beta	translocon-associated protein subunit beta
Sapur.003G047000.3	5.562325867	-0.011103369	0.134158225	-0.08276	0.934039893	0.95698061	grey	0.004894398	0.950598166		AT5G47420.1		Tryptophan RNA-binding attenuator protein-like	tryptophan RNA-binding attenuator-like protein
Sapur.008G272300.5	0.063672308	-0.081727351	1.044846617	-0.08265	0.934077131	0.95706148	grey	0.062620006	0.648771571	GO:0043565,GO:0006355,GO:0003700	AT2G40140.2	WRKY3	WRKY DNA-binding protein 3	WRKY transcription factor, putative
Sapur.009G069700.1	0.123192604	0.077023457	0.943526025	0.082482	0.934203816	0.95704118	grey	0.045518984	0.57133461		AT4G14835.1		RING/U-box superfamily protein	zinc finger-like protein
Sapur.010G051300.1	23.52268832	0.055398652	0.517217056	0.082473	0.934203782	0.95704118	grey	0.015362784	0.7872527	GO:0007165,GO:0055115,GO:0043531	AT4G17680.1		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.010G074000.2	0.08607485	-0.025454519	0.309549668	-0.08223	0.934460048	0.95782443	grey	-0.057324778	0.475788846	GO:0006629	AT4G10955.2		alpha/beta-Hydrolases superfamily protein	triacylglycerol lipase
Sapur.001G155200.1	947.7086995	-0.00447984	0.054568841	-0.08207	0.934500148	0.95828962	grey	0.003394271	0.986346955		AT5G23240.1		CASC5/Barentsz eIF4AIII-binding	CASC5/Barentsz eIF4AIII-binding protein
Sapur.004G384800.2	2.387717776	-0.061454109	0.745459201	-0.08182	0.934570924	0.95839559	grey	-0.023241245	0.777195559	GO:0006468,GO:0004672	AT3G59010.1	ATOST1,OST1,PAS,SNRK2.6	Protein kinase superfamily protein	Serine/Threonine-kinase SAPK10, putative
Sapur.007G103400.1	0.114989364	-0.004182361	1.274607635	-0.08173	0.934850847	0.95743383	grey	0.051686642	0.132039439		AT4G33625.1			COPI associated protein
Sapur.U002G09901.1	0.084618523	-0.011164377	0.140616873	-0.08163	0.935011275	0.95763188	grey	0.005985671	0.941361356	GO:0003677	AT5G03150.1	NGA4	AP2/B3-like transcriptional factor family protein	NA
Sapur.012G102300.4	0.053749626	-0.135765643	1.668775621	-0.08136	0.935158490	0.95765688	grey	-0.139079916	0.082352997	GO:0006355,GO:0005634,GO:0003700,GO:0046983,GO:0003677	AT5G62165.3	AGL42	AGAMOUS-like 42	MADS-box transcription factor
Sapur.006G211300.1	0.574612287	-0.050404143	0.956864774	-0.08128	0.935230087	0.95788904	grey	-0.021943885	0.785012369					transmembrane protein, putative
Sapur.014G035100.1	0.092210207	0.077731427	0.957113233	0.081204	0.935279707	0.95791323	grey	0.003874335	0.9615587		AT3G60340.2		alpha/beta-Hydrolases superfamily protein	palmitoyl-protein thioesterase, putative
Sapur.006G169200.1	0.580454119	0.008172576	0.080172576	0.081173	0.935374543	0.95816064	grey	0.004860204	0.948771571		AT5G61860.2		NAD(P)-binding Rossmann-fold superfamily protein	short-chain alcohol dehydrogenase, putative
Sapur.010G229900.1	347.7179385	-0.004064629	0.050215614	-0.08049	0.935815612	0.95821626	grey	-0.045145173	0.574552077		AT5G43150.1			hypothetical protein
Sapur.002G084100.1	0.3608567	0.034575885	0.430138405	0.080383	0.935925219	0.95827129	grey	-0.00036381	0.996396154	GO:0006950	AT1G09740.1		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress A-like protein
Sapur.011G086001.1	1.146617604	0.008107202	0.251235359	-0.08029	0.936003504	0.95918054	grey	0.005238677	0.998740671		AT2G27230.1		F-box/kelch-repeat protein	NA
Sapur.003G065000.1	4.117693171	0.016487739	0.205730825	0.080148	0.936119174	0.95835624	grey	-0.015152174	0.846796284	GO:0043531	AT5G07040.1	RPM1,RPS3	NB-ARC domain-containing disease resistance protein	NB-ARC domain-containing protein
Sapur.016G177000.1	0.265106756	0.045804767	0.561653037	-0.08013	0.936134846	0.95835624	grey	-0.062426245	0.437265559	GO:0006468,GO:0004672	AT4G26290.1	HERK1	hercules receptor kinase 1	receptor-like kinase, putative
Sapur.006G069300.1	0.190133603	0.048373391	0.606695935	0.079733	0.936450001	0.95852573	grey	-0.02652243	0.76161705	GO:0003824,GO:0006470,GO:0004722	AT5G07630.1	PLL5	pcl-like 5	protein phosphatase 2C, putative
Sapur.002G242500.2	0.124446462	-0.062790453	0.787320364	-0.07929	0.936512239	0.95860708	grey	-0.218316179	0.005054989	GO:0005515	AT2G27190.1		NB-ARC domain-containing disease resistance protein	CC-NBS-resistance protein
Sapur.007G062800.1	74.15098828	-0.005160313	0.064817791	-0.07961	0.936545178	0.95880865	grey	-0.283065108	0.00036382	GO:0006351,GO:0008289,GO:0000439	AT5G55750.1		BSD domain (BTF2-like transcription factors, Synapse-associated proteins and DOS2-like proteins)	RNA polymerase II transcription factor B protein, putative
Sapur.010G212000.1	25.76251412	0.013763187	0.173181206	0.079425	0.936689786	0.95880939	grey	0.006945201	0.906472207		AT5G45480.1		Protein of unknown function (DUF642)	NA
Sapur.019G007800.2	0.058961569	0.120881931	1.523871028	0.079378	0.936732241	0.95880009	grey	0.043749561	0.586424439	GO:0015524,GO:0007165,GO:0005515	AT4G12010.1		Disease resistance protein (TIR-NBS-LRR class) family	TIR-NBS-LRR resistance protein
Sapur.010G166600.1	23.56273872	0.015364418	0.123963465	-0.0793	0.936875727	0.95893013	grey	0.000962129	0.954388089	GO:0043531	AT5G14470.1		NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.002H410800.2	0.09086332	0.117641094	1.487407514	0.079061	0.936959961	0.95896756	grey	-0.084235843	0.294222671					hypothetical protein
Sapur.005G406300.1	0.053849661	0.058374667	2.005862222	0.079054	0.936987887	0.95896756	grey	0.047676968	0.153239025					NA
Sapur.001G021300.1	1515.05549	0.011042065	0.11991009	0.078922	0.937094118	0.95904056	grey	-0.014898376	0.852241783	GO:0055544,GO:0005509	AT2G38750.1	ANNAT4	annexin 4	annexin protein
Sapur.007G084400.2	0.130958227	0.062280119	0.790308205	0.078763	0.937236971	0.95936121	grey	-0.032638798	0.684887315		AT4G39830.1		TLD domain containing nucleolar protein	TLD family protein
Sapur.T042400.1	0.123953468	0.052280159	0.792308248	0.078606	0.937346108	0.95940174	grey	-0.050838525	0.537256815					NA
Sapur.019G043600.1	1.80067949	-0.014972605	0.190579799	-0.07856	0.937282119	0.95940174	grey	0.010275152	0.859697944	GO:0007165,GO:0055115,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.006G133200.2	0.01112334	0.080172204	1.139416879	0.078528	0.937408545	0.95940174	grey	0.402308545	1.7E-07	GO:0006351,GO:0005634,GO:0008289,GO:0003677	AT3G44260.1	ATRNAPC4-3,NRPB5,NRPD	Eukaryotic DNA-dependent RNA polymerase II, subunit 5	DNA-directed RNA polymerase II, putative
Sapur.T056800.1	0.050882298	0.128869649	1.540039145	0.0785	0.937430033	0.95940174	grey	-0.028523511	0.72288555		AT4G28455.1	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.006G118600.1	0.078614245	0.058128124	0.928881126	0.078423	0.937512761	0.95940604	grey	-0.025257241	0.750374488		AT5G47760.1		DNA/RNA helicase protein	NA
Sapur.016G240900.1	0.132574682	0.029013848	0.381260344	0.078051	0.937787495	0.95945558	grey	0.036454327	0.650352883		AT1G17780.2			NA
Sapur.005G154700.1	45.42406002	0.015347508	0.158868347	0.078042	0.937807047	0.95945558	grey	0.002239154	0.977958867	GO:0005515	AT1G60461.1	VIP5	Coatomer, beta' subunit	NA
Sapur.016G213200.2	0.253944119	0.048190849	0.538093847	0.07851	0.937966527	0.95949765	grey	-0.015435374	0.847781102	GO:0006457	AT4G38960.1	AT4G38960,PIB5PES,ROF2	PEBP-type peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl isomerase, putative
Sapur.001G021000.1	75.76783807	0.024088918	0.309555479	0.077818	0.937973008	0.95949765	grey	-0.008063474	0.920162268	GO:0016791,GO:0008152	AT1G17310.1		Pyridoxal phosphate phosphatase-related protein	inorganic diphosphatase
Sapur.006G130000.1	0.053918924	-0.011897688	1.152061126	0.07817	0.937979798	0.95949765	grey	-0.318631006	4.82E-05	GO:0016567,GO:0004842,GO:0005515	AT2G42240.1	PUB15	Plant U-box 15	E3 ubiquitin ligase PUB14, putative
Sapur.013G018200.1	0.072881709	0.09501196	1.221115804	0.077744	0.938018181	0.95949765	grey	-0.025170786	0.735120855		AT5G05470.1		Actin-binding FH2 (formin homology 2) family protein	formin-like 2 domain protein
Sapur.007G136400.1	0.108024669	0.077187622	0.966045015	0.077662	0.938135502	0.95956077	grey	-0.041632006	0.604591008	GO:0055114,GO:0020037,GO:0016705,GO:0005506	CYP78A7	CYP78A7	cytochrome P450, family 78, subfamily A, polypeptide 7	cytochrome P450 family protein
Sapur.014G047000.2	0.096126163	-0.078765475	1.016236584	-0.07749	0.938235859	0.95970564	grey	-0.080299427	0.317440031	GO:0003677	AT4G40040.1		ARID/BRIGHT DNA-binding domain,CLM2 domain protein	ARID/BRIGHT DNA-binding domain protein
Sapur.005G071200.2	91.60064017	0.010133268	0.060138544	-0.07747	0.938238457	0.95970564	grey	-0.117568313	0.145337761		AT4G39910.1		RING/U-box superfamily protein	hypothetical protein
Sapur.T160200.1	3.803638188	0.017328924	0.223706661	0.077463	0.938254554	0.95970564	grey	0.023566807	0.685455507		AT4G24706.2	AETH02,THO2	THO/TEX family protein	NA
Sapur.007G139200.1	0.027713285	0.070864181	1.211163364	0.077427	0.938275533	0.95970564	grey	0.013870087	0.833970572		AT5G45850.1		RING/U-box superfamily protein	ubiquitin-protein ligase, putative
Sapur.002G152800.1	0.5461586	-0.024878652	0.121520402	-0.07738	0.938287227	0.95980558	grey	-0.047632926	0.551578838	GO:0008270,GO:0005622,GO:0005515	AT4G27890.1		B-box type zinc finger protein with CCT domain	zinc finger constans-like protein
Sapur.002G098800.1	2.77042539	0.014275679	0.184554585	0.077255	0.938421055	0.95982317	grey	-0.019801823	0.809797978	GO:0220905,GO:0016651	AT5G57580.1	FRO1	NADH-ubiquinone oxidoreductase-related	NADH-ubiquinone oxidoreductase 18 kDa subunit
Sapur.T032200.1	0.070507248	0.064364691	1.224094721	0.077013	0.938495219	0.95982317	grey	-0.000301027	0.738316165	GO:0005509	AT5G11440.1		Calcium-binding EF-hand family protein	EF-hand pair protein
Sapur.019G072200.2	0.81276896	-0.021128229	0.273666777	-0.0772	0.938487821	0.95984921	grey	-0.033707701	0.675142809	GO:0005515	AT4G27220.1		NB-ARC domain-containing disease resistance protein	BED Finger NBS-LRR resistance protein
Sapur.004G261000.1	0.089087744	-0.010835776	1.01853563	0.077009	0.938663227	0.95997131	grey	0.000965126	0.967027027	GO:0016593,GO:0016570,GO:0006368	AT4G10040.1	VIP5	plus-3-domain containing protein	RNA polymerase-associated protein RTF1, putative
Sapur.005G159000.4	0.117606382	0.060306934	0.788385826	0.076862	0.938733305	0.95986104	grey	-0.066383413	0.48877651		AT1G27750.4			transmembrane protein, putative
Sapur.005G177700.2	0.11663331	0.054266885	1.004029578	0.076858	0.938856138	0.95986395	grey	-0.40367170	1.59E-07	GO:0003677,GO:0008289	AT5G25230.1	HDG2	homeodomain GLABROUS 2	homeobox leucine zipper protein
Sapur.006G189900.2	0.13461743	-0.060202583	0.785648853	-0.07663	0.938918517	0.95986395	grey	-0.078915068	0.177196326	GO:0016020,GO:0008378,GO:0006486	AT2G26100.1		Galactosyltransferase family protein	beta-1K23-galactosyltransferase, putative
Sapur.002G084600.2	0.062562724	0.090124124	1.313370092	-0.07646	0.938929769	0.95987095	grey	-0.022835154	0.868058428	GO:0005524	AT2G39200.1	RCA	rubisco activase	rubulose bisphosphate carboxylase/oxygenase activase
Sapur.002G061300.1	19.06362733	0.006808236	0.089102557	-0.07609	0.938979783	0.96008137	grey	0.00342272	0.969360077		AT3G42146.1			transmembrane protein, putative
Sapur.012G097600.1	0.120576615	0.057364564	0.836138727	-0.07583	0.939054564	0.96047452	grey	-0.073356067	0.33657386	GO:0045500,GO:0008312,GO:0000614	AT5G49100.1		Signal recognition particle, SRP9/SRP14 subunit	signal recognition particle 9 kDa protein
Sapur.004G133800.1	0.088069582	0.077004234	1.015674367	0.075816	0.939565591	0.96047452	grey	-0.030010006	0.70987141	GO:0015114,GO:0016491				amine oxidase, putative
Sapur.006G059200.1	0.115431265	0.075034269	1.011378281	0.07508	0.940502984	0.96100381	grey	-0.020767764	0.796478965	GO:0006661	AT1G64L,MOS1,UBA1	ubq10n-activating enzyme 1	ubq10n-activating enzyme E1	ubq10n-activating enzyme E1
Sapur.009G085700.1	0.111244918	0.059012174	0.9617806	0.074998	0.940519169	0.96182741	grey	-0.056383811	0.493076883	GO:0006488,GO:0004792	AT2G35385.1		Protein kinase family protein	NA
Sapur.011G019900.1	76.07882122	0.007010263	0.094722996	0.074983	0.940282189	0.96182741	grey	-0.005509981	0.999342258		AT5G55890.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.005G181800.1	0.06643153	0.079527119	1.002768092	0.074886	0.940348729	0.96146086	grey	-0.011230976	0.889312465		AT4G00280.1		RING/U-box superfamily protein	NA
Sapur.005G081000.3	0.10834768	0.067396794	0.905277402	0.074449	0.940653	0.96408135	grey	-0.014903055	0.85078836		AT5G09320.1		agenet domain containing protein	agenet domain protein
Sapur.012G028300.1	0.132928337	0.070842419	0.949807755	0.074357	0.940715148	0.96418861	grey	-0.181032167	0.015313883	GO:0046983	AT5G44030.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	BHLH transcription factor, putative
Sapur.008G089800.2	0.136500942	0.048583657	0.654564788	0.074223	0.940833254	0.96152632	grey	-0.016491837	0.837588398	GO:0046872,GO:0000166,GO:0016021,GO:0015914,GO:0005524,GO:0004012,GO:0000028	AT5G68730.1		ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	phospholipid-transporting ATPase, putative
Sapur.010G129800.4	0.814942223	0.007090278	0.280364846	0.074043	0.940875838	0.96164644	grey	0.008349079	0.917349011	GO:0003924,GO:0016020,GO:0005870,GO:0000886	AT1G28330.1	GALT1	galactosyltransferase family protein	beta-1K23-galactosyltransferase
Sapur.016G129400.1	0.056994958	-0.131868713	1.806380878	-0.0741	0.940830249	0.96151721	grey	-0.135293797	0.091119956		AT5G03665.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.006G035100.1	0.088544127	0.079396834	1.074233165	0.07409	0.940839935	0.96151721	grey	-0.003015568	0.970098813	GO:0016787,GO:0005524,GO:0003677,GO:0016817	AT5G17300.1	ATNOB1,INOB1	PNGB1 ortholog	DNA helicase INOB1
Sapur.010G089000.1	1.052885892	0.015192526	0.261080854	0.074023	0.940892293	0.96176318	grey	-0.000924104	0.857767113	GO:0016021,GO:0004190	AT5G45550.1	CYP76C4	cytochrome P450, family 76, subfamily C, polypeptide 4	cytochrome P450 family protein
Sapur.002G149100.1	29.24 1464	-0.005142214	0.070644315	-0.07279	0.941370262	0.96226255	grey	-0.009510106	0.958898866		AT5G28080.1		Tetratricopeptide repeat (TPR)-like superfamily protein	methyltransferase domain protein, putative
Sapur.005G134300.1	0.11774232	0.062880055	0.864815328	-0.07383	0.941484958	0.96267474	grey	-0.021570236	0.884160902		AT5G27410.2	MAPKKK9,MEK2	mitogen-activated protein kinase kinase 2	MAP kinase kinase kinase
Sapur.15WG148800.2	0.053224422	0.120668281	1.665789024	0.072619	0.942109141	0.96291694	grey	-0.007944183	0.921339591	GO:0003677,GO:0008289	AT4G00730.1	AHDP,ANL2	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein	homeobox domain protein
Sapur.015G079000.1	0.098160552	0.069315777	0.935256549	-0.07252	0.942165601	0.96360029	grey	-0.060019249	0.470492126	GO:0016874,GO:0016740,GO:0005524,GO:0004812,GO:0000166,GO:0006421,GO:0005737	AT4G17100.1	ATNS1,NS1,OVA9	Class II aminoacyl-tRNA and biotin synthetases superfamily protein	asparagine-tRNA ligase
Sapur.010G175700.2	0.050033203	0.120971525	1.672029944	0.07235	0.942332295	0.96234773	grey	-0.016519336	0.837178924	GO:0006508,GO:0004185	AT3G15730.1	scp28	serine carboxypeptidase-like 28	serine carboxypeptidase
Sapur.003G177000.6	0.311446601	0.042719147	0.591928265	0.072121	0.942424264	0.96287407	grey	-0.028372235	0.623092737		AT3G03220.1		RNA-binding (RRM/RBD/RNP motifs) family protein	NA
Sapur.011G091600.1	171.9929777	0.002935681	0.040801324	0.071951	0.942641189	0.96297254	grey	-0.010789367	0.883312459		AT5G46630.1		F-box family protein	NA
Sapur.012G154500.1	585.3091875	0.006007966	0.01931716	0.071864	0.942869132	0.96309243	grey	-0.018173136	0.813283936		AT5G57850.2	IK23A,NPH3,PHOT1,RPT1	phototropin 1	NA
Sapur.013G309600.1	2.311074997	-0.013371888	0.187117226	-0.0746	0.943029569	0.96286563	grey	-0.025573322	0.750542437		AT5G62140.1			hypothetical protein
Sapur.003G080800.1	184.9856888	0.003765631	0.052695439	-0.07146	0.943024141	0.96286563	grey	-0.00779471	0.922787742		AT4G22760.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.010G264500.1	0.163932024	0.045356166	0.635247349	0.071389	0.943080025	0.96296459	grey	-0.048882524	0.544863425		AT2G38870.1		Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	NA
Sapur.003G103200.2	0.063941141	0.094161082	1.310682203	0.071351	0.943118155	0.96291569	grey	-0.00013369	0.454382191	GO:0071805,GO:0016020,GO:0015079	AT3G00570.1	ATKT1,ATKT1P,ATKUP,KT1	potassium transporter 1	potassium transporter
Sapur.006G219700.1	0.063641473	0.050281197	1.410406915	0.07113	0.943259646	0.96303751	grey	-0.106828654	0.181160603		AT2G38854.1			Myb/SANT-like DNA-binding protein family
Sapur.004G107400.1	0.082385223	-0.100320847	1.410845178	-0.07111	0.943312461	0.96303751	grey	-0.125523406	0.132696688		AT4G15110.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3	NA
Sapur.007G201700.1	0.095572000	0.052180152	1.015134204	0.071061	0.943325089	0.96303751	grey	-0.016523631	0.819232122					hypothetical protein
Sapur.004G082700.2	0.051929933	0.158631101	2.233743419	0.071015	0.943385446	0.96306942	grey	-0.00593167	0.94122496		AP61		acclimation of photosynthesis to environment	protein acclimation of photosynthesis to environment protein
Sapur.009G081000.1	0.260969819	0.047276507	0.391435324	0.070912	0.943467839	0.96321886	grey	-0.070464064	0.39131185		AT5G57630.1	DVL17,RTL6	ROTUNDIFOLIA 6	NA
Sapur.004G075200.2	0.05817527	-0.003314899	1.417084828	-0.07075	0.943595535	0.96322622	grey	-0.085918316	0.166684466	GO:0055114,GO:0016616,GO:0006694,GO:0003854,GO:0019752	AT4G37520.1	MDH	malate dehydrogenase	NAD-malate dehydrogenase
Sapur.010G199300.1	0.162224325	-0.047369804	0.671294016	-0.07053	0.943788816	0.96340072	grey	-0.046443354	0.563537553	GO:0043130,GO:0032266	AT5G06920.1		EAP30/Vps36 family protein	vacuolar protein sorting protein
Sapur.014G135300.1	0.022153397	0.074378446	0.946126264	0.070647	0.943892912	0.96377789	grey	0.02265674	0.774393594		AT2G25250.1		DNA heat shock N-terminal domain-containing protein	heat shock protein
Sapur.012G093600.1	74.38809027	0.02456245	0.348810388	0.070417	0.943862063	0.96377789	grey	-0.004238685	0.960061749					NA
Sapur.006G123300.1	0.147316147	0.050239213	0.845592386	0.069693	0.944369421	0.96382382	grey	-0.027842952	0.739236473					NA
Sapur.016G227400.2	0.082341274	0.079439991	1.139691664	0.069942	0.944239756	0.96385953	grey	-0.405648815	1.36E-07	GO:0008641	AT5G51330.1	CNX5,SIR1	co-factor for nitrate, reductase and xanthine dehydrogenase 5	adenylyltransferase and sulfurtransferase MOCS3
Sapur.009G051800.2	0.083474864	0.079734347	1.140943647	0.069915	0.944401155	0.96385953	grey	-0.01531751	0.903905858		AT2G27520.1		plectin-related	Cyclin 4
Sapur.U002G09901.1	0.013476548	-0.030087079	0.445402243	-0.06957	0.944535246	0.96387545	grey	-0.013069847	0.870575968					NA
Sapur.002G062500.1	0.074978671	0.067485249	0.966566526	0.069665	0.944566325	0.96387545	grey	-0.027842956	0.739236473		AT5G27160.1		Protein of unknown function (DUF506)	DUF506 family protein
Sapur.T046600.2	0.077369411	0.07974781	1.147643126	0.069488	0.944609318	0.96394729	grey	-0.018451184	0.818546807		AT3G07330.1	ATCS,CB,ATCSLC5,CS,CSC	Cellulose synthase-like C5, glycosyltransferase family 2	cellulose synthase-like C5, glycosyltransferase family 2
Sapur.005G131300.1	5.131330867	0.012343821	0.229070662	0.069444	0.944622554	0.96394729	grey	-0.040247007	0.619430975		AT4G22,H822,MESE8		homeobox protein 22	NA
Sapur.013G057800.1	0.26621849	-0.035114348	0.506365569	-0.06935	0.944707903	0.96397089	grey	-0.07746157	0.134903365	GO:0006396,GO:0000176,GO:0005622,GO:0000376,GO:0008408,GO:0006139	AT5G35931.1		Polynucleotidyl transferase, ribonuclease H fold protein with HRDC domain	2'-5' exonuclease
Sapur.003G162600.1	0.070233154	0.122875284	1.771789411	0.069351	0.944732181	0.96397589	grey	-0.054188557	0.500281557					NA
Sapur.007G087000.1	2.418621933	0.017628388	0.09217229	0.068717	0.945212	0.96445154	grey	0.003729487	0.960455149	GO:0005515,GO:0043531	AT6G27230.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.002G095400.1	0.267828886	-0.033192982	0.483878978	-0.0686	0.945208954	0.96498338	grey	-0.078914913	0.325888806					NA
Sapur.016G138000.2	0.058959737	0.104275502	1.248355685	0.068589	0.945388398	0.96517527	grey	-0.000507251	0.993161464	GO:0005085,GO:0016021	AT5G59250.1		Major facilitator superfamily protein	D-xylose-proton symporter-like protein
Sapur.019G042700.1	0.127283652	0.057519708	0.840807766	0.06841	0.945492015	0.96541463	grey	-0.060017283	0.455107212		AT5G62180.1		Disease resistance protein (TIR-NBS-LRR class) family	TIR-NBS disease resistance-like protein, putative
Sapur.010G170300.1	0.065715217	0.078805673	1.153832193	0.068312	0.945537149	0.96560804	grey	-0.054152762	0.497267728		AT2G27750.2	AT-EXP10,ATEXP10,ATEXPA	expansin A10	alpha-expansin
Sapur.010G047900.1	0.080898766	0.078381128	1.148315063	0.068255	0.945582349	0.96560804	grey	-0.032093832	0.688884766		AT4G24260.2		Protein of unknown function (DUF3664)	6-sp transcription factor
Sapur.015G189600.1	0.127690507	0.058284224	0.739132232	0.068146	0.945627884	0.96560804	grey	-0.054563631	0.435141142		AT5G46240.1		C2H2-like zinc finger protein	C2H2-like zinc finger protein, putative
Sapur.006G070000.2	0.057170501	-0.135642121	1.995149088	-0.06797	0.945807661	0.96470846	grey	0.368908981	1.99E-06	GO:0010338,GO:0006351,GO:0005634	AS1,ATMYB91,ATMYAH,MYI	myb-like HTH transcriptional factor family protein	MYB-related transcription factor, putative	NA
Sapur.001G185500.1	0.054764908	0.121890756	1.809908705	0.067895	0.945888835	0.96476128	grey	0.055872318	0.485935928		AT5G23120.1	CYCP1;1	cyclin p1;1	cyclin protein
Sapur.013G139600.1	0.083018807	-0.060692826	1.01908884	-0.0678	0.945841703	0.96478851	grey	0.058647105	0.281632					NA
Sapur.005G018800.1	0.240061197	0.033397592	0.495810329	0.067763	0.945974299	0.96489354	grey	-0.064070225	0.421002586	GO:0070188,GO:0003697	AT5G62640.1			telomere-capping, CST complex subunit
Sapur.010G062400.1	0.076275544	0.099029154	1.126067015	0.067684	0.946028842	0.96487215	grey	0.454037342	1.34E-07	GO:0005886,GO:0005524,GO:0004672	AT5G38880.1	cki3	casein kinase I-like 3	casein kinase-like protein
Sapur.003G176200.1	0.053748693	-0.119218893	2.006857447	-0.06759	0.946113827	0.96487215	grey	-0.273137352	1.59E-06					NA
Sapur.011G029300.1	0.400668204	0.007208135	0.176844708	-0.06747	0.946126774	0.96488276	grey	-0.005312293	0.958083118	GO:0005096	AT5G54330.1	AGD5,NEV	ARF-GAP domain 5	ARF-GTPase activating protein, putative
Sapur.012G290100.2

Sapur.01G0300400.3	38.17684548	-0.04685237	0.087443474	-0.05495	0.95617631	0.97131083	grey	0.004155159	0.95880706			AT4G04860.1	DER2.2	DERLIN-2.2	derlin-2 protein
Sapur.0096G0630800.2	0.06129023	0.083408249	1.521124628	0.554833	0.95627189	0.97127726	grey	-0.00088753	0.9911998	GO:0046861		AT4G37850.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH35
Sapur.0072G0640005.5	13.13496621	0.050827823	0.926018303	0.554637	0.95647327	0.97138897	grey	-0.00772425	0.92351874	GO:0016168;GO:0006355;GO:0005634		AT4G27280.1		MRG family protein	mortality factor-like protein
Sapur.0142G0410061.1	1.505709583	0.011935514	0.218618557	0.554595	0.95646102	0.97138897	grey	0.033670274	0.675483112			AT3G60430.1		Protein of unknown function (DUF1639)	DUF1639 family protein
Sapur.1596G0800030.3	0.05683788	0.083464464	1.530180612	0.554515	0.95624536	0.97141559	grey	-0.00571254	0.98303481			AT4G18120.1			arginine/serine-rich coiled coil protein, putative
Sapur.1596G1269001.1	0.053307687	0.083416422	1.532988228	0.554414	0.95685145	0.97146755	grey	0.27341685	0.00553651	GO:0016884		AT5G07160.1		Amidase family protein	NA
Sapur.0123G0780001.3	0.08452864	0.054996553	1.010183308	-0.05428	0.95671122	0.97153887	grey	-0.07538398	0.345207048	GO:0008270		AT5G26935.1		DHHC-type zinc finger family protein	palmitoyltransferase ZDHHC5, putative
Sapur.0001G0280100.1	0.085002384	0.088100479	1.021458051	-0.05422	0.95679395	0.97153887	grey	-0.02858009	0.72231052	GO:0003723		AT4G13070.1		RNA-binding CRS1 / YhbY (CRM) domain protein	NA
Sapur.0032G0390600.2	0.15169265	0.083421755	1.540809936	0.554139	0.95682699	0.97157291	grey	0.01692266	0.80854005			AT3G19690.1		NAD(P)-binding Rossmann-fold superfamily protein	NAD-dependent epimerase/dehydratase
Sapur.0020G0601001.1	1.965082934	0.153605263	0.924089233	0.553289	0.95688251	0.97158035	grey	-0.02991179	0.70989344	GO:0006950;GO:0006468;GO:0005524;GO:0004672		AT3G77280.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	adenine nucleotide alpha hydrolases-domain kinase
Sapur.0150G0177001.1	0.353101967	0.098327284	1.820234849	-0.05396	0.95689344	0.97159835	grey	-0.11570708	0.14900561	GO:0005524;GO:0016776		AT5G19210.2		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.0118G0600.1	0.102272722	0.083408556	1.021352264	0.553614	0.95689543	0.97160651	grey	-0.10341417	0.10741884						NA
Sapur.0105G0420000.2	0.206347666	-0.033257576	0.625041411	-0.05364	0.95720135	0.97185082	grey	-0.02597297	0.74678561	GO:0003824;GO:0006470;GO:0004722		AT4G23360.1		Protein phosphatase 2C family protein	protein phosphatase 2C, putative
Sapur.0151G0245001.1	13.11496621	0.053408226	0.926018303	0.554637	0.95726492	0.97188647	grey	-0.09020378	0.87843642			AT2G39410.1		RNI-like superfamily protein	F-box protein At-8 protein
Sapur.0182G0947001.1	1.625.660711	-0.002074012	0.038782424	-0.05348	0.95730955	0.97186726	grey	-0.08930964	0.31742861			AT3G11890.1		adenylate cyclase	adenylate cyclase
Sapur.0062G1310001.5	0.072847938	0.083463831	1.076880234	0.553464	0.95730955	0.97186726	grey	-0.06437552	3.2E-07	GO:0005515		AT5G48450.2	TBR1	TOPLESS-related 2	topless-related protein
Sapur.0061G4800004.4	0.06147249	0.08163282	1.52755876	0.55344	0.95731294	0.97186726	grey	-0.07689523	0.33975272			AT5G57880.1	ATPRD2,MPS1,PRD2	multipolar spindle 1	recombination initiation defect 2 protein, putative
Sapur.0096G0023000.2	0.08798731	0.032387565	0.806760288	0.553277	0.95743177	0.97188755	grey	0.05110259	0.82923173	GO:0055114;GO:0046872;GO:0006801;GO:0071486;GO:0034599;GO:0009507		AT2G28190.1	CSD2,CZSOD2	copper/zinc superoxide dismutase 2	superoxide dismutase [Cu-Zn] protein
Sapur.0182G0413001.1	0.054783799	0.042829492	1.809093637	0.553023	0.95753618	0.97196293	grey	-0.07252318	0.30362915						NA
Sapur.0062G1310000.2	0.690885735	0.015783879	0.297539874	0.553048	0.95769307	0.97205558	grey	0.023077422	0.77419908	GO:0005525		AT2G24765.1	ABR1,ARL1,ATARL1	ADP-ribosylation factor 3	NA
Sapur.0051G2740001.9	0.060309125	0.054996553	1.026088172	0.553019	0.95783129	0.97206051	grey	-0.12482353	0.11932365						NA
Sapur.0021G0180100.1	0.070329915	0.08019694	1.523576327	0.553267	0.95802085	0.97227671	grey	0.413364992	7.29E-08	GO:0006904;GO:0000145		AT3G02350.1	SEC15B	exocyst complex component sec15B	exocyst complex subunit Sec15-like protein
Sapur.0182G0252001.1	0.071125115	0.085320369	1.042884418	0.55216	0.95817763	0.97246944	grey	-0.16445299	0.03573319			AT5G22270.1		Nucleotide transfer family protein	NA
Sapur.0141G1428001.1	196.5525065	-0.002171327	0.041396946	-0.05245	0.95819702	0.97267088	grey	-0.04617722	0.57852617			AT4G07568.1			NA
Sapur.0075G0778001.1	1.346513637	0.013408229	0.102638303	-0.05221	0.95824859	0.97267088	grey	-0.02231606	0.78343522	GO:0006468;GO:0005524;GO:0004672		AT5G66910.1		Protein kinase superfamily protein	NA
Sapur.0013G1290002.2	0.08003799	-0.053015288	1.016783695	-0.05214	0.95841695	0.97263991	grey	-0.10327777	0.20361604			AT5G13200.1		GRAM domain family protein	PH-GRAM-GEM domain protein
Sapur.0182G0890001.1	25.03663854	0.004994837	0.095825251	0.052124	0.95842547	0.97263991	grey	-0.02237971	0.77132215	GO:0006508;GO:0004185		AT4G38630.1	BRS1,SCPL26	alpha/beta-Hydrolases superfamily protein	serine carboxypeptidase
Sapur.0050G0230001.1	664.1374882	-0.002465555	0.047388333	-0.05203	0.95850405	0.97275750	grey	-0.00709276	0.92802306			AT5G07370.1		sequence-specific DNA binding transcription factors	Myb/SANT-like DNA-binding domain protein
Sapur.0120G0691000.1	540.5838290	-0.001686748	0.038198311	-0.05201	0.95851961	0.97275702	grey	0.00390983	0.98255277	GO:0006396		AT5G62640.1	ELF5	proline-rich family protein	WW domain-binding protein
Sapur.0162G0770001.1	0.167338	0.042888893	0.810115228	-0.05195	0.95854183	0.97292166	grey	-0.04804747	0.55129003	GO:0005975;GO:0004553		AT2G29960.1	AtGH9B8,GH9B8	glycosyl hydrolase family 9	glycosyle hydrolase family 9 protein
Sapur.0042G0120002.2	0.058992253	0.085344373	1.649551645	0.551739	0.95873641	0.97256231	grey	0.022008332	0.7844021	GO:0005975;GO:0004553		AT5G01820.1	BGLU46	beta glucosidase 46	NA
Sapur.0062G0440001.1	341.1751127	-0.004793191	-0.059124522	-0.05155	0.95886639	0.97280474	grey	0.03195429	0.87018204	GO:0003779		AT4G34135.1	ATVLN4,VLN4	villin 4	NA
Sapur.0070G0700.1	0.052807848	0.085352197	1.664432809	0.55128	0.95902212	0.97307247	grey	0.028142674	0.72643015	GO:0008234;GO:0006508		AT5G45890.1	SAG12	senescence-associated gene 12	cysteine protease, putative
Sapur.0062G0810001.1	0.072846761	0.056828707	1.082286517	0.55123	0.95915313	0.97287107	grey	0.028463119	0.73254492	GO:0055114;GO:0006633;GO:0016627		AT4G34150.1		calmodulin-binding protein / sperm-specific antigen 2 protein	calmodulin-binding protein / sperm-specific antigen 2 protein
Sapur.0120G0950001.1	1.902591997	0.010476861	0.205215134	0.551044	0.95920374	0.97317624	grey	0.10711398	0.18179536			AT3G15130.1	GRL,NAP5,NAP7	transcription activators	NA
Sapur.0120G0190700.1	0.131011203	0.056828707	0.534665647	0.550893	0.95924981	0.97327165	grey	-0.02119966	0.91332371	GO:0015986;GO:0015078;GO:0000276		AT4G29480.1		Mitochondrial F0F1-ATPase subunit G protein	hydrogen-transporting ATP synthase, rotational mechanism protein%3C putative
Sapur.0041G0185001.1	0.129158457	0.098499895	0.985288028	0.550746	0.95952798	0.97351697	grey	-0.00073901	0.99272187			AT5G03170.1	FASCLN1,FLA11,FLA11	FASCILIN-like arabinogalactan-protein 11	NA
Sapur.0031G1680001.2	0.362089732	0.021606982	0.52188894	-0.0507	0.95962739	0.97365379	grey	-0.00692586	0.94051812	GO:0003676;GO:0006418;GO:0005524;GO:0004812;GO:0000166		AT4G13940.1	ATKRS-2,LYS4S	Lysyl-tRNA synthetase, class II	lysine-tRNA ligase
Sapur.0051G1940001.1	4.387678059	-0.004720632	0.013657954	0.13017928	-0.05059	0.95983677	grey	0.014592223	0.85411547						hypothetical protein
Sapur.0062G0960002.2	0.072814224	0.070886208	1.407623977	0.550366	0.95983804	0.97367719	grey	0.038878504	0.62878905	GO:0005985		AT5G06470.1		Nucleotide/sugar transporter family protein	triose-phosphate transporter family protein
Sapur.0186G0040001.1	0.353965544	0.098327284	1.668836132	0.550022	0.95994008	0.97408708	grey	-0.12460169	0.11992353			AT3G07020.1	GalAK	galactokinase family protein	galactokinase, putative
Sapur.0182G0790001.2	1.327014691	-0.010752868	0.214384652	0.55016	0.95996531	0.97362421	grey	-0.0022419	0.97778642	GO:0005085;GO:0016020;GO:0006811;GO:0005216		AT4G30160.1	ATCNGC13,CNGC17	cyclic nucleotide-gated channel 17	cyclic nucleotide-gated ion channel protein, putative
Sapur.0171G1200.1	0.107258277	-0.003264403	0.080445511	-0.04969	0.96001329	0.97378387	grey	-0.08187208	0.33802817	GO:0046872;GO:0030001		AT2G27260.1		Copper transport protein family	heavy metal-associated domain protein
Sapur.0031G1525001.1	11.66698703	-0.005418428	0.109259344	-0.04959	0.96044728	0.97402608	grey	-0.03904115	0.62747257						NA
Sapur.0120G0190100.1	0.067597522	-0.00468751	-0.036429531	-0.04948	0.96052293	0.97480505	grey	-0.12279246	0.11497667	GO:0016757		AT3G18180.1		Glycosyltransferase family 61 protein	NA
Sapur.0032G0670001.1	0.085435128	-0.066584775	1.392568358	-0.04781	0.96185007	0.97481269	grey	-0.08543005	0.28625332	GO:0046983;GO:0003677		AT5G10140.1	AGL25,FLC,FLF	K-box region and MADS-box transcription factor family protein	NA
Sapur.0194G0331001.1	0.134460207	-0.00386129	0.749439042	-0.04782	0.96187567	0.97481204	grey	0.18737912	0.01877604	GO:0016746;GO:0008168		AT1G08950.1		Phosphatidyl glycerol acyltransferase family protein	1-acyl-sn-glycerol-3-phosphate acyltransferase
Sapur.0042G0870001.2	0.051168807	-0.004488897	1.668805614	-0.04883	0.96187567	0.97400066	grey	-0.14017794	0.06974258	GO:0006468;GO:0005524;GO:0004672		AT5G10580.1		Protein kinase superfamily protein	Serine/Threonine-kinase like protein
Sapur.1596G1190008.8	0.072635688	0.059499167	1.228502157	0.04883	0.96195966	0.97400066	grey	-0.01878614	0.81154581			AT4G8860.2			ribosomal protein
Sapur.0050G0390001.1	0.086839303	-0.004720632	1.142192522	0.04877	0.96196974	0.97400674	grey	-0.03537551	0.68207963			AT2G41610.1	PMP	putative type 1 membrane protein	NA
Sapur.0162G0547000.2	0.0693921	0.059500444	1.122103937	0.04868	0.96198821	0.97426728	grey	-0.01294248	0.87188524			AT3G10140.1	REC42	REC4 homolog 3	DNA repair protein Rec4, putative
Sapur.0131G1010001.1	0.068879795	-0.003661312	1.092455534	0.04804	0.96246172	0.97461694	grey	-0.07360907	0.33917561	GO:0006364;GO:0003723		AT4G24120.2		Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain	regulator of chromosome condensation-like protein with FYVE zinc finger protein
Sapur.0050H0940.1	0.060319587	0.059504244	1.233026622	0.048259	0.96155018	0.97483003	grey	-0.05703165	0.47747927						NA
Sapur.0062G1350001.3	0.055222969	0.059500755	1.236526195	0.048201	0.96155029	0.97499568	grey	-0.05453876	0.49473687	GO:0016579;GO:0006843		AT2G27350.6		OTU-like cysteine protease family protein	ring-finger, C3HC4-type (RING finger) protein
Sapur.0020G0613000.1	0.053079505	0.059505145	1.235682553	0.048156	0.96159142	0.97705896	grey	-0.08160864	0.30950942			AT5G21000.1		PLATZ transcription factor family protein	PLATZ transcription factor family protein
Sapur.0062G0010001.1	0.057557141	0.059505535	1.236807256	0.048112	0.96162832	0.97717774	grey	-0.04406003	0.58435329						NA
Sapur.0021G1530001.2	0.159448266	0.030816771	0.642285431	0.04768	0.96173239	0.97768822	grey	-0.32779671	2.78E-05			AT5G02930.1	LPA1	tetratricopeptide repeat (TPR)-containing protein	LOW PSII ACCUMULATION protein
Sapur.0071G0940001.1	0.086146374	0.064287064	1.390138316	-0.0479	0.96179572	0.97479166	grey	-0.21252971	0.00734193			AT5G61460.1	EDA35	temperature sensing protein-related	cell division cycle-like protein
Sapur.0075G0930001.2	0.108148847	0.057416916	0.786264796	-0.0479	0.96179978	0.97479166	grey	-0.08093928	0.31470978	GO:0009231;GO:0009319		AT5G08340.1		Nucleotidyl transferase superfamily protein	riboflavin biosynthesis protein, putative
Sapur.0030G0274000.1	0.081535528	-0.066584775	1.392568358	-0.04781	0.96185007	0.97481269	grey	0.07854831	0.32814497			AT5G48120.1		ARM repeat superfamily protein	MMS19 nucleotide excision repair-like protein
Sapur.1596G0331300.1	0.134460207	-0.00386129	0.749439042	-0.04782	0.96187567	0.97481204	grey	-0.05191429	0.51859673	GO:0016757		AT3G61630.1		Glycosyltransferase family 61 protein	NA
Sapur.0032G0180001.1	0.100176615	-0.043762275	0.913723868	-0.04736	0.96226662	0.97483584	grey	-0.28702-respective NPH3 family protein				AT5G11570.1		Phototropic-responsive NPH3 family protein	NA
Sapur.0062G0470001.2	0.057944015	0.059504244	1.233026622	0.048156	0.96229378	0.97483584	grey	-0.01987556	0.88492787	GO:0006355;GO:0003677		AT5G05180.1	ANAC008,SOG1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC transcription factor 093
Sapur.0030G0995000.1	84.79296606	-0.025671366	0.470606921	0.047325	0.962539	0.97483584	grey	-0.01354304	0.86631155	GO:0005085;GO:0042626;GO:0016021;GO:0006810;GO:0005524;GO:0016887		AT5G59140.1	ATMRP14,MRP14	multidrug resistance-associated protein 14	multidrug resistance protein ABC transport family protein, putative
Sapur.0194G0472001.1	146.7899964	-0.005882204	0.114452214	-0.04724	0.96232629	0.97483584	grey	-0.00582056	0.94323195						hypothetical protein
Sapur.0192G0391001.1	52.03251564	0.003887596	0.082447186	0.047367	0.96238324	0.97483584	grey	-0.01627614	0.83867049	GO:0005524		AT4G30130.1	AATP1	AAA-ATPase 1	AAA family ATPase
Sapur.0030G0990001.1	0.8614524	0.003887596	0.176368196	0.047175	0.96238324	0.97483584	grey	0.02989058	0.73090868	GO:0006296;GO:0004634;GO:0000287;GO:0000015		AT2G36530.1	EN,CL1,CL2	Enolase	NA
Sapur.0192G0446001.1	1.619174323	0.009005166	0.19115208	0.04711	0.96245592	0.97483584	grey	-0.15238207	0.05675325			AT4G27633.3			transmembrane protein, putative
Sapur.1596G0819000.1	0.051338886	0.085423948	1.822042214	0.046858	0.96282679	0.97537425	grey	0.07342555	0.38077163						NA
Sapur.0135G0010001.3	0.108605741	0.083408249	0.962622219	0.046861	0.96282516	0.97536861	grey	-0.08202515	0.35433657			AT2G37175.1		RING/U-box protein with domain of unknown function (DUF 1232)	C3HC4-type RING finger family protein
Sapur.7041400.1	0.978814882	-0.010507386	0.234137875	0.046713	0.96274237	0.97214809	grey	-0.00890807	0.91831643	GO:0008270;GO:0008022;GO:0006625;GO:0005779		AT3G04660.1	APM4,ATPDX12,PDX12	pyridoxal 5'-phosphate synthase family protein	pyridoxine/pyridoxamine 5'-phosphate oxidase family protein
Sapur.0062G0940001.1	0.08413062	0.053333	1.318863537	0.046613	0.96282102	0.97265055	grey	-0.04245586	0.58481826	GO:0005270;GO:0005515		AT4G26010.1		RING/U-box superfamily protein	NA
Sapur.0032G0967000.2	0.070570732	-0.064716886	1.401943351	-0.04619	0.96316252	0.97550884	grey	-0.06631589	0.40910186			AT4G11270.1		Transducin/WD40 repeat-like superfamily protein	NA
Sapur.0162G0480001.1	0.163654764	0.031150869	0.676202222	-0.04608	0.96324612	0.97580503	grey	-0.06990303	0.38426618	GO:0043565;GO:0006351		AT3G48820.1			transcription factor TGAL
Sapur.0010G0547000.1	0.211682757	0.023107877	0.501621818	-0.04607	0.96326723	0.97586503	grey	-0.08983942	0.26318976						NA
Sapur.0171G0580100.1	0.075569008	0.053522159	1.296544845	0.045805	0.96329339	0.97636517	grey	-0.02607864	0.75723475			AT5G05530.1			hypothetical protein
Sapur.0120G0950100.3	4.885449924	0.005546869	0.121528613	0.045636	0.96360005	0.97585343	grey	-0.05875991	0.46478174			AT4G04640.1		Complex I subunit NDUFS6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-A
Sapur.0062G0920001.1	2.019360899	0.009869888	0.215600127	0.045625	0.96368792	0.97585343	grey	-0.00349489	0.98959187	GO:0005385		AT4G11220.1		Nucleotide-sugar transporter family protein	sugar phosphate/phosphate translocator, putative
Sapur.0120G0190600.1	52.16181154	0.012316857	0.270614661	0.045528	0.96386659	0.97585343	grey	0.01928025	0.81893601	GO:0003824;GO:0006470;GO:0004722		AT4G31600.1		Protein phosphatase 2C family protein	NA
Sapur.0162G0057000.3	0.54421847	0.015092867	0.33263724	0.045373	0.96389721	0.97567262	grey	-0.00838622	0.91974			AT4G27630.1	mtACP3	mitochondrial acyl carrier protein 3	acyl carrier protein
Sapur.0162G0740001.1	0.054853341	0.054301621	1.667862535	0.045123	0.96393237	0.97635054	grey	-0.02570385	0.74836259			AT5G20280.1			DUF4339 domain protein
Sapur.0152G0810001.1	0.061541723	0.059503032	1.317471521	0.045185	0.96395638	0.97650933	grey	-0.02831533	0.71999136			AT5G68630.1		PLACE family protein	fruit weight 2.2-3 protein, putative
Sapur.0162G0120001.1	0.060585819	0.059503007	1.318863537	0.045168	0.96397649	0.97667727	grey	-0.04562742	0.58796867						NA
Sapur.0050G0580001.2	0.10600871	0.038601227	0.862995772	0.045077	0.96404945	0.97686948	grey	-0.04934466	0.61589341			AT5G10010.1			ATP/GTP-binding protein, putative
Sapur.0171G0812000.1	0.095894988	0.085888846	1.913242462	0.04489	0.96434968	0.97820476	grey	0.05737809	0.47352865			AT1G70190.1		Endosomal targeting BORG-like domain-containing protein	BORG-like domain protein
Sapur.0081G1940001.1	1.124483214	0.011982766	0.267411097	0.04481	0.96428531	0.97820476	grey	-0.01674704	0.83509262	GO:0031047		AT3G22430.1			XS domain protein
Sapur.0120G0950700.1	0.065153007	0.042867439	0.955264159	0.044811	0.96429133	0.97820476	grey	-0.16381181	0.04362015						NA
Sapur.0120G0970001.1	0.062182753	-0.06285044	1.408416615	-0.04462	0.96466301	0.97827466	grey	-0.02284158	0.25033767			AT1H5,FH5	ATFH5,FH5	formin homology5	formin-like 2 domain protein
Sapur.0061G1990001.4	0.061254825	0.062869348	1.409021646	-0.04458	0.96464501	0.97828761	grey	0.02855592	0.72358023	GO:0006641		AT5G42270.1	ATSAE2,SMA2764,SAE2	SUMO-activating enzyme 2	SUMO1 activating enzyme subunit 2
Sapur.1596G0100.1	0.091695434	0.048352041	1.094089856	0.044194	0.96479888	0.97526376	grey	-0.04427652	0.18311348	GO:0006468;GO:0005524;GO:0004672		AT4G37570.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.0062G0500001.1	0.112173477	0.035408856	0.802405577	0.044163	0.96479126	0.97525261	grey	-0.04140765	0.57419948	GO:0006629;GO:0006508;GO:0004190		AT5G22290.2		Sugosin-like aspartyl protease family protein	aspertic protease oryzasin protein
Sapur.0120G0950100.2	0.124895413	0.042867439	0.862765636	0.044153	0.96503247	0.97627808	grey	-0.02479646	0.75883961	GO:0006355;GO:0003677		AT5G62430.1	ANAC054,NAC054	NAC domain protein	NAC domain protein
Sapur.0120G0810001.1	28.55613823	-0.011295407	0.258162693	-0.04375	0.96510245	0.97629629	grey	-0.00089849	0.99018008						NA
Sapur.0162G0120001.1	0.187469562	0.029269491	0.627122224	-0.04318	0.96523878	0.97689756	grey	-0.08108355	0.33232181			AT4G29080.1		Ribonuclease H-like superfamily protein	NA
Sapur.0141G0960001.1	651.5823822	0.001175531	0.039432686	0.043556	0.96529309	0.97689756	grey	-0.02208477	0.78366829			AT3G03000.1	NPL41	NPL4-like protein 1	nuclear pore localization protein NPL4
Sapur.0120G0950400.1	0.083481149	0.052648681	1.217621484	0.04346	0.96534295	0.97692764	grey	-0.18052302	0.02650828			AT3G56640.1			NA
Sapur.0132G0540001.3	0.141527111	0.028634528	0.660664239	-0.04334	0.96542893	0.97708624	grey	-0.36589179	2.48E-06			AT3G13480.1	ECT2	evolutionarily conserved C-terminal region 2	YTH domain protein
Sapur.0171G0680.1	0.078577215	-0.064628124	1.148686854	-0.04314	0.96553133	0.97712356	grey	-0.07963038	0.31224874			AT3G17165.1			hydrogen peroxide induced protein
Sapur.1596G0093001.1	0.073407874	0.046963035	1.090331634	0.043073	0.96564375	0.97712878	grey	-0.07562441	0.35013227			AT5G33045.1		RWP-RK domain-containing protein	RWP-RK domain protein
Sapur.0182G0880001.2	1.805199113	-0.012399586	0.288025163	-0.04305	0.96568075	0.97723878	grey	0.00835014	0.91726767	GO:0005975;GO:0004553;GO:0006468;GO:0005524;GO:0004672		AT4G11530.1	CRK34	cysteine-rich RLK (RECEPTOR-like protein kinase) 34	NA
Sapur.0162G2830001.1	0.099563223	-0.003664499	0.086109622	0.042919	0.96595969	0.97750574	grey	0.11393665	0.05423158	GO:0006396;GO:0000724		AT5G55100.2		SWAP (Suppressin of WHP-APricot)/surp domain-containing protein	suppressor-of-white-apricot-like protein, putative
Sapur.0132G0870002.2	0.132651958	0.034351175	0.917521382	0.042019	0.96645801	0.97806896	grey	-0.22084677	0.78366829			AT3G03600.1	ATORC1,ORC3	origin recognition complex subunit 3	origin recognition complex subunit 3
Sapur.0021G0190000.1	0.063132007	0.042867439	0.955264159	0.041966	0.96750151	0.97852068	grey	-0.07160206	0.37102386	GO:0003676		AT5G45630.1		RNA binding (RRM/RBD/RNP motifs) family protein	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.0070G0740001.9	0.352168208	-0.016221375	0.393751956	-0.0412	0.96718384	0.97892223	grey	-0.0107066	0.88412609			AT5G55485.1		UDP-Glycosyltransferase superfamily protein	starch synthase, putative
Sapur.0062G4710001.1	0.514448884	0.015326439	0.377230407	-0.04119	0.96747498	0.97892223	grey	-0.06750279	0.49093872			AT5G12230.1	MED19A		hypothetical protein
Sapur.0162G0810001.2	0.058301011	-0.062766624	1.526836458	-0.0411	0.96751319	0.97836265	grey	-0.06124964	0.18374769	GO:0006468;GO:0006672		AT4G36700.1	CDK9,CTK2	CDPK-related kinase 3	CDPK-related kinase, putative
Sapur.0153G0130001.1	0.075393101	0.042867439	0.955264159	0.041047	0.96764958	0.97836465	grey	0.00255407	0.93798539			AT4G27770.1	EMB2777	Sec61G/14 domain-containing protein (Lrp) family protein	hypothetical protein
Sapur.0062G0510001.5	0.138150335	-0.035792118	0.870958053	-0.0405	0.96774136	0.97829691	grey	-0.07984214	0.32020415	GO:0005634;GO:0006777		AT5G42370.1	SPL2	squamosa promoter binding protein-like 2	promoter-binding protein SPL10, putative
Sapur.0096G0600001.1	0.381976326	0.035881981	0.389737969	0.04075	0.96796876	0.97850413	grey	-0.02073850	0.79637121	GO:0006418;GO:0005524;GO:0004812;GO:0000166;GO:0016874		AT4G33760.1		tRNA synthetase class II (D, K and N) family protein	NA
Sapur.0096G0147500.1	0.091880027	0.042867439	0.955264159	0.040676	0.96852449	0.97888734	grey	-0.02324742	0.69039633			AT3G19540.1		Protein of unknown function (DUF620)	lipase, putative
Sapur.0096G0720001.2	0.234480149	-0.019654429	0.487319797	-0.04033	0.96782835	0.97877788	grey	-0.06840439	0.2276019			AT5G27640.1	AGL48	ARM repeat superfamily protein	Arc5/CT-9 rapidly elicited protein
Sapur.0120G0950900.1	0.516527518	0.004488897	0.412080609	-0.04008	0.96852538	0.97884762	grey	-0.02787835	0.77809128	GO:0016567;GO:0006842		AT5G19610.1	PH11	Tetratricopeptide repeat (TPR)-containing protein	PPR containing plant protein
Sapur.0120G0950900.1	0.10623561	-0.018849851	0.960060229	0.039999	0.96880779	0.97895664	grey	-0.0691254	0.38974136			AT5G09450.1	AXR1	NAD(P)-binding Rossmann-fold superfamily protein	NDD80-activating enzyme E1 regulatory subunit
Sapur.0162G0120001.1	0.105667370	-0.012329986	0.780986051	-0.03996	0.96881375	0.97895664	grey	-0.03873046	0.67895494			AT5G60550.1	EBS	PHD finger family protein / bromo-adjacent homology (BAH) domain-containing protein	Ebs-BAH-PHD domain protein
Sapur.0120G0950200.1	27.72719836	-0.003562291	0.089092251	-0.03992	0.96891936	0.97896304	grey	-0.01215366	0.89397155	GO:0055114;GO:0016491		AT5G79760.1	DTA4	downstream target of AGL15-4	NA
Sapur.0162G0120001.1	0.088827745	-0.003664499	0.086109622	0.042019	0.96892449	0.97900294	grey	-0.05194268	0.48973117			AT5G12230.1			octicrhomid calcium-binding protein
Sapur.0162G0280001.3	0.086361537	0.042120927	1.072863679	0.03926	0.96884285	0.97937247	grey	-0.08519962	0.28643295			AT4G25730.2			zinc finger protein, putative
Sapur.0120G0950300.1	0.118857548	0.035408807	1.007247417	0.038545	0.96907543	0.97974734	grey	-0.03984247	0.62363937	GO:0009378;GO:0006310;GO:0006281		AT4G03980.1		AAA-type ATPase family protein	AAA-type ATPase family protein
Sapur.0162G0620001.2	0.082269222	0.042126116	1.075127618	0.039182	0.96874939	0.97937552	grey	-0.20964908	0.08845715			AT5G68910.3	WIT2	WPP domain-interacting protein 2	WPP domain interacting tail-anchored protein, putative
Sapur.0062G0510001.2	0.078079867	0.042134775	1.078945251	0.039052	0.96888996	0.97940032	grey	-0.03474292	0.66575653	GO:0046872;GO:0030001		AT4G16380.1		Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.0120G0950800.1	0.715494983	0.011537203	0.295882256	0.038003	0.96889722	0.97940032	grey	-0.01572615	0.86501855	GO:0005515;GO:0043531		AT4G27220.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.0192G0870001.1	0.193295441	-0.024484722	0.63270007	-0.0387	0.96913546	0.97961528	grey	0.31041282	7.59E-05	GO:0008887;GO:0000145		AT5G71820.1	SEC6	exocyst complex subunit SEC6, putative	SEC6

Sapur.02G0032900.3	0.38659626	-0.00792765	0.39353146	-0.01989	0.98410089	0.99372495	grey	-0.08578624	0.28539491	ATS2G26670.1		Tetratricopeptide repeat (TPR)-like superfamily protein	plant(P22G2-32 protein, putative
Sapur.01G0135000.4	0.08633040	-0.01994789	1.01241028	0.019703	0.98428	0.99388704	grey	-0.28492906	0.00203178	ATS1G79430.1	APL,WOY	Homeodomain-like superfamily protein	Myb family transcription factor
Sapur.04G0262000.2	0.07896567	-0.02726791	1.18751102	-0.0164	0.98432072	0.99400508	grey	-0.07452348	0.35361251	ATS4G23980.1		NHL domain-containing protein	NHL domain, putative
Sapur.01G0153900.1	0.07668507	0.01956241	1.02079435	0.019548	0.98446145	0.99463355	grey	-0.06742349	0.40145883	AT-HF,HSN4		HIS HF	imidazole glycerol phosphate synthase subunit HisF
Sapur.09G0199100.2	0.56458376	0.07255532	0.37152157	0.019424	0.98450533	0.99232205	grey	0.09106657	0.98057265	ATU8A1,MOS1,LIB4		ubiquitin-activating enzyme 11	ubiquitin-activating enzyme E1
Sapur.02G0380800.1	123.2043939	0.00076954	0.03890424	0.019223	0.98463242	0.99002588	grey	-0.00357378	0.96457298	AT4G32290.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putative
Sapur.01G0239900.1	0.11932802	0.01928086	1.00600867	-0.01921	0.98467836	0.99002588	grey	-0.02529718	0.75239569	AT4G29180.1	DYT1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	helix loop helix DNA-binding domain protein
Sapur.05G0422000.1	8.01806762	0.00522431	0.27050787	0.019398	0.98483446	0.99002588	grey	-0.05178715	0.98203391	AT1G45188.1			late embryogenesis abundant protein
Sapur.15W0G0338800.1	0.12024433	0.01635393	0.85330486	0.019164	0.98470161	0.99002588	grey	0.00603317	0.94219632	AT4G18720.1		F-box family protein	NA
Sapur.01G0293000.1	1.19318552	-0.00668358	0.18875	0.019062	0.98474191	0.99002588	grey	-0.05550892	0.48997384	AT3G07860.1		Ubiquitin-like superfamily protein	Ub11/Ub12 small nuclear ribonucleoprotein 25 kDa protein
Sapur.01G0267600.1	0.57054423	-0.00645268	0.33773877	-0.0191	0.98476234	0.99002588	grey	0.02758189	0.73167088	AT4G36020.1	HIVA2(t)	HIVA2 (HL-phase 1) family	TB2/DP1, HIVA2 family protein
Sapur.11G0390800.4	0.10368884	-0.01888206	0.93096023	-0.01602	0.98481604	0.99035258	grey	-0.02688648	0.77224363	AT1G18160.1		BED zinc finger DNA binding dimerization domain	AC transposase, putative
Sapur.09G0303200.2	0.10242787	-0.01674828	0.86423973	0.018947	0.98488139	0.99066486	grey	-0.04592627	0.54788116	AT3G10250.1		Plant protein 1589 of unknown function	hypothetical protein
Sapur.01G0225800.1	9.70406715	0.01313186	0.76417541	0.018764	0.98493158	0.99072888	grey	0.01102768	0.98817156				transmembrane protein, putative
Sapur.01G0240400.1	2.62360503	0.00354375	0.18816857	-0.01878	0.98504588	0.99275937	grey	-0.03894855	0.62918194	AT4G24240.1		Leucine-rich repeat receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.01G0281700.1	0.08319869	-0.00179475	0.90808949	-0.01872	0.98507364	0.99275304	grey	-0.03154425	0.18003443	AT3G27135.1		transmembrane receptor,ATP binding	NA
Sapur.01G0221700.1	0.09368427	-0.01757213	0.95588352	-0.01808	0.98523471	0.99090726	grey	-0.07461129	0.15304929				NA
Sapur.01G0181700.1	0.41946469	-0.00632126	0.34811324	-0.01816	0.98530803	0.99107666	grey	-0.43025152	1.146-08	AT2G40070.2		RNA recognition motif and CCHC-type zinc finger domains containing protein	zinc finger CCHC-type and RNA-binding motif protein
Sapur.07G0703200.2	0.18865419	0.01922452	0.81713843	0.018104	0.98534168	0.99107666	grey	0.01297936	0.87183391	AT3G19970.1		alpha/beta hydrolase family protein	alpha/beta hydrolase family protein
Sapur.01G0256900.3	0.15308536	0.01360759	0.72578206	0.018135	0.98551072	0.99107666	grey	-0.04542678	0.57211768	AT4G33900.2		Serine/threonine-protein kinase WNK (With No Lysine)-related	Serine/Threonine-kinase WNK (WNK)-like protein, putative
Sapur.04G0264200.2	0.99504353	0.01848864	0.53112	0.018117	0.98553145	0.99147056	grey	-0.04884657	0.61134621	AP2G30.1,HSN3	APG30,HSN3	Aldolase-type TIM barrel family protein	NA
Sapur.01G0195300.1	0.1411388	0.01319021	0.73062582	0.017942	0.98568162	0.99207952	grey	-0.06543378	0.41574289				hypothetical protein
Sapur.05G0133300.1	0.18013875	0.01193879	0.74316466	0.017811	0.98570755	0.99212882	grey	0.01938052	0.83948808			Protein of unknown function, DUF247	electron transporter, putative
Sapur.01G0147900.2	0.07653079	0.02648804	1.49277217	0.017743	0.98584359	0.99147852	grey	-0.04269296	0.95858774	AT2G08270.2,G00635,G0-G0503700	AT6N1L2	sequence-specific DNA binding transcription factors;zinc ion binding;sequence-specific DNA binding transcription f	NF-X1-type zinc finger protein NFX1L1
Sapur.01G0240500.1	0.14303519	0.01313186	0.74517541	0.017624	0.98589385	0.99212327	grey	-0.06601166	0.98419933	AT4G08840.1	EDT2,RAV2,BAV2,TEM2	related to AB1/VP1 2	B1-DNA-binding domain protein
Sapur.01G0260900.1	0.08589454	0.01602882	0.96337985	0.01757	0.98589146	0.99226386	grey	-0.05693362	0.47871819	AT4G20460	ATCYS6,ATCYS8,CYS8	cystatin 8	NA
Sapur.01G0237500.1	162.3410729	0.00200457	0.11422617	0.017531	0.98602288	0.99224807	grey	0.00020587	0.99796268	AT2G26190.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.01G0254400.1	0.18425984	0.01056002	0.54609547	-0.01741	0.98603161	0.99236795	grey	-0.01392426	0.88647141	AT1G59100.1	LEP	Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.01G0254500.3	0.02619911	0.02472963	1.41045433	0.017209	0.98629735	0.99139143	grey	0.08096221	0.31345927	AT1G09410.3		HKH endonuclease	HKH nuclease, putative
Sapur.01G0243300.2	0.10378823	0.01966252	0.92368276	0.017177	0.98629403	0.99139143	grey	-0.02978483	0.71169427	AT1G69500.1	SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	stomatal cytokinesis defective protein, putative
Sapur.01G0231300.1	24.64012048	0.00106118	0.11169854	0.017065	0.98638557	0.99160625	grey	0.00314483	0.98921324	AT5G04870.1	ATCPK1,CPK1	calcium dependent protein kinase 1	transmembrane protein, putative
Sapur.09G0251500.1	0.09831353	0.01819816	1.07053818	0.017	0.98643689	0.99147056	grey	-0.08346767	0.67128907				NA
Sapur.01T0013300.1	31.14959614	0.00378682	0.22437736	0.016877	0.98653471	0.99151174	grey	-0.02763879	0.73538133			Plant protein of unknown function (DUF247)	NA
Sapur.01G0268700.2	1.38169592	0.01916287	0.14543422	0.01669	0.98668422	0.99192383	grey	-0.00648842	0.93307343				DUF2365 family protein
Sapur.01T0269700.2	0.55609045	-0.02537803	1.52741849	-0.01656	0.98679098	0.99195185	grey	-0.0479742	0.5572483	AT3G43320.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase domain protein
Sapur.09G0293200.2	0.05473603	0.02655185	1.45665385	-0.01651	0.98682741	0.99195185	grey	-0.10526042	0.20239946	AT5G07350.1			hypothetical protein
Sapur.15W0G0158800.1	0.05398280	0.02284029	1.53115185	-0.01649	0.98684194	0.99195185	grey	-0.00874918	0.23526715	AT4G16685.2	ATBPC2,BBR/BPC2,BPC2	basic pentacysteine 2	GAGA-binding transcriptional activator
Sapur.01G0119200.1	0.05162092	-0.02528609	1.53534082	-0.01643	0.98688349	0.99195185	grey	-0.07715402	0.33691111	AT5G15810.1		Protein of unknown function (DUF567)	LUHP-one-related protein
Sapur.07G0814500.3	0.15108917	-0.02537831	1.53953928	-0.01642	0.98689893	0.99195185	grey	-0.01392426	0.12724425	AT1G18620.1	GDSL	DHHC-type zinc finger family protein	zinc finger protein, putative
Sapur.01G0256700.2	1.29801798	-0.00645087	0.39292782	-0.01642	0.98690293	0.99195185	grey	-4.73E-05	0.99531016	AT5G01020.2,G00630.1,G00521.2,G	NRT1.5	nitrate transporter 1.5	peptide transporter, putative
Sapur.09G0260000.2	14.65003219	0.00223594	0.19667787	-0.0164	0.98691434	0.99195185	grey	-0.00210449	0.97862045	AT5G59155.1	AIPP2-B15,PP2-B15	phloem protein 2-B15	F-box protein PP2-B15
Sapur.03G0147000.2	0.79221003	0.00508082	0.31238728	0.016264	0.98702346	0.99160743	grey	0.01260045	0.87513858	AT5G42050.1	DCD	DCD (Development and Cell Death) domain protein	development and cell death domain protein
Sapur.01G0242200.1	0.18455164	0.01888556	0.57147613	0.016163	0.98708397	0.99160743	grey	-0.02109294	0.69708261				NA
Sapur.05G0203900.1	173.8307727	-0.00062074	0.03854751	-0.0161	0.98715766	0.99175346	grey	0.01976195	0.85587316			nucleotide repair protein	DNA excision repair protein ERCC-1
Sapur.01G0368100.1	0.28028733	0.01867932	0.51727547	-0.0158	0.98719028	0.99186766	grey	-0.04857051	0.54780425	AT4G08300.1		Peptidyl-tRNA hydrolase family protein PTH2	peptidyl-tRNA hydrolase PTH2
Sapur.09G0791100.1	24.3622485	-0.00286836	0.18164983	-0.0159	0.98739353	0.99186766	grey	0.01735239	0.82918149	AT4G02140.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.01G0184200.1	0.14660302	0.01182920	0.75422026	-0.01589	0.98746495	0.99200642	grey	-0.12487453	0.13916735	AT4G09410.1	amac078,NAC2	NAC domain containing protein 2	NAC transcription factor
Sapur.15W0G0059100.1	0.42864809	0.00433677	0.35935963	0.015577	0.98750561	0.99200642	grey	-0.02499796	0.75593886	AT5G55050.3		alpha/beta-Hydrolases superfamily protein	alpha/beta-fold hydrolase
Sapur.05G0120800.1	0.77362573	0.00394152	0.25423595	0.015504	0.98763293	0.99200564	grey	-0.02018374	0.80189079				NA
Sapur.08G0163200.1	0.85372617	0.00159502	0.19207047	0.015514	0.98765047	0.99203737	grey	-0.24797985	0.05740228	AT4G15830.1		ARM repeat superfamily protein	NA
Sapur.T0529000.4	0.27707214	-0.01787921	1.15185496	-0.01514	0.98769264	0.99203737	grey	0.08841007	0.27086166	G00463.1	ARA8,ATPC51,CAD1,PC51	phytochelatin synthase 1 (PC51)	phytochelatin synthase
Sapur.01G0195600.1	0.38278313	0.01526617	1.66691948	-0.0152	0.98795198	0.99203737	grey	-0.10484648	0.15815529	AT2G18230.1		transcription factor NET2/NOT2/NOT3 family protein	CCR4-NOT transcription complex subunit 3
Sapur.T0946000.1	0.15076684	-0.00925802	0.61364597	-0.01512	0.98793971	0.99203597	grey	-0.05764988	0.47391881	AT5G26455.1	CL22S	CLAVATA(CLE)-RELATED 25	NA
Sapur.15W0G0129800.1	0.35209488	0.01297102	0.54609547	-0.0151	0.98799734	0.99203597	grey	-0.08916228	0.3576146	AT3G07730.2	RPS4b	40s ribosomal protein S4-B	40S ribosomal protein Sa protein
Sapur.08G0257800.1	262.5393412	-0.00537988	0.35632356	-0.0148	0.98819529	0.99237518	grey	0.03136947	0.69658259	AT4G40300.1	ATFER4,FER4	ferritin 4	ferritin
Sapur.15W0G0113700.1	0.07388334	0.01966252	0.98168594	-0.0146	0.98854253	0.99256828	grey	-0.09742273	0.34780768				NA
Sapur.04G0180400.1	2.58700406	0.00268018	0.18565035	0.014317	0.98857694	0.99256828	grey	-0.00365072	0.96376286	AT4G30650.1	ATOST1,OST1,PM4,SNRK2-6,	Protein kinase superfamily protein	Serine/Threonine-kinase SAPK10, putative
Sapur.01G0124300.1	3.93378702	0.00285105	0.15980336	0.014294	0.98859526	0.99256828	grey	-0.00594728	0.94103701			Sec14p-like phosphatidylinositol transfer family protein	SEC14p cytosolic factor family protein
Sapur.01G0264600.1	57.33699905	0.00215065	0.08056988	-0.01442	0.98887247	0.99256828	grey	0.01450205	0.98561938	AT3G62170.1		BRO1-like; Fungal RNA degradation factor family protein	Arc transposase-like protein
Sapur.15W0G0213300.1	0.66866984	-0.02513383	1.78376822	-0.0141	0.98874905	0.99268073	grey	-0.01994503	0.80423584	AT1G73910.2		Rhodanese/Cell cycle control phosphatase superfamily protein	rhodanese-like domain protein
Sapur.01G0283300.4	29.0199821	0.00159409	0.07068607	-0.01424	0.98905456	0.99364563	grey	0.00062062	0.99364563	AT1G08930.1	ERD6	Major facilitator superfamily protein	outer arm dynein light chain 1 protein
Sapur.09G0250600.1	0.10573788	-0.01458584	1.12336507	-0.0138	0.98890288	0.99286598	grey	0.0881971	0.91884074	AT4G00390.1	GFA2	gamma-tubulin complex component 2	chaperone protein Dnj1
Sapur.01G0179100.1	0.07783934	-0.01875306	1.14394276	-0.0133	0.98926512	0.99369721	grey	-0.09103047	0.75542287	AT5G17820.1	CHR9	switch 2	DNA repair and recombination RAD26-like protein, putative
Sapur.01T0107400.1	0.32226655	-0.00516886	0.39361867	-0.0133	0.98952519	0.99246387	grey	-0.02101864	0.79387021	AT2G01780.1		SGNH hydrolase-type esterase superfamily protein	GDSL esterase/lipase
Sapur.01G0149600.1	0.10017864	0.01908404	0.86184169	-0.0129	0.98973664	0.99340364	grey	0.00203546	0.97535475	AT4G24154.1	AT5G60010.1	Ribosomal protein L7Ae family protein	60S acidic ribosomal protein P0
Sapur.07G0870600.1	0.08024278	-0.01547527	1.21855272	-0.0123	0.98984632	0.9934997	grey	-0.06947312	0.18726202	AT2G45970.1		LMBR1-like membrane protein	LMBR1 integral membrane-like protein
Sapur.01G0175100.2	0.16057628	-0.01788167	1.1519	-0.0123	0.98986018	0.9934997	grey	-0.41388806	1.27E-09	AT4G38090.1		Ribosomal L18e/L5e family protein	60S ribosomal protein L18-2
Sapur.01G0164200.2	0.05127696	-0.02507589	2.01061955	-0.0123	0.98988245	0.99342297	grey	-0.04673628	0.24073684	AT4G03720.1		Predicted eukaryotic LigT	activating signal cointegrator 1 complex subunit 1, putative
Sapur.01G0246700.1	0.22196782	0.00565333	0.68713622	0.01223	0.99032782	0.99381339	grey	-0.02568879	0.76491107	G0435.1		Disease resistance protein (CC-NBS-LRR class) family	NA
Sapur.05G0107300.1	10.83313344	0.00320025	0.09158545	-0.01121	0.99039114	0.99488027	grey	0.00682143	0.92441231	AT4G30820.1			NA
Sapur.09G0157700.1	0.07568286	-0.01394737	1.39634752	-0.0103	0.99120348	0.99401617	grey	-0.06861357	0.39181401				NA
Sapur.09G0186100.1	0.06271119	-0.01341383	1.23000463	-0.01077	0.99148806	0.99417735	grey	-0.08894208	0.3576146	AT5G60560.1		Lsm and RanBP2 domains containing protein	non-binding protein in the microtubule-organizing centre protein
Sapur.15W0G0124800.1	1.55717664	-0.00199356	0.18364004	-0.0076	0.99148633	0.99417735	grey	0.03601516	0.65429871	AT4G28240.2	CGL,CGL1,GNT1	alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase, putative	alpha-2N,2G-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
Sapur.01G0270100.1	0.46360074	-0.01425572	0.19188988	-0.0077	0.99149503	0.99417735	grey	0.00990609	0.65124667	AT2G36310.1	DAG1	Dof type zinc finger DNA-binding family protein	Dof zinc finger protein
Sapur.04G0113200.1	0.19606405	-0.00518736	0.48941809	-0.01067	0.99149315	0.99472118	grey	-0.03190055	0.24610918	AT5G21280.1			NA
Sapur.01G0282000.1	0.16224424	-0.00239056	0.22623579	-0.01047	0.99161802	0.99480349	grey	0.02021917	0.85546229				hypothetical protein
Sapur.01G0197900.2	8.89478253	0.00122191	0.11748004	0.01401	0.99170146	0.99489063	grey	-0.01489776	0.85308144				cysteine-rich TM module stress tolerance protein
Sapur.01T0264400.2	0.40376203	0.00406429	0.39507847	0.01025	0.99182079	0.99489849	grey	-0.03352168	0.89788336	AT5G27481.1	ATHIR1,HIR1	DNA binding bromodomain-containing membrane-associated protein family	hypersensitive induced response protein
Sapur.01G0179500.4	0.26403519	-0.00288879	0.58384929	-0.01019	0.99185043	0.99489182	grey	0.17755565	0.02609624	AT4G18020.1	WUS8	GATA type zinc transcription factor family protein	transcription factor LNG1
Sapur.03G0408900.1	17.92315867	0.00085855	0.08491932	0.01026	0.99192001	0.99501972	grey	0.02519918	0.75405039				NA
Sapur.01G0268800.1	585.0115874	0.00319755	0.03314158	-0.0092	0.99208748	0.99515204	grey	-0.04372026	0.5867365	AT5G44610.1	GPX2,GSL1	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	haloacid dehalogenase-like hydrolase
Sapur.T0823100.1	0.19876688	-0.00422569	0.44842039	-0.00942	0.99248684	0.99526942	grey	-0.08235005	0.30520291	AT4G08020.1	APM4,ATPDX12,PDX12	pentam-12	NA
Sapur.01G0185000.1	14.01879	-0.00188322	0.12004786	-0.0089	0.99258769	0.99541732	grey	-0.00801728	0.93617669	AT5G27730.1		F-box/Rho-like/FBD-like domains-containing protein	NA
Sapur.04G0264600.1	556.8525235	-0.00599737	0.06854735	-0.00875	0.99269191	0.99594006	grey	-0.00670901	0.93135329	AT3G27830.1	CRP1	cysteine/histidine-rich RNA binding protein	S-exoproteinase
Sapur.01G0238200.1	0.42839383	0.01388223	0.40338237	-0.00838	0.99319401	0.99617543	grey	-0.04104303	0.57605627	AT4G27450.1		Transducin/WD40 repeat protein	transducin/WD40 domain protein
Sapur.01G0321200.4	0.15210737	0.00547217	0.66304846	0.008253	0.99341095	0.99246539	grey	-0.03404251	0.67210135	AT4G29000.1		Tesmin/TSO1-like CXC domain-containing protein	transcription factor, putative
Sapur.02G0808900.1	0.14667315	0.00268018	0.61044186	0.008383	0.99350769	0.99352389	grey	-0.06426786	0.56256849	AT5G20650.2	HMG BETA 1 HMGB2,NFD5C	HMG box family protein	HMG(high mobility group) box protein
Sapur.01G0124400.1	315.8952258	0.00350805	0.04500824	0.007795	0.99378049	0.99539006	grey	0.01321506	0.88956584	AT4G03430.1		Ankyrin repeat family protein	26S proteasome non-ATPase regulatory subunit 10, putative
Sapur.05G0180800.1	0.27191457	0.00316745	0.40742581	-0.00777	0.99379723	0.99539006	grey	0.02972517	0.7146439	AT4G00460.2,G00635.2,G00635.4		Protein kinase superfamily protein	receptor-like kinase
Sapur.01G0274800.1	0.35207489	0.01421156	1.66633476	0.007361	0.99428149	0.99608126	grey	0.06392416	0.39948783	AT4G20360.1,G00635.2,G00635.4		DEADLIKE/AtRH box helicase family protein	DEAD-box like helicase superfamily protein
Sapur.01G0145100.1	0.49681727	-0.00261455	0.35187658	-0.00735	0.99441437	0.99688599	grey	-0.05185544	0.50506688			Plant protein 1589 of unknown function	octanoyltransferase pyrophosphatase/phosphodiesterase family protein, putative
Sapur.01G0220900.1	-0.07064737	-0.01968387	1.50506828	-0.007	0.99457176	0.99688599	grey	-0.02852806	0.72397465	AT4G01240.1	ATRDV1,REV3	recovery protein 3	DNA polymerase family protein
Sapur.09G0264800.1	1.00615604	-0.00154079	0.21138224	-0.00729	0.99481156	0.99688599	grey	-0.01861975	0.81888945				NA
Sapur.01G0238900.1	0.30018516	-0.01026499	1.40306766	0.007387	0.99491679	0.99688599	grey	-0.06507264	0.41821792	AT4G08870.2,G00300.1		Heavy metal transport/detoxification superfamily protein	heavy metal-associated domain protein
Sapur.01G0277600.1	0.05626302	0.01028211	1.41279101	0.007247	0.99491944	0.99689024	grey	-0.056771	0.48004812	AT4G00550.1	DDL	SMAD/FHA domain-containing protein	hypothetical protein
Sapur.01G0287000.1	0.05526203	0.01238211	1.81123743	0.006829	0.99494832	0.99489364	grey	-0.02274641	0.77351148				NA
Sapur.07G0452900.1	0.06129575	0.01021775	1.52113384	0.006786	0.99495859	0.99489364	grey	-0.03785813	0.63747609	AT4G08130.2,G00630.1	ATPEN2,PEN2	PTEN 2	phosphatidylinositol-3N,3C,4N,5C-trisphosphate 3-phosphatase
Sapur.15W0G0074800.1	0.06018884	0.01031397	1.52109056	0.006777	0.99503496	0.99489364	grey	-0.08553964	0.15469395	AT2G37140.1		Yippee family putative zinc-binding protein	fs(2)k43 binding coordinator/zuo, putative
Sapur.01G0257100.1	0.08109341	0.00184093	1.20973649	0.006736	0.99513221	0.99489364	grey	-0.23657233	0.00285214	AT4G29180.2,G00635.2,G00635.4		Protein phosphatase 2A regulatory B subunit family protein	protein phosphatase 2A, regulatory subunit B'C, putative
Sapur.09G0128700.4	0.07816769	0.00815347	1.21495462	0.006724	0.99524849	0.99489364	grey	-0.00225508	0.97781018	AT4G34560.1,G00635.2,G00635.4		bZIP transcription factor family protein	bZIP transcription factor family
Sapur.01G0186200.2	0.05851158	0.00183527	1.21367609	0.006633	0.99579327	0.99497928	grey	-0.05623849	0.49437885	AT5G58640.1		Plant protein of unknown function (DUF827)	weak movement under blue light protein
Sapur.01G0205500.1	0.07674344	0.00360505	1.29601066	0.006374	0.99614483	0.99697005	grey	0.24161995	0.00234511	AT4G04410.2,G00540.1,G00540.2	GHS1	Ribosomal protein S21 family	ribosomal protein S21
Sapur.01G0161300.2	0.07200034	0.00283937	1.30175253	0.00343	0.99649527	0.99697005	grey	0.02248124	0.76617297	AT1G45188.1	ATU8A1,MOS1,LIB4	ubiquitin-activating enzyme 1	ubiquitin-activating enzyme E1
Sapur.01G0146300.1	0.36393304	0.00280098	1.31413971	0.006301	0.99497196	0.99697005	grey	-0.08511502	0.27031166	AT5G50310.1			transmembrane protein, putative
Sapur.15W0G0041200.1	0.05616333	0.00203267	1.12538479	0.006257	0.99500748	0.99697005	grey	-0.06869771	0.39262751				NA
Sapur.15W0G0021000.2	0.05623134	0.00269338	1.32545129	0.006257	0.99500675	0.99697005	grey	-0.09287543	0.24729634	AT4G01880.2,G00535.2,G00535.4,G00601.2,G00601.4,G00601.6,G00515.2	ATATHL4,ATHL	ABC2 homolog 6	NA
Sapur.09G0050500.2	0.05838293	0.00358345	0.96668859	-0.00607	0.99513896	0.99785313	grey	-0.17438342	0.03809311	AT5G58510.2,G00635.2,G00642		Zinc finger (CCHC-type; RNG-Finger) family protein	NA
Sapur.09G0250600.1	0.07364924	0.00836402	1.39718420	0.005987	0.99523402	0.99798456	grey	-0.02388581	0.76655231	AT4G05085.2,G00635.2,G00635.4,G00601.2,G00601.4,G00601.6,G00601.8,G00601.10,G00601.12,G00720,G00930	ZIP2	28Y/IRT-like protein 2	metal cation transporter, ZIP family protein
Sapur.09G0277900.1	0.06442696	0.00876298	1.41036705	0.005939	0.99526193	0.99798456	grey	-0.04482581	0.57841914	AT4G34100.2		RING/U-box superfamily protein	E3 ubiquitin ligase SUL5, putative
Sapur.01G0282300.1	0.06169365	0.00329721	1.41431341	0.005605	0.99527637	0.99798456	grey	-0.08472525	0.29377832				NA
Sapur.01G0294600.1	0.23651043	0.00285502	0.49013361	0.005764	0.99547254	0.99720493	grey	-0.04378668	0.60218431				hypothetical protein
Sapur.01T0091200.1	0.07989393	0.00511094	1.07409337	0.005689	0.99548577	0.99720493	grey	-0.08672085	0.38218515				NA
Sapur.09G0251000.1	0.07908451	0.00611449	1.05494655	0.005687	0.99562342	0.99720493	grey	-0.04472491	0.5802266			DNAse I-like superfamily protein	chromosome condensation-like protein
Sapur.01G0272500.1	0.06779148	0.00840651	1.15466876	0.005679	0.99564592	0.99737889	grey	0.07253212	0.56360027	AT4G02390.2,G00374.2,G00374.4,G00374.6,G00374.8,G00374.10,G00374.12,G00720,G00930	TUBG1	gamma-tubulin	tubulin gamma chain
Sapur.01G0222300.1	0.08374781	0.00424204	1.13862485	0.005481	0.99566873	0.99918588	grey	-0.05163813	0.52074888	AT4G04610.2,G00540.1,G00540.2,G00735		Ribosomal protein S21 family protein	ribosomal protein S21
Sapur.01G0182600.1	0.20596429	0.00189344	0.40617749	0.005347	0.99574262	0.99718588	grey	-0.06343918	0.41898968	AT5G47460.1	ARIP12,RLP12	receptor like protein 12	receptor-like protein kinase, putative
Sapur.01G0282500.8	0.05062259	0.00876682	1.66939869	-0.00525	0.99581834	0.99718588	grey	-0.04091108	0.63940737	AT5G60960.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	hypothetical protein
Sapur.01G0266300.1	0.08452465	0.00366192	1.11294154	0.005468	0.99583429	0.99718588	grey	-0.14997415	0.08283552	AT5G44680.1	MEE13	myosin heavy chain-related	myosin heavy chain-like protein
Sapur.05G0182700.1	0.07779251	0.00637168	1.21882055	0.005328	0.99588924	0.99718588	grey	-0.07962624	0.32153139	AT5G45155.1	AETL8,TL8	tubby like protein 8	tubby-like F-box protein
Sapur.09G0225500.1	2.76708816	0.00114314	0.22311352	-0.00512	0.99591133	0.99724086	grey	-0.01523944	0.84985645				NA
Sapur.01G0282400.1	1.16417324	0.00387904	0.05331141	0.005025	0.99595444	0.99724086	grey	-0.02929879	0.73651288	AT5G28050.1		Cytidine/deoxycytidylate deaminase family protein	deoxycytidylate deaminase (cytidine deaminase), putative
Sapur.T0415500.1	0.48908246	0.00168494	0.33243575	0.005019	0.99595449	0.99724086	grey	0.02117267	0.79239443	AT5G28455.1	CL22S	CLAVATA(CLE)-RELATED 25	NA
Sapur.09G0165000.2	0.08175	0.00422904	1.28847856	0.004988	0.99602649	0.99724086	grey	-3.26770711	0.99999999	AT5G57420.1	ATCLA1,CLA1	nuclear factor CLA1	CLAN7-binding transcription factor
Sapur.09G0260500.1	0.07068376	0.00622209	1.30345708	0.004973	0.99602034	0.99724086	grey	-0.05049893	0.52997073	AT4G07076.2,G00796	EMB2656	AIR9 repeat family protein	chromosome condensation-like protein
Sapur.09G0260600.1	105.2398616	0.00048748	0.13876741	0.004966	0.99603661	0.99724086	grey	0.00649365	0.93615402	AT5G44260.1	VEA4	AP2/B3-like transcriptional factor family protein	hypothetical protein
Sapur.01G0265300.2	70.19521354	0.00033645	0.06853705	0.004909	0.99608122	0.99724086	grey	-0.01799399	0.82490741	AT4G08870.1	MEE9	maternal effect embryo arrest 9	maternal effect embryo arrest 9 protein, putative
Sapur.01G0263200.1	0.11464615	0.00223018	0.67496074	0.004843	0.99610648	0.99756633	grey	0.16438984	0.18161356	AT4G26180.1	MEE16	G-box binding factor 5	transcription factor
Sapur.01G0180500.1	0.09328831	0.00467467	1.07245965	0.004333	0.99624406	0.99756633	grey	-0.06320243	0.43159717	AT4G05856.2,G00837.2,G00837.4,G00837.6,G00837.8,G00837.10,G00837.12,G00837.14,G00837.16,G00837.18,G00837.20,G00837.22,G00837.24,G00837.26,G00837.28,G00837.30,G00837.32,G00837

Sapur.15ZG041700.1	0.036319546	0.269176571	1.877877141	0.143341	0.886020968	NA	grey	0.143209394	0.073565897		AT1G78172.1			NA
Sapur.T020900.1	0.034073548	0.269180617	1.888843848	0.142511	0.886676562	NA	grey	0.131869371	0.099699488	GO:0005681,GO:0000398,GO:0000387	AT1G54385.1		ARM repeat superfamily protein	NA
Sapur.011G034000.2	0.048133767	0.219982766	1.551993402	0.141742	0.887283739	NA	grey	0.024182642	0.763696464		AT4G21670.1	ATCPL1,CPL1,FRY2	C-terminal domain phosphatase-like 1	double-stranded RNA-binding motif protein
Sapur.003G042800.1	0.042056393	0.260245744	1.855808197	0.140233	0.888475817	NA	grey	0.144338361	0.071300542		AT1G53708.1	RTFL9	ROTUNDIFOLIA like 9	DVL19
Sapur.006G028400.7	0.038293016	0.320020059	2.301176761	0.139068	0.889396412	NA	grey	0.036151683	0.653066339	GO:0043565,GO:0006355,GO:0003700,GO:0006351	AT3G12250.2	BZIP45,TGA6	TGACG motif-binding factor 6	TGA-type basic leucine zipper protein TGA2.2
Sapur.009G011600.1	0.033033202	0.260238397	1.89686534	0.137194	0.890877515	NA	grey	-0.385584133	6.13E-07	GO:0006355,GO:0003677	AT4G34610.1	BLH6	BEL1-like homeodomain 6	BEL1-related homeotic protein, putative
Sapur.005G053600.1	0.042727235	0.231623418	1.693768387	0.13675	0.891228131	NA	grey	0.092524497	0.249099878		AT3G05270.1		Plant protein of unknown function (DUF869)	filament-like plant protein
Sapur.005G035300.2	0.033209027	0.284469988	2.090250413	0.136094	0.89174718	NA	grey	0.159150443	0.04648946	GO:0005515	AT3G05090.1	LRS1	Transducin/WD40 repeat-like superfamily protein	salt-induced WD protein
Sapur.009G101300.1	0.049316658	0.342858433	2.522170469	0.135938	0.891870413	NA	grey	0.134217958	0.093758004	GO:0009733	AT4G34800.1		SAUR-like auxin-responsive protein family	auxin-responsive family protein
Sapur.019G050500.1	0.039100773	0.231471128	1.706086576	0.135674	0.892079217	NA	grey	0.051347928	0.523039044		AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO	exportin 1A	NA
Sapur.005G157800.1	0.030059188	0.286203014	2.124953185	0.134687	0.892859559	NA	grey	0.136584096	0.088060035	GO:0055114,GO:0016491,GO:0005507	AT5G09360.1	LAC14	laccase 14	laccase
Sapur.014G079100.3	0.049169303	0.207523162	1.546785429	0.134164	0.893272769	NA	grey	0.046728172	0.561145365	GO:0010181,GO:0055114,GO:0008615,GO:0004733	AT2G46580.1		Pyridoxamine 5\'-phosphate oxidase family protein	pyridoxamine 5'-phosphate oxidase-related FMN-binding protein
Sapur.T122700.1	0.026482306	0.284472811	2.138840632	0.133003	0.894190789	NA	grey	0.179261501	0.024677125					NA
Sapur.016G032600.3	0.024432826	0.284473791	2.156656314	0.131905	0.895059419	NA	grey	0.176167105	0.027312754	GO:0016787	AT1G18300.1	atnudt4,NUDT4	nudix hydrolase homolog 4	NA
Sapur.008G144000.5	0.034149858	0.306769131	2.327746463	0.131788	0.895151951	NA	grey	0.163654578	0.040557197		AT1G67570.1		Protein of unknown function (DUF3537)	transmembrane protein, putative
Sapur.005G161300.1	0.037267636	0.273321747	2.075515207	0.131689	0.895230582	NA	grey	0.115293164	0.150469654		AT1G53580.1	ETHE1,GLX2-3,GLY3	glyoxalase II 3	hydroxyacylglutathione hydrolase
Sapur.T137500.1	0.033137808	0.306770591	2.335533926	0.131349	0.895499046	NA	grey	0.147623487	0.06502911		AT1G04645.1		Plant self-incompatibility protein S1 family	NA
Sapur.004G067600.1	0.040709106	0.269232746	2.050939682	0.131273	0.89555945	NA	grey	0.123853214	0.122241902					NA
Sapur.007G041100.4	0.039239912	0.269234838	2.058391259	0.130799	0.895934576	NA	grey	0.134126808	0.093983228		AT5G11180.1	ATGLR2.6,GLR2.6	glutamate receptor 2.6	glutamate-gated kainate-type ion channel receptor subunit glur5 protein, putative
Sapur.T029900.1	0.037996489	0.269236661	2.064961765	0.130383	0.896263128	NA	grey	0.121630105	0.129145035		AT5G24280.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.013G071100.2	0.035733467	0.26924012	2.077603438	0.129592	0.896889486	NA	grey	0.123901178	0.122096179	GO:0005524	AT3G54280.1	ATBTAF1.BTAF1.CHA16.CHF	DNA binding;ATP binding;nucleic acid binding;binding;helicases;ATP binding;DNA binding;helicases	TATA-binding protein associated factor
Sapur.003G126800.2	0.029100946	0.306776844	2.369847172	0.12945	0.897001544	NA	grey	0.167314228	0.036217598	GO:0006355,GO:0005634,GO:0003700	AT1G77080.4	AGL27,FLM,MAF1	K-box region and MADS-box transcription factor family protein	NA
Sapur.016G170500.4	0.034013085	0.269242879	2.08786925	0.128956	0.897392612	NA	grey	0.114239381	0.154259796		AT4G33690.1			plant/T16L1-180 protein, putative
Sapur.010G069100.1	0.027130431	0.306780223	2.389074496	0.12841	0.897824794	NA	grey	0.173600148	0.029678207					NA
Sapur.013G106100.2	0.03253114	0.269245356	2.097221079	0.128382	0.897846705	NA	grey	-0.212069099	0.007667243	GO:0003677	AT1G34380.2		5\'-3\' exonuclease family protein	DNA polymerase I
Sapur.016G064300.1	0.045074112	0.260217089	2.033192629	0.127984	0.89816126	NA	grey	0.130132521	0.104281704	GO:0006355,GO:0003677	AT3G52440.1		Dof-type zinc finger DNA-binding family protein	Dof zinc finger protein, putative
Sapur.001G034400.5	0.030583133	0.269084668	2.110317187	0.127509	0.898537463	NA	grey	0.123136705	0.124434875	GO:0016491,GO:0008152	AT4G27760.1	FEY,FEY3	NAD(P)-binding Rossmann-fold superfamily protein	forever young oxidoreductase
Sapur.001G012400.1	0.05002959	0.231684462	1.827199584	0.126798	0.899100621	NA	grey	0.093419145	0.24453285	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G45550.1	CYP76C4	cytochrome P450, family 76, subfamily C, polypeptide 4	NA
Sapur.005G006100.2	0.049678183	0.231684926	1.828342576	0.126719	0.899163161	NA	grey	0.100858736	0.208802484		AT1G10630.1	ARFA1F,ATARFA1F	ADP-ribosylation factor A1F	ADP-ribosylation factor(Arf)/Arf-like (Arl) small GTPase family protein
Sapur.012G035000.1	0.047424009	0.23168797	1.83590586	0.126198	0.899575056	NA	grey	0.094573419	0.238726924	GO:0016790,GO:0006633	AT1G08510.1	FATB	fatty acyl-ACP thioesterases B	NA
Sapur.004G043200.1	0.046002787	0.231689956	1.840893047	0.125857	0.899844829	NA	grey	0.088596471	0.269848736	GO:0043565,GO:0006355,GO:0005634,GO:0003700	AT4G18880.1	AT-HSFA4A,HSF A4A	heat shock transcription factor A4A	heat stress transcription factor A-4a
Sapur.T127900.1	0.044325571	0.231692406	1.847104355	0.125435	0.900178808	NA	grey	0.088670875	0.269445118					NA
Sapur.T160400.1	0.041818327	0.23169616	1.856752011	0.124786	0.900693183	NA	grey	0.068489724	0.394037933					NA
Sapur.012G108300.1	0.044012878	0.193915437	1.557382054	0.124514	0.900908536	NA	grey	0.063990789	0.42590913		AT5G23750.2		Remorin family protein	remorin, carboxy-terminal region protein
Sapur.002G156600.1	0.036931615	0.231542752	1.877679745	0.123313	0.901859066	NA	grey	-0.43956644	8.43E-09	GO:0003676	AT1G02840.2	ATSRP34,SR1,SRP34	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in serine/arginine-rich splicing factor 1 (SRSF1)-like protein
Sapur.009G104300.1	0.045968137	0.227149304	1.854076961	0.122513	0.902492421	NA	grey	0.09093515	0.257358143	GO:0006468,GO:0005524,GO:0004672	AT5G67080.1	MAPKKK19	mitogen-activated protein kinase kinase kinase 19	Serine/Threonine kinase domain protein
Sapur.008G132300.1	0.042140441	0.271055807	2.272126918	0.119296	0.905040799	NA	grey	0.156171864	0.050796814					transmembrane protein, putative
Sapur.15WG115300.1	0.036472923	0.2469966	2.073371892	0.119128	0.905173966	NA	grey	0.108760186	0.175131956					hypothetical protein
Sapur.007G031100.1	0.040607237	0.271057591	2.281251136	0.11882	0.905418195	NA	grey	0.158147105	0.047905059		AT4G17900.1		PLATZ transcription factor family protein	NA
Sapur.T171400.1	0.036747033	0.271062384	2.306358652	0.117528	0.906441429	NA	grey	0.148603656	0.06324774	GO:0005975,GO:0004553	AT4G14130.1	XTH15,XTR7	xyloglucan endotransglucosylase/hydrolase 15	NA
Sapur.008G150100.1	0.036623199	0.271062545	2.307216469	0.117485	0.906475999	NA	grey	0.458887795	1.50E-09	GO:0005515	AT3G26510.2		Octicosapeptide/Phox/Bem1p family protein	PB1 domain protein
Sapur.006G065700.1	0.03866586	0.269291252	2.298741414	0.117147	0.906743362	NA	grey	0.074664117	0.352702173		AT5G58100.1			transmembrane protein, putative
Sapur.004G114700.2	0.037953465	0.269292169	2.303423031	0.11691	0.906931724	NA	grey	0.105758545	0.187416109		AT1G11755.1	LEW1	Undecaprenyl pyrophosphate synthetase family protein	nogo-B receptor
Sapur.003G006000.1	0.032669438	0.271067942	2.33661636	0.116009	0.907645607	NA	grey	0.167709037	0.035773778					NA
Sapur.003G139500.5	0.027478402	0.247000168	2.133396115	0.115778	0.907828549	NA	grey	0.104611508	0.192272968	GO:0016747	AT5G48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase
Sapur.004G145400.1	0.031931332	0.271069011	2.342584552	0.115714	0.907879487	NA	grey	0.171744351	0.031495064		AT5G05800.1			NA
Sapur.010G196300.3	0.033401556	0.269298406	2.33609324	0.115277	0.908225369	NA	grey	0.110053188	0.170027735	GO:0007034	AT3G10640.1	VPS60.1	SNF7 family protein	charged multivesicular body protein
Sapur.001G114400.1	0.032272987	0.269300066	2.345036775	0.114838	0.908573281	NA	grey	0.119609746	0.135675177	GO:0006506,GO:0005789	AT5G46850.2			NA
Sapur.008G056500.2	0.043667168	0.194150822	1.69345846	0.114648	0.908724508	NA	grey	0.034906433	0.664278604		AT5G05550.1		sequence-specific DNA binding transcription factors	transcription factor
Sapur.017G118500.1	0.040344658	0.233531917	2.050122812	0.113911	0.9093082	NA	grey	0.138912819	0.082725573	GO:0006888,GO:0005622,GO:0005801	AT1G51160.1		SNARE-like superfamily protein	trafficking protein particle complex subunit 1
Sapur.018G116600.1	0.045607262	0.209506488	1.842314775	0.113719	0.909460424	NA	grey	0.082351712	0.305192853		AT1G04645.1		Plant self-incompatibility protein S1 family	NA
Sapur.014G002400.15	0.039530175	0.233533042	2.054258401	0.113682	0.909489558	NA	grey	0.136965016	0.087169129	GO:0006334,GO:0005634,GO:0003677,GO:0000786	AT1G49950.2	ATTRB1,TRB1	telomere repeat binding factor 1	single MYB histone
Sapur.007G053800.1	0.026488925	0.271077688	2.392900966	0.113284	0.909805304	NA	grey	0.176452367	0.027060114	GO:0003824,GO:0006470,GO:0004722	AT3G51470.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.016G128100.1	0.025845036	0.271078796	2.399586124	0.112969	0.910055148	NA	grey	0.15412596	0.053943191					NA
Sapur.002G087400.2	0.025494009	0.271079411	2.403318577	0.112794	0.910194042	NA	grey	0.130221346	0.104043411		AT5G64460.3		Phosphoglycerate mutase family protein	phosphoglycerate mutase family protein
Sapur.010G136200.1	0.025484129	0.271079429	2.403424547	0.112789	0.910197979	NA	grey	0.172643589	0.030603227		AT1G79270.1	ECT8	evolutionarily conserved C-terminal region 8	YTH domain protein
Sapur.001G103800.1	0.04679291	-0.206925356	1.838109659	-0.11258	0.910367437	NA	grey	-0.212580722	0.007518386		AT4G25190.1		Family of unknown function (DUF566)	DUF566 family protein
Sapur.004G135100.1	0.024945083	0.271080388	2.409285296	0.112515	0.910415191	NA	grey	0.177694243	0.025983408	GO:0006468,GO:0004672	AT4G38470.1		ACT-like protein tyrosine kinase family protein	tyrosine kinase domain protein
Sapur.007G067700.1	0.035439661	0.233539021	2.076682311	0.112458	0.910460467	NA	grey	0.10745415	0.180401693	GO:0005524,GO:0004386,GO:0006281,GO:0003678,GO:0000723	AT5G28780.1		PIF1 helicase	NA
Sapur.004G034100.1	0.033637156	0.233541849	2.087564011	0.111873	0.910924181	NA	grey	0.117884606	0.141448469	GO:0046983,GO:0008171	AT4G35160.1		O-methyltransferase family protein	orcinol O-methyltransferase-like protein
Sapur.002G199500.2	0.04933457	0.173678452	1.557640221	0.111501	0.911219068	NA	grey	0.027325323	0.734072872		AT2G20370.1	KAM1,MUR3	Exostosin family protein	NA
Sapur.018G108800.1	0.050434077	-0.171451213	1.541099359	-0.11125	0.911416092	NA	grey	-0.189691425	0.017337129	GO:0005515	AT5G57180.2	CIA2	chloroplast import apparatus 2	import apparatus 2 protein, putative
Sapur.005G116900.1	0.022281945	0.271085409	2.440744244	0.111067	0.911563455	NA	grey	0.176797458	0.026757161					NA
Sapur.009G041400.3	0.035060752	0.209510466	1.886574393	0.111053	0.911574016	NA	grey	0.063232854	0.431421343	GO:0051536,GO:0009055,GO:0055114,GO:0046872,GO:0016491	AT4G34890.1	ATXDH1,XDH1	xanthine dehydrogenase 1	xanthine dehydrogenase
Sapur.017G070500.1	0.048804041	-0.171448792	1.544982443	-0.11097	0.911639063	NA	grey	-0.206636281	0.00941678		AT1G69560.1	ATMYB105,LOF2,MYB105	myb domain protein 105	MYB transcription factor, putative
Sapur.006G052100.1	0.03050824	0.23354709	2.108211645	0.11078	0.911791029	NA	grey	0.088630102	0.269666251	GO:0005543	AT5G35200.1		ENTH/ANTH/VHS superfamily protein	clathrin assembly protein, putative
Sapur.005G165200.1	0.029136685	0.233549537	2.118074997	0.110265	0.912199215	NA	grey	0.094882007	0.237191204					hypothetical protein
Sapur.15WG089000.2	0.020294627	0.271089469	2.467182319	0.109878	0.912505999	NA	grey	0.175794536	0.027645748		AT3G48120.1			arginine/serine-rich coiled coil protein, putative
Sapur.003G072700.4	0.027549102	0.233552499	2.130208472	0.109638	0.912696211	NA	grey	0.141671772	0.07674463		AT5G61500.1	ATATG3,ATG3	autophagy 3 (APG3)	autophagy-related protein
Sapur.T017900.1	0.043126588	0.18533409	1.697888098	0.109156	0.913079031	NA	grey	0.053857916	0.502901448					NA
Sapur.008G021300.6	0.032045204	0.22523906	2.100401112	0.107236	0.914601588	NA	grey	-0.230342362	0.003704944		AT5G04440.1		Protein of unknown function (DUF1997)	RAP annotation release 2, galactose-binding-like domain protein
Sapur.019G088600.1	0.045914405	0.271099556	2.537124278	0.106853	0.914905533	NA	grey	0.141341195	0.077442311					NA
Sapur.016G261200.5	0.040664656	0.195998483	1.85876719	0.105445	0.916022379	NA	grey	-0.081608864	0.309590942		AT3G15480.1		Protein of unknown function (DUF1218)	plant/MJK13-14 protein, putative
Sapur.012G039600.1	0.04893444	-0.17669377	1.680327862	-0.10515	0.91625334	NA	grey	-0.19915702	0.012398622					NA
Sapur.019G009200.2	0.039165182	0.196000816	1.86507917	0.10509	0.916304545	NA	grey	0.067055714	0.404038026	GO:0055114,GO:0016491,GO:0008270	AT5G63620.1		GroES-like zinc-binding alcohol dehydrogenase family protein	NA
Sapur.008G164500.2	0.038251132	0.196002278	1.869068092	0.104866	0.91648189	NA	grey	0.060669981	0.450360841		AT5G18540.1			hypothetical protein
Sapur.011G012200.3	0.050352929	-0.191676785	1.828813646	-0.10481	0.916527084	NA	grey	-0.364770576	2.64E-06		AT4G22290.1		Ubiquitin-specific protease family C19-related protein	ubiquitin thiolesterase, putative
Sapur.002G175200.1	0.046871398	-0.176695624	1.686232422	-0.10479	0.916544644	NA	grey	-0.191497529	0.016280703	GO:0016020	AT3G21620.1		ERD (early-responsive to dehydration stress) family protein	early-responsive to dehydration stress-like protein
Sapur.016G311200.1	0.036436892	0.196005275	1.877328598	0.104406	0.916846779	NA	grey	0.048859975	0.543396694		AT1G40390.1		DNAse I-like superfamily protein	NA
Sapur.010G199900.1	0.032821379	0.196011667	1.895336385	0.103418	0.917631324	NA	grey	0.067577981	0.4003787	GO:0016773,GO:0016020,GO:0005524	AT3G10660.1	ATCPK2,CPK2	calmodulin-domain protein kinase cdpk isoform 2	calcium- and calmodulin-dependent kinase, putative
Sapur.T155000.1	0.032455069	0.196012349	1.897290287	0.103312	0.917715563	NA	grey	0.076925067	0.338271683		AT3G28455.1	CLE25	CLAVATA3/ESR-RELATED 25	NA
Sapur.014G041100.2	0.025826125	0.247012628	2.406375923	0.102649	0.918241372	NA	grey	0.101321135	0.206712423		AT3G60480.1			transmembrane protein, putative
Sapur.012G037400.1	0.04935821	-0.17137683	1.676458448	-0.10223	0.918577675	NA	grey	-0.178451062	0.025345402	GO:0008017,GO:0007018,GO:0005524,GO:0003777,GO:0005871	AT1G18370.1	ATNACK1,HIK,NACK1	ATP binding microtubule motor family protein	kinesin-like protein NACK1
Sapur.001G131400.1	0.047105287	-0.206868357	2.024502928	-0.10218	0.91861198	NA	grey	-0.184222145	0.020907243		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.001G131500.1	0.047105287	-0.206868357	2.024502928	-0.10218	0.91861198	NA	grey	-0.184222145	0.020907243		AT5G35405.1		Protein of unknown function (DUF784)	NA
Sapur.006G161400.1	0.030009476	0.271116814	2.673601411	0.101405	0.91922889	NA	grey	0.141687738	0.076711063		AT3G11950.1		TRAF-like superfamily protein	TRAF-type zinc finger protein
Sapur.016G088000.1	0.035576972	0.233592115	2.317231031	0.100807	0.91970401	NA	grey	0.095247258	0.235382439					NA
Sapur.T085100.1	0.033934669	0.233594344	2.329380501	0.100282	0.920120649	NA	grey	0.096640917	0.228569787		AT5G24280.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.006G145600.1	0.027444031	0.271120286	2.704131533	0.100262	0.920136721	NA	grey	0.148863654	0.062781979		AT2G18660.1	PNP-A	plant natriuretic peptide A	NA
Sapur.001G154200.1	0.033757381	0.23359459	2.330734654	0.100224	0.92016682	NA	grey	0.095750445	0.232906469		AT5G11460.1		Protein of unknown function (DUF581)	DUF581 family protein
Sapur.008G023300.2	0.03361951	0.233594782	2.331793725	0.100178	0.920202892	NA	grey	0.095788742	0.232718778		AT5G04320.2		Shugoshin C terminus	hypothetical protein
Sapur.004G006300.1	0.017733758	0.249198706	2.507159377	0.099395	0.920824779	NA	grey	0.162902033	0.04150167		AT1G09890.1		Rhamnogalacturonate lyase family protein	NA
Sapur.010G171000.1	0.026779555	0.211712309	2.136395392	0.099098	0.921060535	NA	grey	-0.11812371	0.140637317	GO:0006468,GO:0004672	AT5G18610.1		Protein kinase superfamily protein	receptor Serine/Threonine kinase, putative
Sapur.018G095300.2	0.030127973	0.233599911	2.360632817	0.098956	0.921172826	NA	grey	-0.006046898	0.940085315					NA
Sapur.008G068100.2	0.016989077	0.284496818	2.884337654	0.098635	0.921428032	NA	grey	0.136460141	0.088351506	GO:0016787	AT2G02970.1		GDA1/CD39 nucleoside phosphatase family protein	nucleoside diphosphatase
Sapur.002G023700.2	0.028102579	0.233603107	2.379197176	0.098186	0.921784849	NA	grey	0.097470211	0.224582539	GO:0016021	AT1G35180.1		TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain protein, putative
Sapur.016G005100.1	0.027133252	0.23360477	2.389048342	0.097782	0.922105785	NA	grey	0.110224207	0.16936098		AT5G47670.1	L1L,NF-YB6	nuclear factor Y, subunit B6	CCAAT-box-binding factor HAP3-like protein
Sapur.014G125100.2	0.021651741	0.271129233	2.788540483	0.09723	0.922543903	NA	grey	0.068482525	0.394087766	GO:0016020,GO:0008378,GO:0006486	AT1G05170.1		Galactosyltransferase family protein	beta-1%2C3-galactosyltransferase, putative
Sapur.007G070000.2	0.021628315	0.271129273	2.788397474	0.097216	0.922554883	NA	grey	0.154898054	0.052737374		AT5G08335.1	ATICMTB,ATSTE14B,ICMTB	Isoprenylcysteine carboxyl methyltransferase (ICMT) family	S-isoprenylcysteine O-methyltransferase
Sapur.017G117300.1	0.024472996	0.233609401	2.417177396	0.096646	0.923007895	NA	grey	0.085191007	0.288762579	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G64940.1	CYP89A6	cytochrome P450, family 87, subfamily A, polypeptide 6	cytochrome P450 family protein
Sapur.001G002700.1	0.044199728	0.163757562	1.695718563	0.096571	0.923066935	NA	grey	0.066558278	0.407541734	GO:0006508,GO:0005622,GO:0004198	AT1G55350.4	ATDEK1.DEK1.EMB1275.EM	calpain-type cysteine protease family	calpain-like protein
Sapur.018G117000.1	0.04981973	0.194277942	2.016208194	0.096358	0.923236188	NA	grey	0.062921999	0.43369388		AT1G04645.1		Plant self-incompatibility protein S1 family	plant self-incompatibility protein S1
Sapur.004G137200.1	0.041602557	0.196058582	2.046564963	0.095799	0.923680326	NA	grey	0.060880702	0.448786241					NA
Sapur.001G016200.1	0.040290288	0.19606035	2.053033031	0.095498	0.923919355	NA	grey	0.08726302	0.277151933	GO:0046872,GO:0030001,GO:0000166	AT1G63440.1	HMA5	heavy metal atpase 5	heavy metal P-type ATPase
Sapur.T191900.1	0.025672683	0.230171328	2.416986161	0.095231	0.924131571	NA	grey	0.094181113	0.240689293	GO:0016844,GO:0009058	AT1G74000.1	SS3	strictosidine synthase 3	NA
Sapur.016G292500.21	0.038812247	0.196062403	2.060624982	0.095147	0.924198021	NA	grey	0.064548373	0.42188011		AT1G10390.2		Nucleoporin autopeptidase	hypothetical protein
Sapur.016G296600.2	0.036695884	0.196065465	2.072116061	0.094621	0.924615957	NA	grey	0.104202568	0.194026494	GO:0005515	AT1G04390.1		BTB/POZ domain-containing protein	NA
Sapur.002G197300.1	0.036610289	0.196065593	2.072597306	0.094599	0.924633359	NA	grey	0.043775348	0.586179001		AT4G28760.1		Protein of unknown function (DUF3741)	DUF4378 domain protein
Sapur.T171200.2	0.047962099	0.158446886	1.677678876	0.094444	0.924756379	NA	grey	0.052724223	0.511946514		AT3G58830.1		haloacid dehalogenase (HAD) superfamily protein	haloacid dehalogenase superfamily protein
Sapur.019G019000.1	0.02855427	0.254492438	2.698760035	0.0943	0.924871036	NA	grey	0.151046146	0.058981975	GO:0016788	AT1G29670.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.018G005400.2	0.046104508	0.158449736	1.683267279	0.094132	0.925004103	NA	grey	0.01059654	0.895208181	GO:0046872,GO:0000166	AT2G24520.1	AHA5,HA5	H(+)-ATPase 5	plasma membrane H+-ATPase
Sapur.019G114000.5	0.045727345	0.158450306	1.684393196	0.09407	0.925053816	NA	grey	0.309967402	7.80E-05		AT5G51340.1		Tetratricopeptide repeat (TPR)-like superfamily protein	maternal effect uncoordination 2-1 protein
Sapur.009G010600.2	0.044210515	0.158452648	1.689038011	0.093812	0.92525821	NA	grey	0.048358234	0.547548998	GO:0055114,GO:0020037,GO:0006979,GO:0004601	AT1G07890.2	APX1.ATAPX01.ATAPX1.CS1	ascorbate peroxidase 1	NA
Sapur.017G028900.2	0.05047683	-0.171312847	1.828414869	-0.09369	0.925351653	NA	grey	0.03854935	0.631696535		AT3G21865.1	PEX22	peroxin 22	peroxin, putative
Sapur.006G143900.1	0.042348335	0.15845563	1.695012001	0.093483	0.925519469	NA	grey	0.297637258	0.000153248	GO:0003968	AT2G19910.1		RNA-dependent RNA polymerase family protein	NA
Sapur.006G218700.3	0.041929149	0.158456318	1.696400704	0.093407	0.92557994	NA	grey	0.03420651	0.67061376	GO:0003824,GO:0006470,GO:0004722	AT4G31860.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.016G232100.1	0.041389423	0.158457214	1.698213651	0.093308	0.925658739	NA	grey	0.031016182	0.699778969		AT5G55630.1	ATKCO1.ATTPK1.KCO1.TPK1	Outward rectifying potassium channel protein	outward rectifying potassium channel protein
Sapur.007G060900.1	0.049389823	0.156671511	1.680286318	0.093241	0.925712134	NA	grey	0.011104068	0.890219871					NA
Sapur.T061300.1	0.045961385	0.235480069	2.534200989	0.092921	0.925966454	NA	grey	0.133519016	0.095496036		AT5G17020.1	ATCRM1.ATXPO1.HIT2.XPO	exportin 1A	NA
Sapur.017G128600.4	0.038721144	0.158461753	1.707488482	0.092804	0.926059277	NA	grey	0.046777505	0.56073151	GO:0016787				ser/thr protein phosphatase family protein
Sapur.008G100300.4	0.019397346	0.262645046	2.83202654	0.092741	0.926109304	NA	grey	0.135677723	0.090209125	GO:0055085,GO:0016020,GO:0006810,GO:0015171,GO:0003333	AT2G01170.1	BAT1	bidirectional amino acid transporter 1	NA
Sapur.014G073100.1	0.029563315	0.196077071	2.117578674	0.092595	0.926225363	NA	grey	0.033057725	0.681061921		AT2G46300.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.006G127400.2	0.037562619	0.158463864	1.711857589	0.092568	0.926246474	NA	grey	0.021831601	0.786086811		AT4G26240.1			transmembrane protein, putative
Sapur.018G010700.1	0.03509644	0.174223819	1.883750247	0.092488	0.926310525	NA	grey	0.069263016	0.388707501	GO:0006508,GO:0004190	AT5G10770.1		Eukaryotic aspartyl protease family protein	aspartyl protease
Sapur.006G005200.1	0.032443653	0.17422488	1.897352562	0.091825	0.926836879	NA	grey	0.062194758	0.439037141	GO:0042545,GO:0030599,GO:0005618	AT1G05310.1		Pectin lyase-like superfamily protein	pectinesterase
Sapur.T149300.1	0.033181464	0.158472402	1.729892414	0.091608	0.927009303	NA	grey	0.047018303	0.558713583					NA
Sapur.007G083400.3	0.029093978	0.174226333	1.916528041	0.090907	0.927566273	NA	grey	0.338706221	1.43E-05	GO:0055085,GO:0016021	AT5G10190.1		Major facilitator superfamily protein	MFS transporter
Sapur.007G079700.1	0.024372218	0.249204098	2.74574869	0.09076	0.92768331	NA	grey	0.11629483	0.146932544	GO:0008270,GO:0005515	AT2G01150.1	RHA2B	RING-H2 finger protein 2B	NA
Sapur.016G265200.2	0.038784661	-0.154211757	1.707261762	-0.09033	0.928027401	NA	grey	-0.211528952	0.007827233	GO:0016788	AT5G03610.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.006G166900.1	0.035167044	0.235490946	2.618428402	0.089936	0.928338083	NA	grey	0.136816333	0.087516013					NA
Sapur.016G270600.1	0.034601604	0.235491589	2.623708194	0.089755	0.928481709	NA	grey	0.138790144	0.08299996	GO:0048544,GO:0006468,GO:0004672	AT4G27290.1		S-locus lectin protein kinase family protein	Serine/Threonine-kinase
Sapur.016G176900.1	0.050017214	-0.135835239	1.544776821	-0.08793	0.929930762	NA	grey	-0.146673812	0.066793945		AT3G43740.1		Leucine-rich repeat (LRR) family protein	somatic embryogenesis receptor kinase
Sapur.009G027600.1	0.029162264	0.235498275	2.680704505	0.087849	0.929996376	NA	grey	0.148852762	0.062801435		AT5G59210.1		myosin heavy chain-related	T-snare
Sapur.010G061800.1	0.028979497	0.235498517	2.682845583	0.087779	0.930052028	NA	grey	0.145730811	0.068584825		AT3G22520.1			hypothetical protein
Sapur.001G179300.1	0.022487696	0.241204242	2.778626052	0.086807	0.930824909	NA	grey	0.15011745	0.060575187					hypothetical protein
Sapur.016G058100.2	0.038552758	0.197969294	2.294236033	0.08629	0.931236003	NA	grey	0.117458382	0.142903249		AT3G58490.2		Phosphatidic acid phosphatase (PAP2) family protein	sphingosine-1-phosphate phosphatase
Sapur.008G086900.1	0.046723035	0.158518353	1.838345936	0.086229	0.931284542	NA	grey	0.057407244	0.475133279	GO:0006950	AT1G69080.1		Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.019G047600.1	0.025106954	0.235503966	2.732614436	0.086183	0.931321219	NA	grey	0.151547138	0.058136913					NA
Sapur.014G100500.1	0.044157204	0.158521939	1.84773424	0.085793	0.931631283	NA	grey	0.004514883	0.955246582		AT3G05700.1		Drought-responsive family protein	dehydration-induced-like protein
Sapur.012G042700.2	0.024243351	0.235505278	2.745070031	0.085792	0.9316317	NA	grey	-0.361285554	3.34E-06		AT3G18520.1	ATHDA15,HDA15	histone deacetylase 15	histone deacetylase family protein
Sapur.008G025000.3	0.014717805	0.249206617	2.904819682	0.085791	0.931632771	NA	grey	0.1438102	0.072353185		AT3G10380.1	ATSEC8,SEC8	subunit of exocyst complex 8	SEC8 exocyst complex component specific domain protein
Sapur.002G147100.1	0.024184645	0.235505368	2.745934258	0.085765	0.931653138	NA	grey	0.149461213	0.061722148		AT2G46320.1		Mitochondrial substrate carrier family protein	carrier CGI-69 protein
Sapur.001G012200.2	0.043392291	0.15852303	1.850620987	0.085659	0.931737201	NA	grey	0.033176018	0.679983213	GO:0055114,GO:0046872,GO:0016702	AT3G45140.1	ATLOX2,LOX2	lipoxygenase 2	lipoxygenase
Sapur.010G010800.2	0.023252211	0.235506827	2.760023425	0.085328	0.932000762	NA	grey	0.152636176	0.056334282	GO:0008138,GO:0006470	AT3G23610.2	DSPTP1	dual specificity protein phosphatase 1	NA
Sapur.005G117800.1	0.039945258	0.158528172	1.864417883	0.085028	0.932238939	NA	grey	-0.031426323	0.696003793		AT1G69700.1	ATHVA22C,HVA22C	HVA22 homologue C	ribonuclease HI
Sapur.010G024600.2	0.022598363	0.235507879	2.770332322	0.085011	0.932252887	NA	grey	0.154589734	0.05321619	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810	AT1G70610.1	ATTAP1,TAP1	transporter associated with antigen processing protein 1	ABC transporter B family protein
Sapur.016G212300.1	0.039817944	0.158528369	1.864954079	0.085004	0.93225829	NA	grey	0.024015294	0.765284005	GO:0016788,GO:0006886,GO:0006505	AT3G27325.2		hydrolases, acting on ester bonds	GPI inositol-deacylase
Sapur.006G137300.3	0.049707349	-0.171253379	2.016655608	-0.08492	0.932325392	NA	grey	-0.140650317	0.078916927		AT3G02920.1	ATRPA32B,RPA32B	Replication protein A, subunit RPA32	NA
Sapur.011G070600.1	0.022412392	0.235508182	2.773332924	0.084919	0.932325923	NA	grey	0.158033031	0.048068252		AT5G35700.1	FIM2	fimbrin-like protein 2	NA
Sapur.008G056700.1	0.036360292	0.196119276	2.314291738	0.084743	0.932465967	NA	grey	0.074515773	0.353662266	GO:0005515,GO:0016567,GO:0004842	AT3G54850.1	ATPUB14,PUB14	plant U-box 14	ubiquitin-protein ligase, putative
Sapur.009G014700.1	0.021739558	0.235509298	2.78445557	0.08458	0.932595287	NA	grey	0.152207136	0.057038871					NA
Sapur.019G002200.1	0.021388053	0.235509893	2.790439568	0.084399	0.932739321	NA	grey	0.153164961	0.055475774					NA
Sapur.008G096800.1	0.045777988	0.144045422	1.709585183	0.084258	0.93285168	NA	grey	-0.002603669	0.97418238					hypothetical protein
Sapur.006G211100.1	0.048769875	-0.244206808	2.904824395	-0.08407	0.933001264	NA	grey	-0.408737644	1.07E-07	GO:0017176	AT4G35530.1		phosphatidylinositolglycan-related	GPI-GlcNAc transferase complex, PIG-H component
Sapur.006G138100.3	0.029805296	0.19798127	2.360864042	0.08386	0.933168008	NA	grey	-0.081608864	0.309590942	GO:0005515	AT2G18850.2		SET domain-containing protein	ribulose-bisphosphate carboxylase, lysine N-methyltransferase%2C putative
Sapur.010G136600.4	0.019926024	0.235512452	2.816723948	0.083612	0.933364776	NA	grey	0.154456729	0.053423851	GO:0055114,GO:0016616,GO:0006102,GO:0004450	AT1G65930.1	cICDH	cytosolic NADP+-dependent isocitrate dehydrogenase	isocitrate dehydrogenase [NADP] protein
Sapur.019G015300.1	0.028648018	0.197983069	2.371419377	0.083487	0.933464186	NA	grey	0.10922917	0.173267679	GO:0016829,GO:0010333,GO:0000287	AT3G25810.1		Terpenoid cyclases/Protein prenyltransferases superfamily protein	NA
Sapur.008G147800.1	0.019554864	0.235513126	2.823784647	0.083403	0.933530817	NA	grey	0.155969226	0.051101496	GO:0005515	AT3G01400.1		ARM repeat superfamily protein	NA
Sapur.001G064500.1	0.019434068	0.235513347	2.826119058	0.083335	0.933585532	NA	grey	0.158234282	0.047780655		AT5G07500.1	PEI1	Zinc finger C-x8-C-x5-C-x3-H type family protein	Zn-finger transcription factor, putative
Sapur.002G105700.2	0.04414682	-0.169393337	2.034696312	-0.08325	0.933650854	NA	grey	-0.186868907	0.019107276	GO:0043531	AT4G33300.1	ADR1-L1	ADR1-like 1	NBS-LRR resistance protein
Sapur.016G297400.1	0.027821639	0.197984392	2.379280811	0.083212	0.933683079	NA	grey	0.096221421	0.230605626	GO:0055114,GO:0050660,GO:0016491	AT1G26420.1		FAD-binding Berberine family protein	reticuline oxidase, putative
Sapur.T030200.1	0.018605414	0.235514915	2.842824648	0.082845	0.933974478	NA	grey	0.155844669	0.05128953		AT5G24280.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.010G060700.2	0.0261738	0.197987185	2.396148406	0.082627	0.934147923	NA	grey	0.071049365	0.376561224	GO:0006468,GO:0005524,GO:0004672	AT3G04910.1	ATWNK1,WNK1,ZIK4	with no lysine (K) kinase 1	Serine/Threonine-kinase WNK1, putative
Sapur.003G015900.2	0.018117542	0.235515852	2.852973062	0.082551	0.934208544	NA	grey	0.152888417	0.055923401	GO:0016773,GO:0005975	AT1G80460.1	GLI1,NHO1	Actin-like ATPase superfamily protein	glycerol kinase-like protein
Sapur.010G063800.1	0.040398056	-0.169388798	2.05250014	-0.08253	0.934226828	NA	grey	-0.184787183	0.020511153					NA
Sapur.004G128500.1	0.025764927	0.197987884	2.400433583	0.08248	0.934264981	NA	grey	0.10671092	0.183452153		AT4G38700.1		Disease resistance-responsive (dirigent-like protein) family protein	NA
Sapur.004G118900.3	0.025611115	0.19798815	2.402067559	0.082424	0.934309508	NA	grey	0.112161929	0.161941498		AT4G39150.2		DNAJ heat shock N-terminal domain-containing protein	DnaJ heat shock amino-terminal domain protein
Sapur.002G077900.2	0.017450986	0.235517165	2.867411761	0.082136	0.934538723	NA	grey	0.157865208	0.048309178	GO:0003824,GO:0006470,GO:0004722	AT1G34750.1		Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.011G113800.1	0.028895282	0.174239252	2.12249884	0.082092	0.934573901	NA	grey	0.036089304	0.653626188	GO:0004674,GO:0048544,GO:0006468,GO:0004672	AT4G21380.1	ARK3,RK3	receptor kinase 3	NA
Sapur.014G028900.1	0.02397518	0.197991065	2.420239046	0.081806	0.93480066	NA	grey	0.105589659	0.188125529	GO:0006468,GO:0005524,GO:0004672	AT2G23450.1		Protein kinase superfamily protein	tyrosine kinase family protein
Sapur.006G040400.2	0.023501816	0.197991941	2.425786344	0.08162	0.934949139	NA	grey	0.120973233	0.131241083		AT3G57520.1	AtSIP2,SIP2	seed imbibition 2	raffinose synthase or seed imbibition protein, putative
Sapur.15WG143600.6	0.016062252	0.235520037	2.899872813	0.081217	0.935269088	NA	grey	0.154212799	0.053806443	GO:0003676	AT4G25500.2	AT-SRP40.ATRSP35.ATRSP4	arginine/serine-rich splicing factor 35	arginine/serine-rich-splicing factor RSP41
Sapur.008G042100.1	0.045416318	0.136732502	1.685331309	0.081131	0.935337826	NA	grey	-0.016358482	0.838863938		AT1G20823.1		RING/U-box superfamily protein	NA
Sapur.013G041300.1	0.028954949	0.235520465	2.904820075	0.081079	0.935378974	NA	grey	0.119672412	0.135468905		AT3G04560.1			hypothetical protein
Sapur.005G104500.1	0.025102512	0.235520465	2.904820075	0.081079	0.935378974	NA	grey	0.097890034	0.222582906		AT5G60150.1			hypothetical protein
Sapur.016G225600.1	0.021050717	0.235520464	2.904820075	0.081079	0.935378974	NA	grey	0.253523506	0.00135644		AT1G29395.1	COR413-TM1.COR413IM1.(	COLD REGULATED 314 INNER MEMBRANE 1	cold acclimation protein WCOR413
Sapur.016G076000.1	0.017141682	0.235520464	2.904820075	0.081079	0.935378974	NA	grey	0.134868856	0.092162122		AT2G37370.1			hypothetical protein
Sapur.001G100500.1	0.015175918	0.235520464	2.904820075	0.081079	0.935378974	NA	grey	0.107482258	0.180287064		AT2G02220.1	ATPSKR1,PSKR1	phytosulfokin receptor 1	NA
Sapur.T179200.1	0.044263134	0.136732905	1.688874751	0.080961	0.935473008	NA	grey	0.035421057	0.659635714		AT3G54750.3			NA
Sapur.005G098900.4	0.021454631	0.197995858	2.451110622	0.080778	0.93561849	NA	grey	0.11459327	0.152979032	GO:0055114,GO:0016491	AT5G66760.1	SDH1-1	succinate dehydrogenase 1-1	succinate dehydrogenase [ubiquinone] flavoprotein subunit
Sapur.009G084700.1	0.021411086	0.197995947	2.451694968	0.080759	0.935633773	NA	grey	0.080829861	0.314247408					NA
Sapur.009G039000.1	0.019197449	0.227687478	2.833345079	0.08036	0.935950977	NA	grey	0.149269355	0.062060816		AT5G12460.1		Protein of unknown function (DUF604)	fringe-like protein
Sapur.003G005700.1	0.040087185	0.136734454	1.70270903	0.080304	0.935995427	NA	grey	0.021363429	0.790567134					hypothetical protein
Sapur.T129500.1	0.020192305	0.197998496	2.46865406	0.080205	0.936074182	NA	grey	0.090281031	0.260810987					NA
Sapur.003G058100.2	0.047130497	0.134544628	1.685465738	0.079826	0.936375343	NA	grey	-0.000396068	0.996071984	GO:0051536,GO:0009055	AT1G32550.1		2Fe-2S ferredoxin-like superfamily protein	ferredoxin 2
Sapur.016G048400.1	0.046313598	-0.133901499	1.682502289	-0.07958	0.936567536	NA	grey	-0.18175897	0.022711978		AT3G57550.2	AGK2,GK-2	guanylate kinase	guanylate kinase
Sapur.005G062400.1	0.044782912	-0.13389924	1.687270274	-0.07936	0.936747476	NA	grey	-0.176892228	0.026674473					NA
Sapur.006G200300.2	0.03302249	0.136737454	1.730598377	0.079012	0.937023347	NA	grey	0.002018848	0.979980006	GO:0051603,GO:0005839,GO:0004298	AT1G56450.1	PBG1	20S proteasome beta subunit G1	proteasome subunit beta type protein
Sapur.004G013500.1	0.048993284	0.158577858	2.016837702	0.078627	0.937329327	NA	grey	0.008861254	0.912293511					hypothetical protein
Sapur.009G107300.2	0.03860285	0.134548044	1.713421612	0.078526	0.937409696	NA	grey	0.005929395	0.941247465	GO:0006468,GO:0005524,GO:0004672	AT2G16750.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	receptor-like kinase
Sapur.006G002700.6	0.041296463	0.160440639	2.045415388	0.078439	0.937478735	NA	grey	0.078324593	0.329530138	GO:0006468,GO:0004672,GO:0005524	AT5G47750.1	D6PKL2,PK5	D6 protein kinase like 2	Serine/Threonine kinase domain protein
Sapur.008G099400.3	0.040883614	0.160441187	2.047441879	0.078362	0.937540276	NA	grey	0.021986474	0.784606235	GO:0008270,GO:0005515	AT3G18290.1	BTS,EMB2454	zinc finger protein-related	zinc finger protein, putative
Sapur.001G030700.1	0.048519758	0.1208974	1.545666584	0.078217	0.937655441	NA	grey	-0.005837293	0.942158477		AT1G79660.1			plant/F20B17-9 protein
Sapur.006G145300.1	0.047439704	0.120899168	1.548339946	0.078083	0.937761958	NA	grey	0.030322	0.706185348		AT2G18660.1	PNP-A	plant natriuretic peptide A	NA
Sapur.008G122500.1	0.045205908	0.120903001	1.554188062	0.077792	0.937993713	NA	grey	0.116973866	0.144570769	GO:0005515,GO:0055114,GO:0046872,GO:0016702	AT3G22400.1	LOX5	PLAT/LH2 domain-containing lipoxygenase family protein	linoleate 9S-lipoxygenase, putative
Sapur.010G112300.1	0.02202607	0.190244973	2.446633824	0.077758	0.93802068	NA	grey	0.055301525	0.491505958	GO:0030418,GO:0030410	AT1G09240.1	ATNAS3,NAS3	nicotianamine synthase 3	nicotianamine synthase
Sapur.006G046200.1	0.036178921	0.160447804	2.072409882	0.077421	0.938288728	NA	grey	0.062982904	0.433248088	GO:0043565,GO:0006355,GO:0003700,GO:0006351	AT5G06839.3	bZIP65,TGA10	bZIP transcription factor family protein	BZIP transcription factor
Sapur.019G047700.1	0.036140251	0.160447862	2.072630863	0.077413	0.938295272	NA	grey	0.079535596	0.322084159					NA
Sapur.017G043300.2	0.034021401	0.179656044	2.339632267	0.076788	0.938792074	NA	grey	-0.102416381	0.201821967		AT4G13630.1		Protein of unknown function, DUF593	zein-binding protein
Sapur.016G309900.1	0.031666706	0.160454901	2.100285652	0.076397	0.939103492	NA	grey	0.017162173	0.831062782		AT5G52552.1	CPuORF14	conserved peptide upstream open reading frame 14	NA
Sapur.012G085500.2	0.031608264	0.160454999	2.100677234	0.076383	0.939114784	NA	grey	0.197175256	0.013315952		AT5G51160.1		Ankyrin repeat family protein	ankyrin repeat protein
Sapur.002G072800.2	0.031437153	0.16045528	2.101828723	0.076341	0.939147967	NA	grey	0.080504047	0.316208409		AT1G12350.1	ATCOAB,COAB	4-phospho-panto-thenoylcysteine synthetase	phosphopantothenate-cysteine ligase
Sapur.006G157500.1	0.031280199	0.16045555	2.102891537	0.076302	0.939178562	NA	grey	0.507276449	1.20E-11		AT2G42040.1			WRC protein
Sapur.019G040600.2	0.02976154	0.160458167	2.113515597	0.07592	0.939482721	NA	grey	0.039229868	0.625685369		AT4G15830.1		ARM repeat superfamily protein	NA
Sapur.014G132800.2	0.046936684	-0.171197912	2.261082161	-0.07572	0.939645815	NA	grey	-0.115542491	0.149583273	GO:0043039,GO:0016876,GO:0005524,GO:0006418,GO:0004812,GO:0000166	AT2G04842.1	EMB2761	threonyl-tRNA synthetase, putative / threonine--tRNA ligase, putative	threonyl-tRNA synthetase/threonine-tRNA ligase, putative
Sapur.15WG038600.1	0.027726736	0.160461863	2.128811267	0.075376	0.939915336	NA	grey	0.038127866	0.635431759		AT1G37113.1			NA
Sapur.006G154000.1	0.01777694	0.213923594	2.860266011	0.074792	0.940380603	NA	grey	0.237325867	0.00276431	GO:0046872,GO:0000166	AT3G42640.1	AHA8,HA8	H(+)-ATPase 8	plasma membrane H+ ATPase
Sapur.016G051700.1	0.013780024	0.213924139	2.904820703	0.073645	0.941293242	NA	grey	0.113951973	0.155305879					NA
Sapur.014G139700.1	0.017655233	0.213924139	2.904820703	0.073645	0.941293242	NA	grey	0.098063796	0.221758974		AT3G23810.1	ATSAHH2,SAHH2	S-adenosyl-l-homocysteine (SAH) hydrolase 2	NA
Sapur.005G147900.1	0.018148329	0.213924138	2.904820703	0.073645	0.941293242	NA	grey	0.1160557	0.14777119		AT1G77220.1		Protein of unknown function (DUF300)	organic solute transporter ostalpha protein
Sapur.008G033900.1	0.019616993	0.213924138	2.904820703	0.073645	0.941293242	NA	grey	0.115908449	0.148289409		AT1G49290.1			hypothetical protein
Sapur.014G027900.1	0.013931286	0.213924138	2.904820703	0.073645	0.941293242	NA	grey	0.145162758	0.069682363	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G31940.1	CYP82C4	cytochrome P450, family 82, subfamily C, polypeptide 4	NA
Sapur.T078800.1	0.014140494	0.213924138	2.904820703	0.073645	0.941293242	NA	grey	0.144502566	0.070975821		AT1G18210.2		Calcium-binding EF-hand family protein	NA
Sapur.T091600.1	0.038423286	-0.169336551	2.300332413	-0.07361	0.941317572	NA	grey	0.29327637	0.000193246		AT3G59480.1		pfkB-like carbohydrate kinase family protein	pfkB-type carbohydrate kinase family protein
Sapur.15WG068100.1	0.037524844	-0.169335274	2.307626783	-0.07338	0.941503173	NA	grey	-0.163806509	0.040368724	GO:0005525	AT1G73640.1	AtRABA6a,RABA6a	RAB GTPase homolog A6A	small GTPase family Rab protein
Sapur.15WG130800.2	0.02466585	0.176442435	2.412385498	0.07314	0.941694527	NA	grey	0.084196048	0.294451631	GO:0046872,GO:0016567,GO:0004842	AT4G19670.2		RING/U-box superfamily protein	zinc finger protein, putative
Sapur.011G082400.2	0.026636884	0.19802984	2.714482512	0.072953	0.941843461	NA	grey	0.072240729	0.368590953	GO:0006468,GO:0005524,GO:0004672	AT1G53050.1		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.15ZG040900.1	0.024003274	0.176442652	2.419914859	0.072913	0.941875546	NA	grey	0.020654455	0.797364917		AT3G42723.1		aminoacyl-tRNA ligases;ATP binding;nucleotide binding	NA
Sapur.009G073900.4	0.045141149	-0.133834785	1.84401408	-0.07258	0.942141964	NA	grey	0.020265462	0.801101173	GO:0006281,GO:0003684	AT5G44750.1	ATREV1,REV1	DNA-directed DNA polymerases	DNA repair protein REV1
Sapur.014G002100.1	0.0302597	0.152810243	2.112591614	0.072333	0.942336845	NA	grey	0.046914109	0.559586323		AT2G22620.1		Rhamnogalacturonate lyase family protein	rhamnogalacturonate lyase family protein
Sapur.018G025500.2	0.024511127	0.198032967	2.743728268	0.072177	0.94246137	NA	grey	0.084559377	0.292365597		AT4G32440.1		Plant Tudor-like RNA-binding protein	agenet domain protein, putative
Sapur.006G000200.1	0.048934102	0.120974422	1.677629373	0.07211	0.942514099	NA	grey	-0.115182859	0.150863064		AT4G17150.1		alpha/beta-Hydrolases superfamily protein	esterase/lipase domain protein
Sapur.016G305000.2	0.047260396	0.120976858	1.682400408	0.071907	0.942675687	NA	grey	0.024902298	0.756880756		AT1G30540.1		Actin-like ATPase superfamily protein	BadF/BadG/BcrA/BcrD ATPase family protein
Sapur.019G038700.1	0.046892588	0.120977404	1.683475588	0.071862	0.942711977	NA	grey	-0.198393709	0.012745169	GO:0006468,GO:0004672	AT3G03770.2		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.001G113400.1	0.040276589	-0.133828088	1.86303854	-0.07183	0.942734622	NA	grey	-0.154904106	0.052728011					plant self-incompatibility protein S1
Sapur.002G102500.2	0.049835968	-0.208587337	2.904282275	-0.07181	0.942755312	NA	grey	0.319119404	4.63E-05		AT5G42900.2	COR27	cold regulated gene 27	transmembrane protein, putative
Sapur.018G020500.1	0.044271998	0.120981475	1.691560783	0.071521	0.942983415	NA	grey	0.093420307	0.244526956	GO:0016798,GO:0016020	AT5G34940.2	AtGUS3,GUS3	glucuronidase 3	glycoside hydrolase family 79 amino-terminal domain protein
Sapur.017G005900.2	0.025817148	0.152805519	2.147065796	0.071169	0.943262885	NA	grey	0.000364466	0.996385392	GO:0016787,GO:0005524,GO:0003677	AT1G03750.1	CHR9	switch 2	DNA repair and recombination RAD26-like protein, putative
Sapur.010G188800.1	0.0187139	0.176444562	2.490961614	0.070834	0.94352994	NA	grey	0.078548531	0.32814497					NA
Sapur.006G081700.1	0.047692361	-0.118962305	1.68115689	-0.07076	0.943587042	NA	grey	-0.166434197	0.037223624	GO:0055085,GO:0016021	AT3G51860.1	ATCAX3.ATHCX1.CAX1-LIKE	cation exchanger 3	vacuolar cation/proton exchanger
Sapur.018G113900.1	0.04401943	0.14231734	2.046248495	0.06955	0.94455154	NA	grey	0.009324252	0.907730654	GO:0005515	AT1G74170.1	AtRLP13,RLP13	receptor like protein 13	NA
Sapur.001G030600.2	0.036753779	0.160499737	2.308937784	0.069512	0.944581787	NA	grey	-0.022438112	0.780293045	GO:0016020	AT1G16180.1		Serinc-domain containing serine and sphingolipid biosynthesis protein	TMS membrane protein/tumor differentially protein
Sapur.010G088600.1	0.02943782	0.19990083	2.904821116	0.068817	0.945135353	NA	grey	0.117008859	0.144449845					TPR protein
Sapur.016G042800.3	0.021485419	0.199900829	2.904821116	0.068817	0.945135353	NA	grey	0.110186556	0.169507601		AT5G06800.1		myb-like HTH transcriptional regulator family protein	Myb-like DNA-binding domain protein
Sapur.011G042300.1	0.019552637	0.199900829	2.904821116	0.068817	0.945135353	NA	grey	0.136387684	0.08852224					DUF260 family protein
Sapur.018G023700.2	0.019894122	0.199900829	2.904821116	0.068817	0.945135353	NA	grey	0.312610026	6.72E-05		AT5G25360.1			DUF4050 family protein
Sapur.002G107300.2	0.02385743	0.199900829	2.904821116	0.068817	0.945135353	NA	grey	0.109858216	0.17079025	GO:0016567,GO:0004842	AT2G31510.1	ARI7,ATARI7	IBR domain-containing protein	ariadne-1 protein, putative

Sapur.012G102800.1	0.01945433	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.129649786	0.105584255	GO:0000160	ATSG07210.1	AR821,RR21	response regulator 21	NA
Sapur.004G054100.2	0.01774298	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.114665555	0.093148374		ATSG05810.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.005G139400.2	0.01647271	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.132752283	0.113673032		ATSG01990.1			hypothetical protein
Sapur.006G095400.1	0.01797305	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.130812362	0.10236289		ATSG44750.1	ATHD2A,HD2A,HDA1,HDT1	histone deacetylase 2	histone deacetylase 2a, putative
Sapur.006G094900.1	0.01793034	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.136129065	0.08838804					NA
Sapur.017G065800.1	0.01891927	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.128389561	0.10818830					NA
Sapur.017G104300.1	0.02009437	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.116518187	0.146152476		ATSG66370.1	AtMYB113,MYB113	myb domain protein 113	transcription factor MYB43
Sapur.003G030500.1	0.01686764	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.113820274	0.09292674	GO:0006355,GO:0005634	ATSG15481.1	IAA18,AUX22	indole-3-acetic acid inducible 19	indole-3-acetic acid inducible protein
Sapur.005G032500.2	0.01629982	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	-0.325834711	3.12E-05		ATSG27240.1		DNAJ heat shock N-terminal domain-containing protein	chaperone protein DnaJ, putative
Sapur.019G118800.6	0.01640235	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.124201227	0.09379025		ATSG41130.1			meiosis chromosome segregation family protein
Sapur.016G143700.5	0.01612641	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.113003638	0.101963207	GO:0016788	ATSG05510.1		indigoidine synthase A family protein	indigoidine synthase A-like protein
Sapur.002G095000.2	0.01576193	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.113202714	0.09663178	GO:0006355,GO:0006289,GO:0000439	ATSG12400.1		Nucleotide-excision repair, TFIIH, subunit TTDA	general transcription factor IIH subunit
Sapur.010G134500.1	0.01628344	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.132017602	0.104053446		ATSG47460.1		O-Glycosyl hydrolases family 17 protein	carbohydrate-binding module family 43 protein
Sapur.016G147800.2	0.01561765	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.115670898	0.103886654		ATSG46610.1		5-adenosylmethionine-dependent methyltransferases superfamily protein	aspmidine synthase-related/putrescine aminopropylltransferase, putative
Sapur.002G092000.2	0.01595888	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.135757513	0.09001823		ATSG57910.1	ATMYB68,MYB68	myb domain protein 68	R2R3-MYB transcription factor MYB1.1
Sapur.002G034900.2	0.01513721	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.135205213	0.09169017	GO:0005525,GO:0003924	ATSG38840.1		Guanylate-binding family protein	guanylate-binding family protein, putative
Sapur.007G105800.1	0.01521027	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.1311317	0.101625821	GO:0003677				B3 DNA binding domain protein
Sapur.016G209400.1	0.01518561	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.12995501	0.104891581	GO:0005515	ATSG27220.1		Galactose oxidase/kelch repeat superfamily protein	kelch motif protein
Sapur.T003580.1	0.01447409	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.136161792	0.089042018					NA
Sapur.011G021900.3	0.01448334	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.135938821	0.089590556	GO:0048544	ATSG11340.1		S-locus lectin protein kinase family protein	Serine/Threonine kinase domain protein
Sapur.017G091100.1	0.01447834	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.113838561	0.094698442					NA
Sapur.T000400.1	0.01450383	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.113188963	0.095872361					hypothetical protein
Sapur.019G164000.1	0.01370987	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.1383875	0.088243659	GO:0016829,GO:0010333,GO:0008152,GO:0000287	ATSG39660.2	ATTPS21,TPS21	terpene synthase 21	NA
Sapur.016G061200.1	0.01541606	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	-0.01854933	0.817637251	GO:0016887,GO:0005524,GO:0016020	ATSG06530.1		ABC-2 type transporter family protein	ABC transporter G family protein
Sapur.006G088100.5	0.01563673	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.1642044	0.038804618		ATSG20370.1		6-aminohexanoate dehydrogenase family protein	nucleoside diphosphatase
Sapur.T154500.1	0.01350366	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.13679702	0.0875982		ATSG42480.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.004G208800.1	0.01325791	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.136172661	0.088193747	GO:0003677				B3 DNA-binding domain protein
Sapur.15WG069760.2	0.01329452	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.020192314	0.82013079		ATSG48230.1			chromosome segregation protein Spc25
Sapur.15WG012500.1	0.0131881	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.111441299	0.164671868	GO:0003677	ATSG34390.1	ARF22	auxin response factor 22	NA
Sapur.15WG046790.1	0.01267574	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.13623681	0.088883321					NA
Sapur.017G042300.1	0.01254162	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.13250637	0.08846491		ATSG09680.1		zinc knuckle (CCHC-type) family protein	NA
Sapur.016G241100.1	0.01153775	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.136281515	0.088539995		ATSG27760.1			DNA ligase-like protein
Sapur.005G108600.2	0.01185097	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.13623589	0.08866024		ATSG67130.1		SEC-C motif-containing protein / OTU-like cysteine protease family protein	OTU-like cysteine protease
Sapur.T000100.1	0.01178842	0.19990829	2.904821116	0.068817	0.945135353	NA	grey	grey	0.136562761	0.08810679					NA
Sapur.004G147000.1	0.02502801	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.518663134	3.46E-12		ATSG11755.1	LEW1	U nucleoamyl pyrophosphate synthetase family protein	nogo-B receptor
Sapur.006G205700.1	0.01510317	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.113923908	0.094488628	GO:0016887,GO:0005524,GO:0016020	ATSG15120.1	ABCG40,ATABCG40,ATPDR1	pleiotropic drug resistance 12	transporter family ABC domain protein
Sapur.018G010000.2	0.01090107	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.13517564	0.091417474		ATSG24970.1		Protein kinase superfamily protein	AxrE domain kinase, putative
Sapur.014G135200.1	0.02595906	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.102808981	0.20088949	GO:0005737,GO:0000045	ATSG05630.1	ATGID	Ubiquitin-like superfamily protein	gelsA(A)receptor-associated protein, putative
Sapur.005G172900.1	0.01791666	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.113052804	0.088127554		ATSG11400.3	PNX2	partner of Y14-mago protein, putative	partner of Y14-mago protein, putative
Sapur.009G054600.2	0.01772413	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.10529252	0.18937845	GO:0016788	ATSG26870.1	NPC2	non-specific phospholipase C2	NA
Sapur.006G205600.1	0.01612393	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.11134155	0.105052233	GO:0003824,GO:0006470,GO:0004722	ATSG18610.1	AtDBP1,DBP1	DNA-binding protein phosphatase 1	protein phosphatase 2C
Sapur.005G189400.2	0.01460288	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.110493417	0.107090916		ATSG19860.1		Zinc finger C-x8-C-x5-C-x3-H type family protein	zinc finger CCCH domain protein
Sapur.T084300.1	0.0158895	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.096834763	0.227623684					NA
Sapur.013G030200.1	0.01371159	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.106994608	0.18275973					NA
Sapur.016G284000.2	0.01320177	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	-0.081609854	0.399369942	GO:0008173,GO:0008175,GO:0001510	AT4G20910.2	CRM2,HEN1	double-stranded RNA binding protein-related / DsRBD protein-related	small RNA methyltransferase
Sapur.005G172200.1	0.01288772	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.106117157	0.18593835					NA
Sapur.005G163800.1	0.01344049	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.106407968	0.184789441					NA
Sapur.T057600.1	0.01005744	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.110089935	0.169884305					NA
Sapur.008G156300.3	0.02227209	0.19990829	2.904821116	0.068817	0.945135354	NA	grey	grey	0.07654531	0.32814497		ATSG27100.1		Actin cross-linking protein, putative	actin cross-linking protein, putative
Sapur.008G113200.4	0.01801334	0.15845498	2.30630776	0.068786	0.945140074	NA	grey	grey	0.051417524	0.52247520		ATSG47524.1		hydroxyproline-rich glycoprotein family protein	hydroxyproline-rich glycoprotein family protein, putative
Sapur.003G204200.1	0.02394632	0.16050483	2.33706281	0.068678	0.945149554	NA	grey	grey	0.058623586	0.45179281		ATSG18500.1	ATOPT7,OPT7	ovate family protein 7	hypothetical protein
Sapur.005G088400.2	0.02032111	0.16056139	2.34447065	0.068462	0.945158218	NA	grey	grey	0.093366025	0.24482382		ATSG09610.1		Nucleotide-sugar transporter family protein	nucleotide-sugar transporter protein
Sapur.006G154400.1	0.02024837	0.18808346	2.904820075	0.068179	0.945642974	NA	grey	grey	0.034318753	0.669596245	GO:0008289	ATSG51680.2		Protein of unknown function (DUF1334)	plant/T25C13-40 protein
Sapur.016G021200.2	0.05004764	0.19390572	2.012878485	0.067943	0.945810365	NA	grey	grey	0.039031018	0.627232025	GO:0005515,GO:0016491,GO:0008270	ATSG36620.2		Grx5-like protein	glutaredoxin family protein
Sapur.016G029700.1	0.02063368	0.19216912	2.809276681	0.06771	0.945926265	NA	grey	grey	0.012811623	0.87348626	GO:0006351,GO:0005634,GO:0003677	ATSG18720.1		Transcription factor 65 protein	transcription factor S-II, central domain protein
Sapur.006G034300.1	0.04683558	0.18703181	1.436023959	0.067541	0.946310386	NA	grey	grey	-0.020604063	0.83218291	GO:0005515,GO:0003723	ATSG17860.1		binding RNA binding	NA
Sapur.008G108300.1	0.04695522	0.12886517	1.824659575	0.067353	0.946420589	NA	grey	grey	-0.138537774	0.083571218		ATSG17860.1	JAI3,JAZ3,TIFY6B	jasmonate-zim-domain protein 3	jasmonate ZIM-domain protein
Sapur.T010900.1	0.04834664	0.12888598	1.830049162	0.067156	0.946457593	NA	grey	grey	0.027692772	0.732739949					NA
Sapur.008G084800.1	0.04692049	0.12565155	1.836860851	0.066808	0.946549843	NA	grey	grey	-0.011737107	0.884004016					NA
Sapur.010G034400.1	0.05607543	0.13457561	2.019235629	0.066647	0.946882348	NA	grey	grey	0.107004336	0.182243386		ATSG17900.1			plant/WEB1-12 protein
Sapur.T180500.1	0.04412419	0.12306146	1.845195	0.066608	0.946899195	NA	grey	grey	0.038049027	0.63631462		ATSG46880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.018G060000.3	0.03150584	0.19276058	2.904821228	0.063852	0.947256470	NA	grey	grey	0.128665539	0.108833801		ATSG26000.1		TesmirpTSO1-like CXC domain-containing protein	transcription factor, putative
Sapur.019G289000.2	0.02692953	0.19276058	2.904821228	0.063152	0.947676516	NA	grey	grey	0.122202133	0.09927616	GO:0003824,GO:0006470,GO:0004722	ATSG04151.1		Protein phosphatase 2C family protein	protein phosphatase 2C family protein, putative
Sapur.007G072800.1	0.04128479	0.12308846	1.856239288	0.062214	0.947207701	NA	grey	grey	0.017829882	0.824594045					NA
Sapur.004G174700.1	0.04128118	0.12308641	1.856252621	0.062143	0.947230804	NA	grey	grey	-0.081608854	0.309369942	GO:0008270,GO:0005515	ATSG01960.1		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.002G018800.2	0.04119069	0.12308573	1.856585183	0.062021	0.947237467	NA	grey	grey	0.009363453	0.907344668	GO:0006096,GO:0003872	ATSG76550.1		Phosphofructokinase family protein	Phosphofructose-fructose 6-phosphotransferase alpha subunit
Sapur.T165000.1	0.04033835	0.12308082	1.860117187	0.060676	0.947316692	NA	grey	grey	0.005184756	0.948614601		ATCG00180.1	ATCRR1,ATRPO1,HT2,XPO	exoprim 1A	NA
Sapur.002G026000.2	0.03808421	0.12291325	1.864123212	0.065935	0.947429421	NA	grey	grey	-0.25107214	0.005155241	GO:0016758,GO:0016021,GO:0006506	ATSG22130.2	PNT1	mannosyltransferase family protein	GPI mannosyltransferase
Sapur.019G206600.3	0.02768758	0.12291016	1.871585278	0.065674	0.947635758	NA	grey	grey	0.003894248	0.96141137	GO:0003767	ATSG37140.1	PPO,TOP2	pyruvate orthophosphate dikinase family protein	serine/threonine-protein phosphatase
Sapur.011G053000.2	0.04329919	0.13377432	2.04255841	-0.06549	0.947781149	NA	grey	grey	0.008394927	0.918860178	GO:0003723	ATSG20740.1		Transcription factor jumonji (jmj) family protein	tetraspanin family protein
Sapur.T032100.1	0.03633916	0.12291228	1.877788609	0.065458	0.947809371	NA	grey	grey	0.013640043	0.865362962	GO:0003677,GO:0046983	ATSG42170.1		BED zinc finger ;hAT family dimerization domain	hAT family dimerization domain protein, putative
Sapur.008G074000.1	0.03388163	0.12291191	1.88695391	0.1237667	0.945641	0.947830649	NA	grey	-0.04050678	0.61837765		ATSG10640.1	AETR5120,TRS120	TRS120	TRS120
Sapur.014G018900.1	0.03850839	0.16392788	2.609192227	-0.06506	0.948122659	NA	grey	grey	-0.341097919	1.23E-05		ATSG10150.1		Tc22-like family protein	Tc22 family plant component
Sapur.013G107500.1	0.05012363	0.18860233	2.14181885	0.948879	0.948270413	NA	grey	grey	0.012041616	0.681470046		ATSG21280.1			NA
Sapur.018G108600.1	0.02595826	0.18866296	2.141232135	0.064837	0.948303947	NA	grey	grey	0.02193934	0.785056755	GO:0046983	ATSG57150.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH protein
Sapur.004G064500.3	0.04227697	0.13318142	2.045767483	-0.06448	0.948585026	NA	grey	grey	-0.203850706	0.011243655		ATSMAP33,ATSWAP33B,SWA	soluble N-ethylmaleimide-sensitive factor adaptor protein 33	SNAP family protein	vesicle-associated membrane protein, putative
Sapur.003G102700.1	0.03821725	-0.1319143	2.01073053	-0.064	0.948868054	NA	grey	grey	0.201646421	0.011438299		ATSG64385.1			transmembrane protein, putative
Sapur.005G012300.1	0.01853823	0.18327325	2.854798042	0.063988	0.948979442	NA	grey	grey	0.049843579	0.130942952		ATSG24100.1			NA
Sapur.T041300.1	0.04641779	0.17864986	2.904821749	0.061501	0.949060994	NA	grey	grey	-0.077860938	0.102409969					NA
Sapur.014G071200.2	0.03760108	0.13191189	2.065567859	-0.06386	0.949079381	NA	grey	grey	0.029140632	0.717135155		ATSG46200.1			programmed cell death protein, putative
Sapur.T011120.1	0.03730348	0.13191355	2.066116099	-0.06385	0.949087777	NA	grey	grey	-0.202542706	0.010949177		ATSG27000.1	AEPLA,PLA NB,PLP5	PATATIN-like protein 5	NA
Sapur.005G139300.1	0.04269109	0.09924036	1.561600364	0.063553	0.949282652	NA	grey	grey	0.003262149	0.9795507					NA
Sapur.005G085900.1	0.04243287	0.09924061	1.561772857	0.063546	0.949303913	NA	grey	grey	-0.049357215	0.610799179	GO:0006468,GO:0004672	ATSG54380.1	THE1	protein kinase family protein	NA
Sapur.006G024040.1	0.04524125	-0.09835695	1.554100896	-0.06329	0.94853666	NA	grey	grey	-0.158713069	0.047101199	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATSG40890.1	CYP98A3	cytochrome P450, family 98, subfamily A, polypeptide 3	P-coumaroyl shikimate 3'-hydroxylase
Sapur.006G028300.1	0.02628115	0.16239184	2.028445763	-0.062259	0.950263788	NA	grey	grey	0.078802758	0.31011812		ATSG47060.1		DNAse I-like superfamily protein	NA
Sapur.017G119300.1	0.03565527	0.16239897	2.013615848	0.062136	0.950547371	NA	grey	grey	0.079215264	0.323810408		ATSG21190.1	emb1417	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.005G200300.1	0.03647355	-0.16278996	1.888306429	-0.06181	0.950703188	NA	grey	grey	-0.194010042	0.014685617		ATSG75170.2		Sec14p-like phosphatidylinositol transfer family protein	transporter, putative
Sapur.003G074000.1	0.03374197	0.16240123	2.013154462	0.061713	0.950776012	NA	grey	grey	0.195839538	0.013967262	GO:0005515	ATSG10790.1		UBX domain-containing protein	Fas-associated factor-like protein
Sapur.005G147300.1	0.04379116	0.30432931	1.695788067	-0.06152	0.950945302	NA	grey	grey	-0.32275532	3.76E-05	GO:0006508,GO:0004185	ATSG42240.1	scpl42	serine carboxypeptidase-like 42	serine carboxypeptidase
Sapur.011G032200.3	0.01362488	0.17864986	2.904821749	0.061501	0.950860094	NA	grey	grey	-0.084886551	0.280477361	GO:0008146	ATSGT3E,ATSTSA CDR-7-SC	sulfotransferase 36	sulfotransferase 36	flavonol 3-sulfotransferase, putative
Sapur.T037300.1	0.00629622	0.17864985	2.904821749	0.061501	0.950860094	NA	grey	grey	0.12125831	0.136320701					NA
Sapur.010G007202.2	-0.00661348	0.17864985	2.904821749	0.061501	0.950860094	NA	grey	grey	0.123041817	0.134752209	GO:0003682	ATSG85580.2		agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein	agenet and bromo-adjacent-like (BAH) domain-like protein
Sapur.012G090800.5	0.01145974	0.17864985	2.904821749	0.061501	0.950860094	NA	grey	grey	0.122323892	0.136959355		ATSG45030.2		Trypsin family protein	peptidase, trypsin-like serine and cysteine protease
Sapur.019G204100.1	0.01307827	0.17864985	2.904821749	0.061501	0.950860094	NA	grey	grey	0.114926997	0.154032659		ATSG47721.1		aminoacyl-tRNA ligases;ATP binding;nucleotide binding	NA
Sapur.018G043400.1	0.01179277	0.17864985	2.904821749	0.061501	0.950860094	NA	grey	grey	0.120581269	0.13249127					NA
Sapur.018G189200.1	0.01183451	0.17864985	2.904821749	0.061501	0.950860094	NA	grey	grey	0.078648241	0.32814497		ATSG29660.1			transmembrane protein, putative
Sapur.002G016000.2	0.01327619	0.17864985	2.904821749	0.061501	0.950860094	NA	grey	grey	-0.018947185	0.8137962	GO:0003676	ATSG14300.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA-recognition motif 2 in heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1)-like protein
Sapur.003G047000.2	0.01617264	0.17864984	2.904821749	0.061501	0.950860094	NA	grey	grey	0.095813867	0.232058688					NA
Sapur.003G047700.2	0.02788264	0.17864984	2.904821749	0.061501	0.950860094	NA	grey	grey	-0.075819929	0.345277668	GO:0055114,GO:0016491	ATSG16770.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	flavonol synthase/flavanone 3-hydroxylase
Sapur.013G102100.3	0.05069001	0.22957709	2.007572224	0.061247	0.951825236	NA	grey	grey	-0.019938856	0.843021204		ATSG18330.1		pfkB-like carbohydrate kinase family protein	fructokinase
Sapur.004G182000.5	0.02660753	0.16240622	2.675158146	0.0607	0.951918182	NA	grey	grey	0.079419117	0.32846979		ATSG27400.1		3'(-5')-exoribonuclease family protein	exosome complex exonuclease MTR3
Sapur.15WG095300.1	0.02894204	0.16240707	2.683287507	0.060525	0.951737179	NA	grey	grey	0.096690132	0.228311775	GO:0008270,GO:0004089	ATBCA4,BCA4,CA4	ATBCA4	beta carbonic anhydrase 4	beta carbonic anhydrase 4
Sapur.005G148800.4	0.04667308	0.12368828	2.051115628	0.059662	0.952194188	NA	grey	grey	0.006936836	0.910608391		ATUBP5,SUP22,UBP26	ubiquitin-specific protease 26	ubiquitin-specific protease, putative	ubiquitin carboxyl-terminal hydrolase
Sapur.010G118500.2	0.04050239	0.12307064	2.051968491	0.059928	0.952231127	NA	grey	grey	-0.062708874	0.435134599		ATSG17310.2		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	DNA methyltransferase, putative
Sapur.006G080800.1	0.03051149	0.16240609	2.715618805	0.059806	0.952310266	NA	grey	grey	-0.08850248	0.270045391		ATSG13100.2	VCS	Vanadium chloroperoxidase family protein, U-MD40-like protein, putative	peptidase S26A, signal peptidase I, MD40-like protein, putative
Sapur.001G175900.1	0.03937810	0.12307154	2.057679932	0.059762	0.952344995	NA	grey	grey	0.013069409	0.870792	GO:0006468,GO:0005524,GO:0004672	ATSN8Z-10,SNRK2-10,SPK2B	SNF1-related protein kinase 2.10		Serine/Threonine kinase
Sapur.015G033300.1	0.03992885	0.16240138	2.731663386	0.059674	0.952455158	NA	grey	grey	0.072818751	0.36476178		ATSG41572.1			COP1-interacting-like protein, putative
Sapur.009G129200.1	0.03737602	0.12307384	2.068233494	0.059456	0.952588956	NA	grey	grey	-0.020246679	0.90851464	GO:0020037,GO:0009055	ATSG40810.1		Cytochrome C1 family	cytochrome c1 heme protein
Sapur.005G082200.2	0.02463715	0.16241368	2.738920774	0.059298	0.952745196	NA	grey	grey	0.030894795	0.738379299	GO:0016020,GO:0009570	ATSG51480.1	ATGLR3.6,GLR3.6	glutamate receptor 3.6	glutamate receptor
Sapur.013G054200.3	0.01918024	0.18868214	2.948772843	0.059169	0.952839654	NA	grey	grey	-0.010182808	0.883103907		ATSG13690.1	CYL1,NAG1J	alpha-N-acetylglucosaminidase family / NAGLU family	alpha-N-acetylglucosaminidase
Sapur.005G093000.1	0.02369133	0.16241455	2.753303922	0.058989	0.952960288	NA	grey	grey	0.084889313	0.290478026					NA
Sapur.006G199000.1	0.02322687	0.16241384	2.765513	0.058805	0.953083189	NA	grey	grey	0.064583813	0.42200666		ATSG11530.1	EMF1	embryonic flower 1 (EMF1)	EMBRYO flowering-like protein, putative
Sapur.019G089900.1	0.02310724	0.1624153	2.760667789	0.058882	0.953086509	NA	grey	grey	0.134607072	0.092633433		ATSG03420.1		Protein of unknown function (DUF789)	plant/F21B7-13 protein
Sapur.T000900.1	0.02322893	0.16241385	2.771469051	0.058623	0.953179899	NA	grey	grey	0.072837023	0.36120557					NA
Sapur.T074300.1	0.02668534	0.13869061	2.375137605	0.0585	0.953503331	NA	grey	grey	0.009787242	0.90317083		ATSG33380.1		ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	NA
Sapur.002G016100.5	0.02715417	0.16241716	2.784664422	0.058262	0.953611977	NA	grey	grey	0.068849297	0.398140654	GO:0016799,GO:0008270,GO:0006289,GO:0003906,GO:0003684	ATFRG-1,ATFPG-2,ATMMH4	ATMMH4	8-oxoguanine DNA glycosylase family protein	8-oxoguanine/pyrimidine-DNA glycosylase
Sapur.019G090500.1	0.03972625	0.16926254	2.904820495	-0.05827	0.953933987	NA	grey	grey	-0.031937146	0.00012151		ATSG39730.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH protein
Sapur.013G198600.1	0.01656631	0.16241873	2.787487388	0.058237	0.953962112	NA	grey	grey	0.06273879	0.39938705		ATSG37360.1		Copper transport protein family protein	metal-ion binding protein, putative
Sapur.008G210000.1	0.02162086	0.16241877	2.792563207	0.05816	0.953615106	NA	grey	grey	0.04574691	0.589407331		ATSG04460.3		RING/U-box superfamily protein	neuralized protein
Sapur.017G062900.1	0.04761975	0.28932967	1.435460421	0.05806	0.953700107	NA	grey	grey	-0.050542463	0.529587066	GO:0006468,GO:0005524,GO:0004672	ATSG15080.1		Protein kinase superfamily protein	Serine/Threonine kinase-like protein
Sapur.013G051900.1	0.02091823	0.16241659	2.798624179	0.058035	0.953726517	NA	grey	grey	0.06682712	0.43987839		ATSG78172.1			NA
Sapur.T076200.1	0.02060956	0.16241594	2.804179137	0.057921	0.953851915	NA	grey	grey	0.062696587	0.453460059		ATSG60050.1		BTB/POZ domain-containing protein	NA
Sapur.016G064500.1	0.04238760	-0.09827926	1.697594225	-0.05789	0.953916437	NA	grey	grey	0.143314755	0.077075327	GO:0016567,GO:0006842	ATSG11840.1	PUB24	plant U-box 24	spotted leaf protein, putative
Sapur.T043100.1	0.02015741	0.16242003	2.80872674	0.057827	0.953886491	NA	grey	grey	0.080634115	0.315436611					NA
Sapur.T016620.1	0.02056612	0.16242017	2.808660202	0.057804	0.953947164	NA	grey	grey	0.064604164	0.39227782					NA
Sapur.009G119700.1	0.02027305	0.16242079	2.810276682	0.057795	0.953991903	NA	grey	grey	0.061933306	0.440962785	GO:0006468,GO:0005524,GO:0004672	ATSG46850.1		Protein kinase superfamily protein	ser/arg-rich kinase
Sapur.016G197700.1	0.01945255	0.16242127	2.825165462	0.057661	0.954154126	NA	grey	grey	0.059956561	0.454816893		ATSG45000.1		ARM repeat superfamily protein	proteasome-associated ECM29-like protein
Sapur.004G149100.4	0.01903204	0.16242243	2.834234172	0.057308	0.954302021	NA	grey	grey	0.196549289	0.016617793		ATSG20730.1	AtEIN3,EIN3	Ethylene insensitive 3 family protein	ethylene insensitive transcription factor, putative
Sapur.006G189900.1	0.01902906	0.16242246	2.834285184	0.057304	0.954302799	NA	grey	grey	0.05624563	0.484152222	GO:0008236,GO:0006508	ATSG24280.1		alpha/beta-Hydrolases superfamily protein	lysosomal pro-X carboxypeptidase
Sapur.019G022000.1	0.01859761	0.16242329	2.842981281	0.057131	0.954603597	NA	grey	grey	0.055052204	0.493462668	GO:0071949	ATSG68440.1	SQE1,KF1	FAD/NAD(P)-binding oxidoreductase family protein	squalene monooxygenase
Sapur.003G062300.4	0.01858903	0.16243262	2.843225087	0.057126	0.954644493	NA	grey	grey	-0.02109062	0.785375559		ATPB,CEO1,EOL1,KCD1	WWE protein-protein interaction domain protein family	inactive poly [ADP-ribose] polymerase	inactive poly [ADP-ribose] polymerase

Sapur.017G045400.1	0.007044331	0.164281246	2.904822183	0.056555	0.954899949	NA	grey	0.078548531	0.32814487															
Sapur.003G036000.2	0.005739053	0.164281246	2.904822183	0.056555	0.954899949	NA	grey	0.078548531	0.32814487															
Sapur.004G064700.1	0.005463855	0.164281246	2.904822183	0.056555	0.954899949	NA	grey	0.078548531	0.32814487															
Sapur.006G213200.1	0.016765572	0.162426827	2.883007975	0.056339	0.955074558	NA	grey	-0.025491691	0.751312618	GO:0005515														
Sapur.006G176000.1	0.016826174	0.162426391	2.89060226	0.056053	0.955325231	NA	grey	0.096050081	0.258859033															
Sapur.010G057900.2	0.025628664	0.162428751	2.904821116	0.055967	0.955497975	NA	grey	0.064834309	0.425521441	GO:0006468;GO:0005524;GO:0004672														
Sapur.006G215800.2	0.020593346	0.162428751	2.904821116	0.055967	0.955497975	NA	grey	0.070739504	0.37861133	GO:0006468;GO:0004672														
Sapur.013G012900.1	0.022982161	0.162428751	2.904821116	0.055967	0.955497975	NA	grey	0.055791808	0.487667251	GO:0005524														
Sapur.7.1G0600.1	0.022291173	0.162428751	2.904821116	0.055967	0.955497975	NA	grey	0.054831046	0.495206651															
Sapur.010G079000.2	0.020079987	0.162428751	2.904821116	0.055967	0.955497975	NA	grey	0.060907573	0.491002851	GO:0006468;GO:0004672														
Sapur.010G130700.3	0.018454526	0.162428751	2.904821116	0.055967	0.955497975	NA	grey	-0.488555868	8.51E-11	GO:0005975														
Sapur.007G131300.1	0.018460871	0.162428751	2.904821116	0.055967	0.955497975	NA	grey	-0.126426576	0.059988866	GO:0006355														
Sapur.004G077100.1	0.021576235	0.15527586	2.789824384	0.055658	0.956164283	NA	grey	0.060492284	0.18674628															
Sapur.003G125500.1	0.036617713	0.15076229	2.904820075	0.055279	0.956560606	NA	grey	0.040606106	1.27E-05	GO:0005515														
Sapur.003G027700.1	0.032634415	0.151339792	2.099188868	0.054945	0.956832334	NA	grey	0.153842205	0.054233502	GO:0007034														
Sapur.7.1G0900.1	0.041439564	0.151070989	1.855488779	0.054687	0.956938788	NA	grey	0.055256566	0.947906925															
Sapur.008G045100.1	0.007117824	0.157814943	2.904822379	0.054329	0.956573388	NA	grey	0.102610103	0.20096754															
Sapur.7.0T1700.1	0.007078388	0.157814943	2.904822379	0.054329	0.956573388	NA	grey	0.102599004	0.201054723	GO:0016788														
Sapur.002G169200.1	0.006868073	0.157814943	2.904822379	0.054329	0.956573388	NA	grey	0.102457996	0.201637812	GO:0006298														
Sapur.005G189300.1	0.053575835	0.08342319	1.543027951	0.054064	0.956889374	NA	grey	-0.02131141	0.791065374	GO:0005515														
Sapur.005G038100.1	0.034913034	0.164881375	2.910438293	0.053947	0.957000556	NA	grey	-0.43181456	1.64E-08															
Sapur.006G073000.1	0.032149771	0.10147427	1.858964124	0.053847	0.957283556	NA	grey	-0.026380217	0.743640592	GO:0009611;GO:0004867														
Sapur.010G131000.1	0.031470362	0.101470386	1.902917736	0.053192	0.957967027	NA	grey	0.096960512	0.21412725															
Sapur.004G079000.1	0.046787415	0.096819254	1.842124244	-0.05332	0.957678119	NA	grey	0.119303408	0.13668868	GO:0006813;GO:0003677;GO:0006355;GO:0005634;GO:0003700														
Sapur.005G187700.2	0.020719332	0.101470427	1.906017838	0.053229	0.957641423	NA	grey	0.032364831	0.837365543	GO:0006468;GO:0004672														
Sapur.016G142900.2	0.030623267	0.101470716	1.907476026	0.053108	0.957578312	NA	grey	-0.047565275	0.554218167															
Sapur.006G299600.1	0.039692426	0.099277698	1.867268727	0.053168	0.95258813	NA	grey	-0.00041587	0.995875596															
Sapur.013G088200.1	0.029872719	0.124890286	2.382026887	0.052629	0.957807077	NA	grey	0.008219767	0.918620284	GO:0006412;GO:0005840;GO:0005622;GO:0003735;GO:0015935														
Sapur.7.1G1800.1	0.029000585	0.124891614	2.388105559	0.052738	0.957904631	NA	grey	0.027949221	0.72823665															
Sapur.008G160200.1	0.028405581	0.124891545	2.37374864	0.052614	0.958039421	NA	grey	0.131513619	0.105520474															
Sapur.015G053400.1	0.028376602	0.124892586	2.373973654	0.052609	0.958043277	NA	grey	0.01008894	0.901021901	GO:0004518;GO:0006281														
Sapur.003G079100.1	0.028297531	0.124892711	2.374734197	0.052593	0.958058257	NA	grey	0.04046426	0.537284969															
Sapur.015G172300.4	0.028237586	0.124892805	2.375289986	0.05258	0.958066533	NA	grey	0.017964585	0.823466429															
Sapur.015G172300.1	0.027913849	0.124892319	2.378368654	0.052512	0.958120982	NA	grey	0.027694727	0.639261986	GO:0006468;GO:0005524;GO:0004672														
Sapur.016G134100.1	0.027544417	0.124893911	2.381985515	0.052433	0.958183891	NA	grey	0.003072313	0.989365564															
Sapur.005G156600.1	0.027523737	0.124893911	2.382195669	0.052429	0.958188313	NA	grey	0.073317961	0.342763366	GO:0008270;GO:0005515														
Sapur.012G088400.1	0.027507763	0.12489397	2.382343184	0.052425	0.958190179	NA	grey	0.01728523	0.829869746	GO:0006508;GO:0004190														
Sapur.003G144300.1	0.027387084	0.12489455	2.385879783	0.052347	0.958251903	NA	grey	0.043942661	0.584796606															
Sapur.005G172900.3	0.02710466	0.124894284	2.386607728	0.052329	0.958268153	NA	grey	0.001419976	0.98222015	GO:0006481														
Sapur.15W0G011000.1	0.026760854	0.124895245	2.390140578	0.052254	0.958326028	NA	grey	0.024978024	0.756160863															
Sapur.017G300000.2	0.026733026	0.124895294	2.390441679	0.052248	0.958352154	NA	grey	0.011130007	0.889906099	GO:0005085;GO:0016020;GO:0015297;GO:0015238;GO:0006855														
Sapur.014G120900.2	0.026285684	0.124896032	2.394995186	0.052149	0.958410098	NA	grey	0.017650223	0.836817668	GO:0005085;GO:0003916;GO:0003677;GO:0003917														
Sapur.007G074200.2	0.025816164	0.124896033	2.398334971	0.052066	0.958476466	NA	grey	0.029369665	0.747402107															
Sapur.002G079900.3	0.064165806	-0.096195971	1.852707373	-0.05206	0.958477593	NA	grey	-0.141537338	0.070027738	GO:0008324;GO:0006470;GO:0004722														
Sapur.016G082800.1	0.026516019	0.141175403	2.712881391	0.052028	0.958497686	NA	grey	0.144797084	0.070416019	GO:0005515;GO:0071165 (NR-LBD class) family														
Sapur.015G269600.1	0.02563693	0.124897127	2.401790739	0.052002	0.958527415	NA	grey	0.016100629	0.84137019	GO:0004674;GO:0048544;GO:0006468;GO:0004672														
Sapur.002G073800.1	0.025237856	0.124897581	2.406634944	0.05194	0.958762233	NA	grey	0.011358846	0.885459158	GO:0005515														
Sapur.013G031300.1	0.04123315	-0.096357881	1.854652278	-0.0519	0.958868692	NA	grey	-0.157446058	0.031831281															
Sapur.003G056000.1	0.024915059	0.124898371	2.409618847	0.051833	0.958861562	NA	grey	-0.137945807	1.55E-05	GO:0016021														
Sapur.013G045100.1	0.024847635	0.124899215	2.414959701	0.051719	0.958972474	NA	grey	-0.000542031	0.996461767															
Sapur.003G118200.1	0.043028559	0.131835726	2.559615558	-0.0515	0.958929559	NA	grey	-0.152854568	0.055993186															
Sapur.004G095100.1	0.037556136	0.096329168	1.872029923	-0.05147	0.958951339	NA	grey	-0.17264413	0.030581009															
Sapur.002G169300.1	0.023002285	0.124901837	2.431796073	0.051362	0.959307055	NA	grey	0.003104145	0.969249031	GO:0016887;GO:0005524;GO:0006508;GO:0004222														
Sapur.013G054400.2	0.022817264	0.124902491	2.434060567	0.051314	0.959375041	NA	grey	0.004934679	0.951913305	GO:0006952;GO:0005516														
Sapur.013G111100.1	0.022796335	0.124902225	2.434313794	0.051309	0.959379358	NA	grey	0.053843426	0.502238555	GO:0006351														
Sapur.005G201100.1	0.021833445	0.124903687	2.761107365	0.05113	0.959521744	NA	grey	0.058350427	0.465197325															
Sapur.018G068100.1	0.02263912	0.141176202	2.769679147	0.050972	0.959547796	NA	grey	0.062404035	0.437227887															
Sapur.005G098700.2	0.047616276	0.085360131	1.679889519	0.05081	0.959675771	NA	grey	-0.275428138	0.00048067															
Sapur.017G091000.1	-0.045847924	0.085362162	1.684003614	0.050689	0.959757207	NA	grey	0.005059325	0.941037383															
Sapur.010G057700.2	0.04291912	0.08356667	1.691149285	0.050419	0.959788603	NA	grey	-0.019579323	0.807773763	GO:0005524;GO:0003676														
Sapur.005G073800.1	0.042727174	0.085364885	1.693790585	0.05042	0.959788603	NA	grey	-0.010438939	0.696163663	GO:0016747;GO:0006355														
Sapur.009G069300.3	0.020632315	0.14417664	2.803735746	0.050353	0.959814051	NA	grey	0.050464178	0.732225678															
Sapur.003G035200.1	0.020379778	0.131818547	2.619205764	0.05033	0.959861927	NA	grey	0.014184317	0.85835266															
Sapur.002G185500.1	0.04023138	0.085371093	1.702238515	0.050152	0.960001063	NA	grey	-0.029487876	0.713902296															
Sapur.003G028800.2	0.033686794	-0.13181513	2.648903123	-0.04976	0.960312566	NA	grey	-0.166818108	0.036672732	GO:0006412;GO:0005840;GO:0005622;GO:0003735														
Sapur.012G013300.1	0.031990805	-0.13181426	2.656669649	-0.04961	0.960423132	NA	grey	-0.146706999	0.066731618	GO:0003677														
Sapur.003G056900.1	0.016442047	0.193809505	2.818363243	0.049658	0.960431311	NA	grey	-0.15687171	0.04983636	GO:0006813;GO:0003677														
Sapur.016G130400.1	0.017856165	0.141177288	2.85855516	0.049388	0.96261038	NA	grey	-0.033091189	0.680692857															
Sapur.005G088200.3	0.003737646	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.101365629	0.206112105	GO:0008270;GO:0005515														
Sapur.019G082700.1	0.004457724	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.007925742	0.723413412	GO:0005515;GO:0071165 (NR-LBD class) family														
Sapur.018G070900.2	0.004127884	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.007802716	0.22299776	GO:0006950;GO:0005516														
Sapur.010G068300.1	0.00458316	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.007122661	0.226247527															
Sapur.006G115600.1	0.004787167	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.096560092	0.228931984															
Sapur.005G151400.1	0.00511874	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.005494984	0.234161897	GO:0007165;GO:0005515														
Sapur.002G039700.1	0.005378265	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.094760815	0.227752046															
Sapur.009G241800.1	0.00534176	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.094638378	0.238898744															
Sapur.006G165600.1	0.005469516	0.183840881	2.904822821	0.049361	0.96263849	NA	grey	0.094171238	0.240962213	GO:0005515;GO:0003677														
Sapur.017G087200.1	0.017043087	0.141177483	2.876649166	0.049077	0.96285817	NA	grey	0.039132809	0.426830982															
Sapur.003G012600.1	0.015861461	0.101484751	2.076867743	0.048864	0.96327415	NA	grey	-0.025227003	0.753746206	GO:0003700														
Sapur.009G097800.1	0.024971306	0.117835174	2.411629436	0.048861	0.96329888	NA	grey	-0.000760194	0.992996356	GO:0003677;GO:0008289														
Sapur.016G051300.1	0.015982504	0.141177766	2.901846015	0.048857	0.96334716	NA	grey	0.009001276	0.626765012	GO:0006355;GO:0003700														
Sapur.015G072100.5	0.01255014	0.141177777	2.904821749	0.048601	0.96123726	NA	grey	0.029451518	0.71421628															
Sapur.005G160000.2	0.014413667	0.141177776	2.904821749	0.048601	0.96123726	NA	grey	-0.029864704	0.710582827	GO:0006468;GO:0005524;GO:0004672														
Sapur.15W0G129000.3	0.015016602	0.141177776	2.904821749	0.048601	0.96123726	NA	grey	-0.023125408	0.791784476	GO:0006412;GO:0005840;GO:0005622;GO:0003735;GO:0015935														
Sapur.014G078200.1	0.015220944	0.141177776	2.904821749	0.048601	0.96123726	NA	grey	0.011330206	0.89020806															
Sapur.7.1G1700.1	0.015701194	0.141177776	2.904821749	0.048601	0.96123726	NA	grey	0.015208065	0.493804004															
Sapur.006G150300.3	0.049263339	0.098182512	2.015368081	0.048456	0.96127608	NA	grey	-0.006740296	0.238074865	GO:0016746;GO:0008152														
Sapur.014G028200.1	0.04539573	-0.081489512	1.685399179	-0.04835	0.961437085	NA	grey	-0.15180604	0.059298458															
Sapur.004G082400.1	0.045231948	-0.08183948	1.685896014	-0.04834	0.961484959	NA	grey	-0.12626702	0.139395454															
Sapur.016G193300.1	0.042333033	-0.081488737	1.695075656	-0.04807	0.961657421	NA	grey	-0.167592673	0.031899956	GO:0005515														
Sapur.005G173700.2	0.03853004	0.12492582	2.605932025	0.047939	0.961767151	NA	grey	0.0439047	0.185071713															
Sapur.004G177300.1	0.018323138	0.124926825	2.614961189	0.047774	0.961884486	NA	grey	0.475723826	3.04E-10	GO:0003993														
Sapur.009G027900.2	0.03696786	-0.081487236	1.714167367	-0.04754	0.962068839	NA	grey	-0.157585874	0.048318866	GO:0006883														
Sapur.003G154300.2	0.031943025	0.124931403	2.652664429	0.047697	0.962432277	NA	grey	0.019919047	0.836377088	GO:0044237														
Sapur.013G190100.1	0.031708192	0.124931687	2.655133994	0.047053	0.962470945	NA	grey	-0.035951709	0.654861767															
Sapur.003G068500.1	0.018817752	0.124932783	2.664652818	0.046885	0.962604727	NA	grey	0.045830192	1.58E-09	GO:0016813;GO:0019001;GO:0007186;GO:0004871;GO:0003924														
Sapur.002G037000.1	0.03813933	0.096298465	2.055469209	-0.04685	0.962632519	NA	grey	-0.152167706	0.057138693															
Sapur.013G107000.1	0.029800139	0.124934066	2.679595041	0.046688	0.962762169	NA	grey	0.442937788	6.28E-09															
Sapur.004G016800.1	0.046931886	0.085426281	1.829878717	0.046687	0.962764344	NA	grey	-0.012436651	0.889289026															
Sapur.001G045400.4	0.047623926	0.085428173	1.831235808	0.046549	0.962872573	NA	grey	0.11329228	0.157727133	GO:0008270														
Sapur.005G180100.1	0.038950943	0.124935149	2.685425038	0.046652	0.962895632	NA	grey	-0.114790065	0.152523211	GO:0004881														
Sapur.013G049100.1	0.028808635	0.124935356	2.687478964	0.046488	0.962921348	NA	grey	-0.006613362	0.993916994															
Sapur.007G153600.1	0.027553069	0.124937039	2.702777254	0.046211	0.963135574	NA	grey	0.268705365	0.00066271															
Sapur.017G107000.2	0.046234428	0.085435065	1.853458358	0.046029	0.963327091	NA	grey	-0.007157574	0.928920041	GO:0019898;GO:0015979;GO:0009654;GO:0009523;GO:0005509														
Sapur.006G177700.2	0.026361147	0.124938669	2.718189946	0.045903	0.963339213	NA	grey	0.252436152	0.000429586															
Sapur.002G061000.1	0.046845077	0.085437673	1.860683604	0.045917	0.963376173	NA	grey	-0.027910319	0.728600108	GO:0008152;GO:0008324														
Sapur.015G158700.1	0.025178875	0.124945425	2.73423917	0.045477	0.963727032	NA	grey	0.006682551	0.919398383															
Sapur.001G176700.1	0.040771976	0.103693423	2.28012425	0.045477	0.963727033	NA	grey	-0.036241631	0.651365552															
Sapur.001G087100.2	0.039343836	0.085445429	1.882313367	0.045394	0.963793148	NA	grey	-0.008108589	0.919717101															
Sapur.003G051000.1	0.023726226	-0.131790456	2.904822495	-0.04537	0.963827784	NA	grey	-0.120076216	0.111284807	GO:0006468														
Sapur.014G093400.1	0.030688808	0.131790456	2.904822495	-0.04537	0.963827784	NA	grey	0.020252943	0.80122149	GO:0006351;GO:0005669														
Sapur.005G162500.1	0.023438097	0.124950819	2.708887274	0.045273	0.963882828	NA	grey	0.025283035	0.752393837	GO:0006468;GO:0005524;GO:0004672														
Sapur.010G025000.3	0.047636505	-0.060195499	1.552238146	-0.04465	0.963482482	NA	grey	-0.117523954	0.142678703	GO:0003677														
Sapur.003G052500.1	0.023950729	0.12866172	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0008270														
Sapur.008G039400.1	0.023370509	0.12866172	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.016G198100.1	0.023370509	0.12866172	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.010G053200.2	0.01776012	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.017G070800.2	0.01776012	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.017G070800.1	0.01776012	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	-0.28860864	0.000311561															
Sapur.018G189200.2	0.01776012	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.018G189200.1	0.01776012	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.08830011	0.27102758															
Sapur.008G144100.1	0.017279309	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0006468;GO:0005524;GO:0004672														
Sapur.006G162700.1	0.01602745	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.013G050200.1	0.011245118	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0005515;GO:0016020														
Sapur.018G081000.1	0.011245118	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.079737864	0.225024093	GO:0006614;GO:0005525;GO:0008886;GO:0005785;GO:0005047;GO:0003924														
Sapur.016G113200.6	0.011245118	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.060157182	0.434518716															
Sapur.010G075800.1	0.010088279	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0045454;GO:0005105;GO:0090055;GO:0035556														
Sapur.013G039700.3	0.010088279	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	-0.23382766	0.000303779															
Sapur.7.0S9600.1	0.010088279	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0016020;GO:0005515														
Sapur.005G112900.7	0.009040412	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0005515														
Sapur.004G162700.1	0.009040412	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.007G064900.2	0.009160513	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	NA	NA	GO:0009378;GO:0006310;GO:0006281														
Sapur.013G049900.2	0.009160513	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0006468;GO:0005524;GO:0004672														
Sapur.017G065900.2	0.009160513	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0005511;GO:0005622;GO:0004843														
Sapur.008G234400.7	0.00863243	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.202521249	0.010967844															
Sapur.009G086600.2	0.008284818	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0008152;GO:0008324														
Sapur.016G007200.1	0.008284818	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0006470;GO:0017068;GO:0000398														
Sapur.7.1G6600.1	0.008284818	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.003G073800.1	0.008166449	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	-0.00840004	0.896025587															
Sapur.7.0B8800.1	0.008106149	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0043531														
Sapur.004G081300.1	0.00778933	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.004G081400.1	0.00778933	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.005G171400.2	0.00778933	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.325665503	1.15E-05															
Sapur.005G171400.1	0.00778933	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.017G071200.1	0.00778933	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0005515;GO:0043531														
Sapur.016G194200.2	0.00774334	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0016020;GO:0016021;GO:0016020														
Sapur.016G091500.1	0.007343142	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0006556;GO:0004378;GO:0005524														
Sapur.009G133600.1	0.006855972	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	-0.172264366	0.010283691	Peptidase M20/M40 family protein														
Sapur.002G127700.1	0.007690457	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	-0.055925451	0.460275969	GO:0016787														
Sapur.016G188900.3	0.007690457	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0003824														
Sapur.012G041600.1	0.007690457	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	-0.066065665	0.488522313	GO:0006396;GO:0003723														
Sapur.013G030300.2	0.007690457	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	-0.143162193	0.073661864															
Sapur.016G212900.1	0.007690457	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.017G087000.6	0.007690457	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.015W0G111400.2	0.007690457	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0016020;GO:0015031;GO:0070130														
Sapur.003G171300.3	0.007611915	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	-0.002154878	0.250487746															
Sapur.005G137800.1	0.007611915	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.012G102300.3	0.007611915	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0016491;GO:0008152														
Sapur.017G305000.1	0.007611915	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487	GO:0004222														
Sapur.003G090800.1	0.00749087	0.12866179	2.904822376	0.044962	0.964261295	NA	grey	0.078548531	0.32814487															
Sapur.7.0B4800.1	0.00749087	0.12866179	2.

Sapur.003G024900.2	0.00512044	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.014604671	0.855941117	GO:0006468;GO:0006672			ATSG13680.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
Sapur.007G064900.5	0.00508565	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0009378;GO:0006310;GO:0006281			ATSG50140.2		F-box containing nucleotide triphosphate hydrolases superfamily protein
Sapur.010G171800.1	0.00508565	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	NA	NA	GO:0005515;GO:0003723			ATSG39260.1		binding RNA binding
Sapur.011G084900.1	0.00506695	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG12560.1	CPR30	F-box and associated interaction domain-containing protein
Sapur.004G057400.1	0.00497463	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.135652295	0.316858013	GO:0003676			ATSG41382.2	SUA	suppressor of abi3-5
Sapur.003G151600.3	0.00489475	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG13500.1		suppressor of abi3-5
Sapur.010G020500.1	0.00489475	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.164753864	0.039211613				ATSG26115.1		root determined nodulation protein
Sapur.010G025500.1	0.00489475	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871			ATSG16060.1		pyridoxal-5'-phosphate-dependent enzyme family protein
Sapur.010G057600.1	0.00489475	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0008017;GO:0007018			ATSG16060.1		ATP-binding microtubule motor family protein
Sapur.T036900.2	0.00489475	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0008270			ATSG51390.1		kinesin motor protein
Sapur.002G160500.2	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497		ATSLKR4		ATSG42630.1		DHHC-type zinc finger family protein
Sapur.006G045500.1	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP93D1		ATSG06900.1		Myb-like DNA-binding domain, shaqkyf class protein
Sapur.006G062300.2	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055085;GO:0046873;GO:0030001;GO:0016020			ATSG04355.1		cytochrome P450 family 93, subfamily D, polypeptide 1
Sapur.013G135100.1	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG73165.1	CLE1	Magnesium transporter CorA-like family protein
Sapur.014G031900.3	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016746;GO:0008152			ATSG40950.1		CLAVATA/ESR-RELATED 1
Sapur.016G006200.1	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.092128567	0.251139766				ATSG61380.1		Phosphoglycolate phosphatase family protein
Sapur.016G229800.1	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0003677;GO:0009725;GO:0006355;GO:0005634			ATSG37020.1		Heavy metal transport/detoxification superfamily protein
Sapur.018G079500.3	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497		ARF8,ATARF8		ATSG37030.1		auxin response factor 8
Sapur.I18G029600.1	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG60710.1		Family of unknown function (DUF566)
Sapur.I15G029600.1	0.00485832	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG42760.1		DNAse I-like superfamily protein
Sapur.005G193500.1	0.00481954	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.112024669	0.159109489	GO:0005524;GO:0003676			ATSG41630.1		DEAD/H(D/H) box RNA helicase family protein
Sapur.007G009400.4	0.00481954	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0003723			ATSG64390.3	HEN4	RNA-binding KH domain-containing protein
Sapur.011G009400.1	0.00481954	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG51020.1	NGA4	AP2/B3-like transcriptional factor family protein
Sapur.012G016700.2	0.00481954	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0003824;GO:0006470;GO:0004722			ATSG07430.1	HA12	highly ABA-induced PP2C gene 2
Sapur.T075300.2	0.00481954	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.10445495	0.102944028	GO:0005525			ATSG07520.1	ARA4,RAB5A	RAB GTPase homolog A5A
Sapur.008G033600.2	0.00476894	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG03950.1		Tudor/PWWP/MBT superfamily protein
Sapur.008G070900.1	0.00476894	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.42576945	1.16E-07	GO:0015934;GO:0006412;GO:0007735			ATSG42740.1		Ribosomal L22p protein family
Sapur.012G014900.1	0.00476894	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0003677			ATSG21510.1	VAL3	VP1/ABI3-like 3
Sapur.016G001100.3	0.00476894	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.41884972	4.76E-08				ATSG47800.1		Phototropic-responsive NPH3 family protein
Sapur.018G079400.2	0.00476894	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.027729874	0.73471433				ATSG37730.1		Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region
Sapur.T037600.1	0.00476894	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG42780.1		DNAse I-like superfamily protein
Sapur.005G198800.2	0.00472948	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG38690.1		DEAD/H(D/H) box RNA helicase family protein
Sapur.005G003600.2	0.00472948	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016787			ATSG47650.1	ATNUDT2,ATNUDX2,NUDT2	nudix hydrolase homolog 2
Sapur.006G213800.2	0.00472948	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.02021708	0.80441242				ATSG52570.1		transmembrane protein, putative
Sapur.018G105200.2	0.00472948	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0005975;GO:0004553			ATSG36600.1		Glycosyl hydrolase superfamily protein
Sapur.I03G029100.2	0.00472606	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016887;GO:0005524;GO:0016820			ATSG15520.1	ABCG40,ATABCG40,ATPDR1	pleiotropic drug resistance 1
Sapur.010G096600.1	0.00472606	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0006412;GO:0005840;GO:0003735			ATSG07730.2	RPS15A	ribosomal protein S15A
Sapur.I03G130800.2	0.00472606	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.513078	5.90E-12		SSP5		ATSG11660.4		CTD-small phosphatase-like 5
Sapur.005G119000.1	0.00472606	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.010G138900.1	0.00472606	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.109213858	0.173249118				ATSG43810.2		Small nuclear ribonucleoprotein family protein
Sapur.011G123400.3	0.00472606	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.060557179	0.949931843	GO:0055085;GO:0016021	atcax2,CAX2		ATSG13120.1		cation exchanger 2
Sapur.014G008300.3	0.00472606	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG27750.1		nucleic acid binding
Sapur.016G084800.2	0.00472606	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG60960.3		transmembrane protein
Sapur.002G079300.1	0.00462797	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0019211			ATSG08960.1		phosphotyrosyl phosphatase activator (PTPA) family protein
Sapur.004G046100.2	0.00462797	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055114;GO:0016702			ATSG42670.1		Protein of unknown function (DUF1637)
Sapur.005G190500.4	0.00462797	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0004527;GO:0003676			ATSG75660.1	AtXRN3,XRN3	5'-3' exoribonuclease 3
Sapur.I03G188800.1	0.00462797	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.011G107600.11	0.00462797	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055085;GO:0016021			ATSG20925.1		Auxin efflux carrier family protein
Sapur.016G143000.2	0.00462797	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016787;GO:0005524;GO:0003677	CHR5		ATSG13370.1		chromatin remodeling 5
Sapur.018G038500.1	0.00462797	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG26060.1		Ribosomal protein L18ae family
Sapur.I59W0G018000.1	0.00462797	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055115;GO:0006468;GO:0005524;GO:0004672			ATSG47570.1		Leucine-rich repeat protein kinase family protein
Sapur.005G142300.1	0.00453802	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0046872;GO:0016567;GO:0008842			ATSG48230.1		RING/U-box superfamily protein
Sapur.010G101200.4	0.00453609	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.098808315	0.215642886		CHUP1		ATSG56980.1	CHUP1	Hydroxyproline-rich glycoprotein family protein
Sapur.I01G127300.1	0.00453609	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.067314055	0.22609677				ATSG14020.1		O-fucosyltransferase family protein
Sapur.010G012300.1	0.00453609	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.105776418	0.187341145				ATSG24600.1	HT1	Protein kinase superfamily protein
Sapur.I14G084300.2	0.00453609	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG45270.1	GCP1	Peptidase family M48 family protein
Sapur.014G057200.1	0.00453609	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055085;GO:0016021			ATSG22990.2		Major facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein
Sapur.014G059700.1	0.00453609	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016021	ATSUSE,ATSK31,COP11,CSN		ATSG61461.1		26S proteasome, regulatory subunit Rpn7/Proteasome component (PC) domain
Sapur.016G146300.2	0.00453609	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0005515			ATSG12430.1		Heat shock protein Dnaj with tetratricopeptide repeat
Sapur.T085700.1	0.00453809	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055114;GO:0016491			ATSG35190.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.003G017700.2	0.00448302	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG34705.1		hypothetical protein
Sapur.002G047700.2	0.00448302	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.081608864	0.309369942	GO:0003676			ATSG29400.1	AMI1,MLS	MEI2-like protein 5
Sapur.004G082700.3	0.00448302	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG38660.1	AHK14	acclimation of photosynthesis to environment
Sapur.005G068300.2	0.00448302	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG08930.1		Nucleotide-sugar transporter family protein
Sapur.005G071100.2	0.00448302	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.217658685	0.0061645		SDE3		ATSG54610.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.014G137000.5	0.00448302	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055085;GO:0016021			ATSG48020.1		Major facilitator superfamily protein
Sapur.016G113600.2	0.00448302	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG03970.1		
Sapur.I01G121100.2	0.00440041	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016021			ATSG12400.1	TOM20A	tobamovirus multiplication 2A
Sapur.I03G027400.1	0.00440041	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.058773038	0.46464389				ATSG48120.1		ARM repeat superfamily protein
Sapur.008G172000.2	0.00440041	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG21530.1		DNAse I-like superfamily protein
Sapur.014G037500.1	0.00440041	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG02602.4		ELMO/CED-12 domain protein
Sapur.I16G309000.1	0.00440041	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0005515			ATSG61881.1	ARP8,ATARP8	actin-related protein 8
Sapur.005G135600.1	0.00432069	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.007G082300.2	0.00432069	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055114;GO:0016627;GO:0006635;GO:0005777;GO:0003997			ATSG51130.1	ACX2,ATACX2	acyl-CoA oxidase 2
Sapur.I01G156900.4	0.00431588	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG25360.1		
Sapur.I03G029500.1	0.00431588	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG02820.1		kinase interacting (KIP1-like) family protein
Sapur.008G033200.2	0.00431588	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.066609812	0.407177922				ATSG63220.1		
Sapur.008G136400.3	0.00431588	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.398809971	2.44E-07	GO:0006468;GO:0005524;GO:0004672			ATSG41461.1	CKI1,CKL11	casein kinase I
Sapur.009G064500.1	0.00431588	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG36980.1		hypothetical protein
Sapur.010G088800.1	0.00431588	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016020			ATSG25320.1		transmembrane protein PFT27
Sapur.I16G067800.4	0.00431588	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG11620.3		alpha/beta-Hydrolase superfamily protein
Sapur.007G095800.1	0.00427246	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						transmembrane protein, putative
Sapur.007G177800.1	0.00427246	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0006468;GO:0004672			ATSG43850.1		integrin-linked protein kinase family
Sapur.T007500.1	0.00427246	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.316999147	5.23E-05	GO:0006468;GO:0004672			ATSG03770.2		Leucine-rich repeat protein kinase family protein
Sapur.T057200.1	0.00427246	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG28455.1	CLE25	CLAVATA/ESR-RELATED 25
Sapur.002G105800.3	0.00427132	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055085;GO:0016020;GO:0006810;GO:0005215	PDI-LSH		ATSG26510.1		Xanthine/uracil permease family protein
Sapur.006G175200.1	0.00427132	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0009084;GO:0004664	AOT2		ATSG07620.1		arogenate/prephenate dehydratase
Sapur.009G096600.1	0.00427132	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG28310.1		Protein of unknown function (DUF707)
Sapur.017G038900.11	0.00427132	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG04630.2		
Sapur.010G050100.1	0.00412536	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG33490.1		hydroxyproline-rich glycoprotein family protein
Sapur.005G132400.1	0.00412536	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.006G002100.4	0.00412536	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.293720023	0.000188772				ATSG47800.1		Phototropic-responsive NPH3 family protein
Sapur.010G071000.1	0.00412536	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.011G081800.1	0.00412536	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.228202182	0.050496164				ATSG02670.1		transducin family protein / WD-40 repeat family protein
Sapur.016G163700.3	0.00412536	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG07120.1		
Sapur.I01G088600.1	0.00412536	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.001G172500.1	0.00408228	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0043565;GO:0006355;GO:0003700			ATSG68150.1	ATWRKY9,WRKY9	WRKY DNA-binding protein 9
Sapur.I03G029000.1	0.00408228	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG50680.1		RING/U-box superfamily protein
Sapur.I05G103000.4	0.00408228	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0005515;GO:0042393;GO:0006355			ATSG42790.1	AL3	alfin-like 3
Sapur.I05G156000.2	0.00408228	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.074578889	0.352635583						hypothetical protein
Sapur.I01G111200.2	0.00408228	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055114;GO:0016491			ATSG10580.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.I01G189100.2	0.00408228	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0006508;GO:0004185			ATSG35480.1	scp18	serine carboxypeptidase-like 18
Sapur.I05G107000.1	0.00388351	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.370884016	1.75E-06				ATSG28855.1		Plectorin homology (PH) domain-containing protein
Sapur.I01G014000.2	0.00388351	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.122930137	0.125077716				ATSG54930.1		AT hook motif-containing protein
Sapur.I01G026800.2	0.00388351	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.015158377	0.866161576				ATSG76060.1		transducin/WD40 domain protein
Sapur.I01G181000.2	0.00385605	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG06376.1		topoisomerase II-associated protein PAT1
Sapur.I09G094900.2	0.00385605	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.154917165	0.052645954	GO:0006396;GO:0003723;GO:0003676			ATSG21120.1		etoposide-induced protein
Sapur.I01G100800.1	0.00385605	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016020;GO:0015179;GO:0003333			AATL,CAT1		SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein
Sapur.I03G070700.2	0.00379737	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.137376618	0.112745158	GO:0005525	EIF2-GAMMA		ATSG04170.1		splicing factor like protein
Sapur.I05G060400.2	0.00379737	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0055114;GO:0016627;GO:0006635;GO:0005777;GO:0003997;GO:0003995	ACX2,ATACX2		ATSG51130.1		cationic amino acid transporter
Sapur.I06G079400.2	0.00379737	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497		ATPUMP1,ATUCP1,PUMP1		ATSG54110.1		eukaryotic translation initiation factor 2 gamma subunit
Sapur.I06G079500.2	0.00379737	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.160993926	0.016618431				ATSG28130.1		acyl-coenzyme A oxidase, peroxisomal protein
Sapur.I07G102100.3	0.00379737	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0007275;GO:0006511;GO:0005634			ATSG37930.1		uncoupling protein
Sapur.I01G160600.9	0.00379149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG26160.1		lactoylglutathione lyase / glyoxalase I family protein / glyoxalase I family protein
Sapur.I01G021200.3	0.00379149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG37930.1		Protein with RING/U-box and TRAF-like domains
Sapur.I01G156900.9	0.00379149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG26362.1		
Sapur.I06G059000.7	0.00379149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG28430.1		
Sapur.I09G094300.2	0.00379149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.007G035500.2	0.00378149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0043531			ATSG60900.1		Disease resistance protein (CC-NBS-LRR class) family
Sapur.I08G167000.1	0.00378149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497		ATFRF1,FRF1		ATSG24860.1		flowering promoting factor 1
Sapur.I09G086600.1	0.00378149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0008152;GO:0003824	LACS2,LIR2		ATSG49430.1		long-chain acyl-CoA synthetase 2
Sapur.I09G118200.1	0.00378149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0004693;GO:0004501;GO:0015986	DLO3		ATSG45570.1		Homodomain-like superfamily protein
Sapur.I14G062100.2	0.00378149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0016787			ATSG05590.1		N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein
Sapur.I02G064000.10	0.00378149	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.022169863	0.782954049	GO:0006355;GO:0003677			ATSG59440.3	BLH1,EDA29	BELL-like homeodomain 1
Sapur.I03G088900.2	0.00377543	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0005975			ATSG22281.1		Aldolase superfamily protein
Sapur.005G172900.1	0.00377543	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0046983			ATSG02590.1	UNE12	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.I09G097700.2	0.00377543	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG46660.3		SnrG domain-containing protein
Sapur.I03G157800.2	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0008270;GO:0003677			ATSG11200.3		A20/AN1-like zinc finger family protein
Sapur.I03G161200.1	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0007275;GO:0005515;GO:0005634			ATSG40461.1	SINAT2	seven in absentia 2
Sapur.006G073200.1	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497				ATSG53820.1		C2H2 and C2HC zinc fingers superfamily protein
Sapur.I03G050400.3	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.318188181	4.83E-05	GO:0016787;GO:0008152			ATSG47420.1		2n-dependent exopeptidases superfamily protein
Sapur.012G051100.1	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497	GO:0003677	VAL3		ATSG21510.1	VAL3	VP1/ABI3-like 3
Sapur.I08G037900.1	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497		AT-GT1,LAT-GT1,2,GT1,1		ATSG32440.1	AT-GT1,LAT-GT1,2,GT1,1	GT-2-like 1
Sapur.I08G180200.2	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	-0.074162687	0.276022595	GO:0005515	TPRA,WSXF2		ATSG16880.1	TPRA,WSXF2	WUS-interacting protein 2
Sapur.T027000.1	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.T172700.1	0.00334244	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.078548531	0.32814497						
Sapur.I01G176400.1	0.00317642	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.159126233	0.046531024	GO:0003677					B3 DNA-binding domain protein
Sapur.I02G060100.1	0.00317642	0.12866759	2.984823276	0.044292	0.964675295	NA	grey	0.114604104	0.146542111				ATSG14920.1		Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type

Sapur.01G0237050.1	0.014953944	0.126809129	2.904822183	0.043655	0.965179652	NA	grey	grey	0.013672237	0.865038423					NA
Sapur.003G022700.1	0.016898657	0.126809129	2.904822183	0.043655	0.965179652	NA	grey	grey	0.03954271	0.622932281		ATSG13845.1			transmembrane protein, putative
Sapur.01G0201100.1	0.009993223	0.126809129	2.904822183	0.043655	0.965179652	NA	grey	grey	0.014352997	0.854396584					NA
Sapur.008G002700.1	0.037153883	0.081476416	1.876667748	-0.04342	0.965330344	NA	grey	grey	-0.151572313	0.05817033	GO:0008270	ATSG50448.1		RING/FYVE/PHD zinc finger superfamily protein	zinc finger protein
Sapur.009G046100.1	0.048651268	0.087341853	2.012895526	0.043391	0.965389697	NA	grey	grey	0.017846236	0.82794138	GO:0055114,GO:0050660,GO:0017170,GO:0008033	ATSG63510.1		FMN-linked oxidoreductases superfamily protein	RNA-dihydrouridine synthase
Sapur.001G063000.1	0.040707818	0.061769801	1.432432798	0.043108	0.96561517	NA	grey	grey	-0.028239407	0.72748583					NA
Sapur.016G134500.1	0.021706694	0.124956594	2.904821116	0.043017	0.965888009	NA	grey	grey	0.16264221	0.041837735	GO:0006511	ATSG29070.2		Ubiquitin fusion degradation UFD1 family protein	ubiquitin fusion degradation 1 protein
Sapur.010G005700.1	0.03418857	0.124956593	2.904821116	0.043017	0.965888009	NA	grey	grey	0.020737175	0.70247704		ATSG60660.1	PDE320,TGD4	pigment defective 320	plastid;TGD4-1 protein
Sapur.016G029900.2	0.023697327	0.103897557	2.425881639	0.042747	0.965903179	NA	grey	grey	-0.012767579	0.873901004	GO:0005634	ATSG06150.1	CYC3B4T,CYC3L2	Cyclin family protein	NA
Sapur.003G044500.1	0.043178243	0.087356391	2.04604714	0.042734	0.966047589	NA	grey	grey	0.000315175	0.956671589		ATSG18450.1	ARP4,ATARP4	actin-related protein 4	actin-related protein ARP4
Sapur.008G016000.5	0.046877812	0.087351304	2.047472023	0.042663	0.965970172	NA	grey	grey	-0.030047411	0.681156919		ATSG52870.1		IQ calmodulin-binding motif family protein	calmodulin-binding family protein, putative
Sapur.005G138800.1	0.018912466	0.087352581	2.052307603	0.042563	0.966049806	NA	grey	grey	-0.017458621	0.831859378	GO:0006468,GO:0005634,GO:0004672	ATSG28281.1	PRSK	PRS-like receptor kinase	NA
Sapur.017G009700.2	0.038563167	0.087356424	2.059304956	0.042419	0.966164385	NA	grey	grey	-0.069455532	0.187380382	GO:0003677	ATSG56170.2	ATHAP5B,HAP5B,NF-YC2	nuclear factor Y, subunit C2	histone-like transcription factor, putative
Sapur.003G004800.1	0.037968888	0.087356384	2.062869392	0.042368	0.966231192	NA	grey	grey	0.014393399	0.915931133	GO:0006355,GO:0003700	ATSG7450.1		Integrase (IN) DNA binding superfamily protein	ethylene-responsive transcription factor ERF021
Sapur.01G071400.1	0.037923715	0.087355456	2.063204279	0.042338	0.966238877	NA	grey	grey	0.45257586	2.67E-09		ATSG17110.2	UBP15	ubiquitin-specific protease 15	ubiquitin carboxyl-terminal hydrolase
Sapur.001G183900.1	0.023219817	0.117804273	2.782968024	0.042331	0.966358181	NA	grey	grey	-0.020291758	0.83848624					NA
Sapur.01G088100.2	0.021331556	0.103882216	2.452767896	0.042278	0.966277052	NA	grey	grey	0.354134848	5.36E-06	GO:0008270	ATSG01275.2		RING/FYVE/PHD zinc finger superfamily protein	NA
Sapur.01G025100.1	0.021125581	0.103882281	2.455563919	0.04223	0.966235456	NA	grey	grey	-0.030763809	0.702105621					membrane associated RING finger protein 1%2C8, putative
Sapur.004G029639	0.046229639	0.085409361	2.027764845	0.04216	0.966237955	NA	grey	grey	-0.101147677	0.207498785	GO:0008017,GO:0000910,GO:0000226	ATSG27920.1	MAPRS-8	microtubule-associated protein 65-8	microtubule-associated protein MAPRS-1a
Sapur.T166100.1	0.034007965	0.087360615	2.083437836	0.041931	0.96653171	NA	grey	grey	0.001834516	0.981906764					NA
Sapur.T166800.2	0.031312506	0.087360615	2.083437836	0.041931	0.96653171	NA	grey	grey	-0.025880819	0.747454425		ATSG76700.1		DNA/ heat shock N-terminal domain-containing protein	Dnaj heat shock amino-terminal domain protein
Sapur.01G051400.1	0.033097968	0.087362499	2.090960764	0.041781	0.96682726	NA	grey	grey	-0.029693102	0.709215666		AHL1,ATAHL1	AT-hook motif nuclear-localized protein 1	AT-hook motif nuclear-localized protein	DNA-binding family protein
Sapur.01G0230100.1	0.032767256	0.087362499	2.090960561	0.041719	0.966765472	NA	grey	grey	-0.131033633	2.22E-05	GO:0006351,GO:0003899,GO:0003677,GO:0032549	ATSG27362.2	DMD2,DRD2,NRPD2,NRPD2a	Nucleotide binding protein D2A	DNA-directed RNA polymerase
Sapur.01G0243500.5	0.033441174	0.087363546	2.095177975	0.041697	0.966739898	NA	grey	grey	-0.020277177	0.800988585	GO:0003676	ATSG33435.1		RNA-binding (RNA/RBD/RNP motifs) family protein	splicing factor U2AF large subunit, putative
Sapur.01G0260600.4	0.032318845	0.087364568	2.097088759	0.041675	0.966773156	NA	grey	grey	0.047568622	0.532664883	GO:0005515	ATSG36600.1		BTB/POZ domain-containing protein	BTB/POZ domain protein
Sapur.002G015100.2	0.031284023	0.087365438	2.102867026	0.041546	0.966880726	NA	grey	grey	-0.030683649	0.702845203	GO:0005525	ATSG05670.1		signal recognition particle binding	signal recognition particle receptor subunit beta
Sapur.01G089700.1	0.032161033	0.08736556	2.103368138	0.041536	0.966888857	NA	grey	grey	-0.031517865	0.695570104					NA
Sapur.01G0282200.1	0.017905938	0.103267272	2.904822379	0.041429	0.966954213	NA	grey	grey	0.053834516	0.506201367	GO:0006468,GO:0006672	ATSG11340.1		S-locus lectin protein kinase family protein	alks/lectin receptor kinase family
Sapur.01G4120100.1	0.012287309	0.103267272	2.904822379	0.041429	0.966954213	NA	grey	grey	-0.16375563	0.040431758		ATSG07310.1	ATB2	NADP(+)-linked oxidoreductase superfamily protein	NADH dehydrogenase
Sapur.005G084900.1	0.013387348	0.103267272	2.904822379	0.041429	0.966954213	NA	grey	grey	-0.132603237	0.097688654	GO:0055114,GO:0016491	ATSG07401.1	NDC1	NADP(H) dehydrogenase C1	NADH dehydrogenase
Sapur.01G0889100.1	0.03717825	0.085303005	2.070358635	0.041265	0.967068826	NA	grey	grey	-0.02266695	0.778383838	GO:0016747	ATSG36040.1		HXXXD-type acyl-transferase family protein	NA
Sapur.15WG054700.1	0.035968631	0.084389974	2.11173161	-0.04083	0.967424267	NA	grey	grey	-0.179856629	0.024236173		ATSG21280.1			NA
Sapur.008G104300.1	0.015437893	0.087362499	2.084923513	0.040669	0.967560075	NA	grey	grey	-0.027610305	0.785670045	GO:0005634,GO:0006355,GO:0003700,GO:0003677	ATHB-17,ATHB17,HB17	homeobox-leucine zipper protein 17	homeobox-leucine zipper protein	homeobox leucine zipper protein
Sapur.01G0320300.1	0.016466044	-0.09482627	2.35506679	-0.04006	0.968184018	NA	grey	grey	-0.018423964	0.020903945		ATSG57661.2	GDSL	GDSL-like Lipase/Acylhydrolase superfamily protein	NA
Sapur.15WG064900.2	0.030003853	0.084382477	2.35475231	-0.04005	0.968185356	NA	grey	grey	-0.018203369	0.020921932		ATSG60880.1	BASL	breaking of asymmetry in the stomatal lineage protein	breaking of asymmetry in the stomatal lineage protein, putative
Sapur.01G037000.5	0.030288203	0.084382477	2.35685251	-0.04003	0.968188122	NA	grey	grey	-0.491464869	5.6E-11		ATSG27130.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase N-acetylstarfeasterase	heparan-alpha-glucosamine N-acetyltransferase
Sapur.006G070000.3	0.029583071	-0.09481491	2.362857014	-0.03994	0.968137946	NA	grey	grey	-0.184216687	0.020911101	GO:0010338,GO:0006355,GO:0005634	ATSG37630.1	AS1,ATMYB81,ATMYAH,MYH	myb-like HTH transcriptional regulator family protein	MYB-related transcription factor, putative
Sapur.017G027300.1	0.029577535	-0.09481497	2.362906762	-0.03994	0.968138619	NA	grey	grey	-0.183910519	0.021128504		ATSG42760.1		DNAse I-like superfamily protein	DNA/RNA
Sapur.15WG051100.2	0.047517629	0.061769801	1.510694386	0.03983	0.968238735	NA	grey	grey	-0.113622091	0.156499175	GO:0016773,GO:0016020,GO:0005524	ATSG44630.1		Calcium-dependent protein kinase (CDPK) family protein	calcium/calmodulin-dependent kinase, putative
Sapur.15WG065000.3	0.028502148	-0.09479854	2.37279208	-0.03978	0.968278019	NA	grey	grey	-0.500871203	2.38E-11		ATSG08910.4		18S pre-ribosomal assembly protein gar2-related	hypothetical protein
Sapur.01G2360600.1	0.037950323	0.080406393	2.065735425	0.03804	0.968892994	NA	grey	grey	-0.134033218	0.004220662		ATSG13677.2			hypothetical protein
Sapur.008G084800.2	0.029060825	0.103702783	2.684498851	0.03863	0.969182519	NA	grey	grey	0.00715064	0.929177336	GO:0005515	ATSG49430.1		WD40/YVTN repeat-like-containing domain;Bromodomain	cytochrome c1l-nitrite reductase-like, carbox-terminal heme protein d1, putative
Sapur.01G0261200.1	0.029048872	0.087404206	2.18672851	0.03826	0.969403688	NA	grey	grey	0.000880658	0.932042274		ATSG48880.2		RNA-binding	NA
Sapur.01G1004100.1	0.043073569	-0.098059658	2.56357149	-0.03825	0.969487409	NA	grey	grey	-0.35472476	5.16E-05	GO:0016021,GO:0004659	ATSG51820.1	ATGALCHLG,G4	Ulsk prenylcysteine family protein	bacteriorhodopsin synthase, putative
Sapur.008G008300.1	0.028808037	0.087408824	2.338062244	0.03791	0.969704666	NA	grey	grey	0.021338203	0.782680005	GO:0016788	ATSG47963.3		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.01G0580900.1	0.036354754	0.08760949	2.311751006	0.03782	0.969837948	NA	grey	grey	-0.01871889	0.815998713	GO:0005524,GO:0003676	ATSG42520.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.01G0280300.3	0.028582057	0.087409134	2.315278037	0.03775	0.969884122	NA	grey	grey	-0.007837432	0.92283557	GO:0008080	ATSG15730.1	AtGNA1,GNA1	glucose-6-phosphate acetyltransferase 1	glucosamine-6-phosphate N-acetyltransferase
Sapur.01G0231500.1	0.031211606	-0.07924793	2.103227246	-0.03768	0.969943454	NA	grey	grey	-0.178928389	0.026642979					transmembrane protein, putative
Sapur.01G1411400.3	0.034505972	0.087412498	2.32849941	0.03754	0.970054232	NA	grey	grey	-0.036967673	0.645790012	GO:0006468,GO:0006672	ATSG70530.1	CRK3	cysteine-rich RLK (RECEPTOR-like protein kinase) 3	cysteine-rich receptor-like kinase
Sapur.007G028000.1	0.037591723	0.063886288	1.71751794	0.03764	0.970094885	NA	grey	grey	-0.052501895	0.513296027					NA
Sapur.01G1134000.1	0.033677955	0.087727976	2.344233476	0.037329	0.970302583	NA	grey	grey	-0.026883085	0.73821902	GO:0006474,GO:0048544,GO:0006468,GO:0004672	ATSG21880.1	ARK2,RK3	receptor kinase 3	Serine/Threonine-kinase
Sapur.008G110200.2	0.030507214	0.10816284	2.904821918	0.037223	0.970307026	NA	grey	grey	-0.232532276	0.033379016		ATSG47861.1		MAC/Perforin domain-containing protein	MAC/perforin domain protein
Sapur.009G049400.1	0.030105719	0.10816284	2.904821918	0.037223	0.970307026	NA	grey	grey	-0.029717439	0.225762616	GO:0006629,GO:0003824	ATSG19440.1		NADP(+)-binding Rossmann-fold superfamily protein	cinnamyl alcohol dehydrogenase-like family protein
Sapur.009G105100.1	0.030105719	0.10816284	2.904821918	0.037223	0.970307026	NA	grey	grey	-0.045123157	0.573031046		ATSG38570.1		Pathogenesis-related thaumatin superfamily protein	thaumatin and allergens;antifungal thaumatin-like; plant-like protein
Sapur.01G2170000.2	0.030105719	0.10816284	2.904821918	0.037223	0.970307026	NA	grey	grey	-0.194013513	0.016469407		ATSG50180.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.01G0820100.1	0.030105719	0.10816284	2.904821918	0.037223	0.970307026	NA	grey	grey	0.111410236	0.164728867	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATSG25780.1		Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.15WG100200.1	0.030105719	0.10816284	2.904821918	0.037223	0.970307026	NA	grey	grey	-0.267892624	0.000693522	GO:0016866	ATSG26670.2	TAR2	tryptophan aminotransferase related 2	tryptophan aminotransferase
Sapur.01G0210400.4	0.031014581	0.087416763	2.352982576	0.037151	0.970394232	NA	grey	grey	-0.02239777	0.786678045	GO:0055114,GO:0020037,GO:0006979,GO:0004601	APX6	ascorbate peroxidase 6	ascorbate peroxidase 6	L-ascorbate peroxidase, putative
Sapur.009G151300.1	0.030769391	0.087417084	2.354861656	0.037122	0.970397704	NA	grey	grey	-0.075649747	0.925084167	GO:0006397,GO:0003729	ATSG21645.1		RNA binding (RRM/RBD/RNP motifs) family protein	polyadenylate-binding protein 2-A
Sapur.01G0410400.4	0.030635701	0.087417317	2.356239158	0.037101	0.970404574	NA	grey	grey	-0.021325581	0.791600199	GO:0016021,GO:0004659	ATSG51820.1	ATGALCHLG,G4	Ulsk prenylcysteine family protein	bacteriorhodopsin synthase, putative
Sapur.01G0620200.2	0.029218147	0.08741946	2.351778037	0.037054	0.970488122	NA	grey	grey	-0.020416057	0.799673388	GO:0016787,GO:0005524,GO:0003677	ATSG40700.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.01G0221500.2	0.027573276	0.087420221	2.384320046	0.036665	0.970715831	NA	grey	grey	-0.020957059	0.79446192		ATSG26380.1		Melibiase family protein	alpha-galactosidase
Sapur.01G1511900.4	0.030885213	0.087421003	2.390822811	0.036549	0.970814399	NA	grey	grey	0.468050988	6.36E-10	GO:0005515	ATSG49520.1		WD40/YVTN repeat-like-containing domain;Bromodomain	cytochrome c1l-nitrite reductase-like, carbox-terminal heme protein d1, putative
Sapur.15ZG051800.2	0.031037916	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.36302607	2.60E-06	GO:0009446,GO:0006468	ATSG08170.1	ATAHL,EMB1873	porphyromonas-type peptidyl-arginine deiminase family protein	NA
Sapur.002G095200.1	0.031493898	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.02244602	0.77072222		ATSG56600.1	ZCW7	ZCW7	ZCW7
Sapur.004G162800.2	0.031854958	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.025737836	0.748674946		ATSG28120.1		Major facilitator superfamily protein	NA
Sapur.01G1308500.1	0.031057919	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.006405251	0.936561626					NA
Sapur.003G073700.3	0.031516272	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.021622911	0.788083079		ATSG22060.1			EEIG1/EHBP1 protein amino-terminal domain protein
Sapur.004G164700.1	0.011328829	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.112485521	0.160726523		ATSG27900.1		disease resistance protein (TIR-NBS-LRR class), putative	DUF2450 family protein
Sapur.T017700.1	0.010321507	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	0.012030094	0.881217604	GO:0006629,GO:0007165,GO:0055115,GO:0045131	ATSG17680.1		LysM domain receptor-like kinase family protein	NA
Sapur.006G083000.1	0.013316557	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.00157949	0.946687851	GO:0016747	ATSG36040.1		HXXXD-type acyl-transferase family protein	NA
Sapur.01G1308400.1	0.012559313	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.017454629	0.474768285		ATSG49520.1		Kinase interacting (KIP1-like) family protein	60S-like protein
Sapur.006G092300.2	0.014020804	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.001149356	0.988601558	GO:0009058,GO:0003824	ATSG38670.1	PECT1	phosphoethylethanolamine cytidylyltransferase	ethanolamine-phosphate cytidylyltransferase
Sapur.01G0650700.1	0.015651519	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	0.008421238	0.932022887		ATSG27370.2		Tol1-interaction-factor (TIF) domain family protein	Leucine-rich receptor-like protein kinase family protein
Sapur.006G073000.2	0.014520105	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.082248114	0.305801373		ATSG35830.1		Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator RCC1 repeat protein
Sapur.01G1681300.2	0.015238815	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.028978786	0.71862982	GO:0008641	ATUBA1,MOSS,LIB41	ATUBA1	Ubiquitin-activating enzyme 1	ubiquitin-activating enzyme E1
Sapur.009G049600.2	0.015172426	0.105911962	2.904821821	0.036461	0.970914499	NA	grey	grey	-0.019339529	0.810047386		ATCOMS,ATGRI,COMS,GRI1	gamma response gene 1	gamma response protein	gamma response protein
Sapur.007G091800.2	0.049391569	-0.06081341	1.683787897	-0.03612	0.971189044	NA	grey	grey	-0.138785829	0.102029516		ATSG26330.3		wound-responsive family protein	hypothetical protein
Sapur.003G091600.1	0.049416812	-0.06081341	1.681594205	-0.03608	0.971215923	NA	grey	grey	-0.000924257	0.993057512	GO:0003887,GO:0006351	ATSG11560.1		bromo-adjacent homology (BAH) domain-containing protein	transcription factor S-II domain protein
Sapur.005G055600.1	0.046503138	-0.06081109	1.68115515	-0.03602	0.971264152	NA	grey	grey	-0.203583801	0.010547587	GO:0006412,GO:0005840,GO:0005622,GO:0003735	ATSG10360.1	EMB3010,RPS6B	Ribosomal protein S6e	40S ribosomal protein S6
Sapur.01G0280500.2	0.030978832	-0.09434489	2.662907282	-0.03543	0.971784779	NA	grey	grey	-0.148831611	0.064317067		ATSG21160.1		Ankyrin repeat family protein	transmembrane protein
Sapur.01G0651000.1	0.030349233	-0.09434065	2.669808536	-0.03534	0.971811728	NA	grey	grey	-0.149739145	0.061234228		ATSG31400.1	CTF7	damaged DNA binding;DNA-directed DNA polymerases	ESCO1/2 acetyl-transferase, putative
Sapur.01G0220500.3	0.029413265	-0.09434161	2.68038605	-0.0352	0.971853207	NA	grey	grey	-0.148831611	0.064820928		ATSG40630.3		Homeodomain-like superfamily protein	Myb/SANT-like DNA-binding family
Sapur.003G149600.1	0.050124827	0.054383451	1.548569895	0.035053	0.972027213	NA	grey	grey	-0.097804654	0.222988499	GO:0008146	ATST2A,ST2A	sulfotransferase 2A	sulfotransferase family protein	flavonol 4'-sulfotransferase, putative
Sapur.003G024700.1	0.047626279	0.088924617	2.56323187	0.03484	0.972207707	NA	grey	grey	0.055000453	0.488130005		ATSG45910.1		HSP20-like chaperones superfamily protein	NA
Sapur.01G0850900.1	0.045353231	0.063986279	1.850087235	0.034592	0.972450598	NA	grey	grey	-0.020757046	0.7963803					NA
Sapur.005G129800.1	0.035544484	0.080331396	2.664817446	0.033516	0.973132134	NA	grey	grey	0.158844051	0.066775175	GO:0032446,GO:0016020,GO:0008378,GO:0006486	ATSG26930.1	GALT1	galactosyltransferase1	beta-1%2C3-galactosyltransferase
Sapur.01G1332000.4	0.046026897	-0.06075135	1.830465551	-0.03319	0.973243356	NA	grey	grey	-0.108167833	0.177507776		ATSG14172.1			COPS-interacting-like protein, putative
Sapur.01G0291900.1	0.029876386	-0.07926223	2.401894028	-0.03299	0.973881991	NA	grey	grey	-0.147781777	0.064738688					NA
Sapur.007G047800.1	0.026422897	0.089319035	2.716687922	0.033002	0.973752628	NA	grey	grey	-0.000942274	0.99005712		ATSG42104.3		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.01G4127700.3	0.029328691	0.089319731	2.721287521	0.032823	0.97381656	NA	grey	grey	-0.42983699	1.93E-08		ATSG05660.1			hypothetical protein
Sapur.006G140100.1	0.031174324	0.087460597	2.664718277	0.032823	0.973874779	NA	grey	grey	0.166918248	0.015431466	GO:0008152,GO:0008824,GO:0016149,GO:0008661	ATSG15540.1	CLA,CLA1,DEF,DXPS2,DXS	Deoxyxylulose-5-phosphate synthase	1-deoxy-D-xylulose-5-phosphate synthase
Sapur.001G147400.1	0.043056646	-0.06074336	1.851931704	-0.0328	0.973881819	NA	grey	grey	-0.112973677	0.158906589	GO:0008601,GO:0000159	ATSG17720.1	ATB BETA	Protein phosphatase 2A, regulatory subunit PR55	serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B beta
Sapur.01G0222500.3	0.025244153	0.089320712	2.70069316	0.03271	0.973956526	NA	grey	grey	0.005169119	0.946132806	GO:0005515,GO:0000773	ATSG14045.2			associate of C-myc protein; putative
Sapur.01G1347004.4	0.025227243	0.089320736	2.730692524	0.032707	0.973988176	NA	grey	grey	-0.009494799	0.950495311	GO:0005515,GO:0006777	ATSG03390.1		uvrR/uvrC motif-containing protein	hemimethylated DNA-binding domain protein
Sapur.01G0288200.1	0.024138477	0.089322285	2.74602768	0.032151	0.974032182	NA	grey	grey	-0.021728854	0.768041574	GO:0004842	UFL2	ubiquitin protein ligase 2	ubiquitin protein ligase UFL1, putative	E3 ubiquitin protein ligase UFL1
Sapur.01G1594000.1	0.01091252	0.094318339	2.904824395	-0.03247	0.974097599	NA	grey	grey	-0.113748397	0.10001405		ATSG35405.1		Protein of unknown function (DUF784)	NA
Sapur.01G0200900.1	0.027394222	0.094318339	2.904824395	-0.03247	0.974097599	NA	grey	grey	-0.36110033	3.38E-06	GO:0005975,GO:0004553	ATSG16230.1		O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase, putative
Sapur.005G021200.1	0.029625822	0.094318339	2.904824395	-0.03247	0.974097599	NA	grey	grey	-0.175726069	0.027707318	GO:0019901,GO:0006355,GO:0000979,GO:0070985,GO:0016538,GO:0006355	ATSG27620.1	CYC1-L	cyclin H-1	cyclin H-1
Sapur.01G1212000.2	0.025223114	0.094318339	2.904824395	-0.03247	0.974097599	NA	grey	grey	-0.293090159	0.000195153		ATSG46540.1		ENTH/ANTH family protein	hypothetical protein
Sapur.01G1388800.1	0.01541125	0.094318339	2.904824395	-0.03247	0.974097599	NA	grey	grey	-0.141828476	0.07681884	GO:0007275	ATSG7180.2	CIA2	chloroplast import apparatus 2	import apparatus 2 protein, putative
Sapur.15WG125400.1	0.028753959	0.094318339	2.904824395	-0.03247	0.974097599	NA	grey	grey	-0.214432083	0.007000947		ATSG27060.1		Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator RCC1 repeat protein
Sapur.01G0240900.4	0.023540016	0.089322157	2.75560456	-0.03245	0.974098984	NA	grey	grey	-0.003160625	0.968661854	GO:0016021,GO:0008233,GO:0006465,GO:0005787	ATSG27420.1		Signal peptidase subunit	signal peptidase subunit
Sapur.002G136800.1	0.023688025	0.089322337	2.756396458	0.032406	0.974148407	NA	grey	grey	-0.036456689	0.650331723					NA
Sapur.01G0251400.1	0.023455006	0.089322394	2.756970824	0.032399	0.974171774	NA	grey	grey	-0.00071769	0.992483878		ATSG19380.1			transmembrane protein, putative
Sapur.01G1374000.2	0.023052436	0.089324052	2.761136461	0.032327	0.974311249	NA	grey	grey	-0.034362273	3.21E-07	GO:0006397	ATSG03330.1		Small nuclear ribonucleoprotein family protein	snRNP core Sm Sm-like protein
Sapur.01G0290600.1	0.023427375	0.089324052	2.761136461	0.032327	0.974311249	NA	grey	grey	-0.132397535	0.088595207	GO:0006468,GO:0006139	ATSG16060.1		Protein kinase family protein;Purine-nucleotide alpha hydrolases-like domain	tyrosine kinase domain protein
Sapur.01G0221200.1	0.023242792	0.089325163	2.774759367	0.032192	0.974918905	NA	grey	grey	-0.01313407	0.870312644	GO:0005975,GO:0004553	ATSG13130.1		Cellulase (glycosyl hydrolase family 5) protein	glycosyl hydrolase family 5 protein
Sapur.01G0810800.2	0.023232871	0.089325164	2.774779382	0.032192	0.974919043	NA	grey	grey	-0.285176109	0.000288475	GO:0006259,GO:0005694,GO:0005524,GO:0003824,GO:0003677,GO:000737	ATSG26980.1	SPO11-2	sporulation 11-2	meiotic recombination protein SPO11, putative
Sapur.01G0270700.2	0.022737767	0.089325248	2.775625864	0.032181	0.974928894	NA	grey	grey	-0.020852148	0.795436508	GO:0005643	ATSR72,SRT2	sirtuin 2	NAD-dependent protein deacetylase	NAD-dependent protein deacetylase
Sapur.01B0293000.1	0.022112081	0.089325505	2.778247095	0.032152	0.974953194	NA	grey	grey	-0.006708387	0.93354525		ATSG25250.1		SPFH/Band 7/PHB domain-containing membrane-associated protein family	flotillin-like protein
Sapur.01G4111700.2	0.021919928	0.089325817	2.781443008	0.032115	0.974983124	NA	grey	grey	-0.101452248	0.886770755	GO:0007005,GO:0006842	ATSG26060.1		E3 ubiquitin ligase	E3 ubiquitin ligase
Sapur.T151000.1	0.021805151	0.089326004	2.783356561	0.032093	0.974997941	NA	grey	grey	-0.023397535	0.779152777					NA
Sapur.01G1724300.2	0.021724838	0.089326136	2.784715125	0.032077	0.975008249	NA	grey	grey	0.017393895	0.865546878	GO:0016491	ATSG27230.1		Quinone reductase family protein	quinone oxidoreductase, putative
Sapur.008G224400.1	0.021649949	0.089326259	2.785868141	0.032063	0.974991988	NA	grey	grey	-0.00084836	0.991587709					transmembrane protein, putative
Sapur.01G0261100.1	0.021688604	0.089326259	2.785701383	0.032065	0.974991988	NA	grey	grey	0.268204408	0.000681386	GO:0005515	ATSG27480.2		Galactose oxidase/kelch repeat superfamily protein	kelch repeat F-box protein
Sapur.01T0292500.1	0.021189714	0.089327321	2.793875041	0.031972	0.974994006	NA	grey	grey	-0.295694166	0.000170008	GO:0044237	ATSG38640.1		Nga8/Prp18/CwC15 protein family protein	translation initiation factor 2B, delta subunit%2C putative
Sapur.01G0651500.1	0.020655715	0.089327321	2.803315426	0.031865	0.974576232	NA	grey	grey	-0.055488204	0.490056269	GO:0016021,GO:0006629	ATSG38620.1	FADS2,FAD2	Fatty acid desaturase family protein	protein phosphatase 2C, putative
Sapur.009G121800.4	0.02062142	0.089327982	2.803923201	0.031858	0.974585205	NA	grey	grey	-0.278197741	0.000464651	GO:0006468,GO:0004672	ATSG20930.1	TSL	Protein kinase superfamily protein	touched-like kinase
Sapur.004G164600.1	0.020608291	0.089328935	2.804168805	0.031855	0.974587342	NA	grey	grey	-0.030256717	0.756788898					NA
Sapur.01G0010902	0.020010392	0.089328976	2.819432174	0.031751	0.974659018	NA	grey	grey	-0.026793438	0.647452303		ATSG27630.1			transmembrane protein, putative
Sapur.001G0020300.1	0.020030333	0.089329005	2.814775553	0.031736	0.974682751	NA	grey	grey	-0.00524646	0.948222224		ATSG58170.1		Disease resistance-responsive (dirigent-like protein) family protein	dirigent-like protein pDIR11
Sapur.013G080400.2	0.019762988	0.089329477	2.818918245	0.031697	0.974705449	NA	grey	grey	-0.017914174	0.823804386	GO:0006351,GO:0003714	ATSG35570.1		Protein of unknown function (DUF1421)	signal transducer, putative
Sapur.01B0090600.1	0.019749503	0.089329499	2.820063313	0.031676	0.974710103	NA	grey	grey	-0

Sapur.00G177700.4	0.01035651	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.02183681	0.78603699		ATG13G0D0.2	Protein of unknown function, DUF547	electron transporter, putative
Sapur.01G041100.2	0.01050825	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.02238936	0.78076403	G0D0G60	ATG26594.1	response regulator 24	NA
Sapur.07G080100.1	0.00839857	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.00958218	0.94092015	G0D6442.G0D5840,G0.G0D5622,G0-G0D3735	ATG27940.1	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L30
Sapur.7I02400.1	0.00897904	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.02020193	0.80171179		ATMYB4;MYB4	myb domain protein 4	NA
Sapur.01G122000.5	0.00937869	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.01741543	0.82863853		ATG35163.1	SPFH/Band 7/PHB domain-containing membrane-associated protein family	SPFH domain/Band 7 family protein
Sapur.01G251100.3	0.00832449	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.00732597	0.92749535	G0.0G9058,G0.0G0824,G0.0G1679,G0-G0G9435	ATG35832.1	AENNMN,AT_NMNAT	nicotinamide/nicotinamide mononucleotide adenylyltransferase
Sapur.01G029900.1	0.00896203	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.22608176	0.00392027	G0.0G5511,G0.0G6448,G0.0G6472	ATG02390.1	SRF3	STRUBBELIG-receptor family 3
Sapur.05G094900.1	0.01060201	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.02726596	0.73461629	G0.0G6355,G0.0G0667	ATG45193.1	BEL1	BEL1-related homeotic protein, putative
Sapur.7I18400.1	0.00916932	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.01827335	0.82030437		ATG42680.1	GM6	gamma-irradiation and mitomycin c induced 1
Sapur.01G026800.4	0.01032858	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	0.31239179	6.00E-06	G0.0G4361,G0.0G6289,G0.0G3684,G0-G0G5515	ATG25145.1	RAD23 -1,RAD23C	RAD23 UV excision repair protein RAD23, putative
Sapur.7I024400.1	0.00968205	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.02688277	0.73722742				
Sapur.01G067010.6	0.00972478	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.12966142	0.10717882	G0.0G0850	ATG14680.1	Adenine nucleotide alpha hydrolases-like superfamily protein	ethylene-responsive-like protein
Sapur.00G119100.1	0.00971850	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.02658593	0.74101238				NA
Sapur.7I040700.3	0.00882839	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.00987948	0.90223245	G0.0G9558,G0.0G5515	ATG02730.1	Sterile alpha motif (SAM) domain-containing protein	SAM domain protein
Sapur.00G002800.3	0.00792026	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.01291857	0.87242049		ATG47740.1	Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein
Sapur.01G080300.1	0.00847939	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	0.10844875	0.51273795		ATG26603.1	Homeodomain like superfamily protein	MYB transcription factor
Sapur.00G138200.1	0.00940634	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.02753626	0.73583239	G0.0G6872	ATG19331.1	RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.00G139200.2	0.01027456	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.03703621	0.64518759	G0.0G5085,G0.0G4673,G0-G0.0G0001,G0-G0.0G1820	ATG16010.2	MGT2,MRS2-1	magnesium transporter
Sapur.00G131600.1	0.00960751	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.16213625	0.04251003	G0.0G6633,G0.0G5534,G0.0G3989	ATG36160.2	ACC1,AT-ACC1,EMB2232,GP	acetyl-CoA carboxylase
Sapur.00TG105200.3	0.00543631	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	0.08572849	0.28567884		ATG32106.1	Phototropic-responsive NPH3 family protein	root phototropism protein, putative
Sapur.01TG034800.1	0.01072873	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.03324106	0.67863181	G0.0G6881,G0-G0G6777	AGU64045.1	AGAMOUS-like 5	agamous-like MADS-box protein AGL62
Sapur.01G148200.5	0.00845284	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	0.13789851	0.08501693	G0.0G5515	ATG01590.1	HS,HWS	Galactose oxidase/kelch repeat superfamily protein
Sapur.7I084400.1	0.00912468	0.09118602	2.90483276	0.031182	0.97695654	NA	grey	-0.02992266	0.70868091				NA
Sapur.00G094700.1	0.01072524	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	0.44678614	4.48E-09		ATG36430.1	Family of unknown function (DUF662)	transcriptional activator
Sapur.00G139200.1	0.00955345	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	0.47665497	2.78E-10		ATG25760.1	persephin	ubiquitin-conjugating enzyme E2, putative
Sapur.01G029800.1	0.00895269	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	-0.03874899	0.62993154		ATG59650.1	CW14	Protein of unknown function (DUF1336)
Sapur.01G080800.1	0.00905265	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	0.01164218	0.88493565	G0.0G6205	ATG22120.4	ERD (early-responsive to dehydration stress) family protein	early-responsive to dehydration-like protein
Sapur.01TG127300.3	0.00796451	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	0.19758645	0.15132366	G0.0G5085,G0.0G6021,G0.0G1820,G0-G0G8610,G0-G0G5215	ATG14940.1	Major facilitator superfamily protein	peptide transporter
Sapur.01BG103200.1	0.01347202	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	-0.05672325	0.48027093	G0.0G0220,G0-G0B375	ATG19160.1	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	core-2/I-branching enzyme
Sapur.00G024300.1	0.00854143	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	-0.04004304	0.61834267	G0.0G4648,G0-G0G6457	ATG15130.1	KEG	E3 ubiquitin-protein ligase KEG
Sapur.00G103300.2	0.00891894	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	-0.04233063	0.59816925	G0.0G8270,G0.0G5515,G0-G0G4872	ATG08505.1	zinc finger (CCCH-type/C3HC4-type RING finger) family protein	RING-zinc finger protein, putative
Sapur.00G415500.1	0.01072872	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	-0.05097758	0.53016291		ATG39139.1	RmlC-like cupin superfamily protein	rhizaffinin receptor, putative
Sapur.00G005400.1	0.01072872	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	-0.05097758	0.53016291				NA
Sapur.00G028300.5	0.00967615	0.09118603	2.90483276	0.031182	0.97695654	NA	grey	-0.04700925	0.51853061	G0.0G6747,G0-G0B152	ATG07720.2	Thiolase family protein	cytosolic acetyl-CoA acetyltransferase
Sapur.01G182400.7	0.01686150	0.09334957	2.88077879	0.031011	0.97526101	NA	grey	0.00950826	0.95916444		ATG09812.1		transmembrane protein, putative
Sapur.00TG009900.1	0.00874907	0.09118603	1.54517403	0.03043	0.97523138	NA	grey	-0.06541108	0.57246313		ATG14870.1	PCR2	PLANT CADMIUM RESISTANCE 2
Sapur.09G100800.1	0.06765215	0.07861745	1.54713260	0.0309	0.97493363	NA	grey	-0.05135908	0.52148868	G0.0G6872,G0-G0G001	ATG04900.1		Heavy metal transport/detoxification superfamily protein
Sapur.09G051300.2	0.07272998	0.07812744	1.54884892	0.03087	0.97373329	NA	grey	0.15282762	0.05347884	G0.0G5085,G0.0G6020,G0-G0G8621,G0-G0G5247	ATG32280.1	Voltage-gated chloride channel family protein	NA
Sapur.00G000200.1	0.04707266	0.04781014	1.54106281	0.03082	0.97279822	NA	grey	-0.06103764	0.44709891	G0.0G3824,G0-G0B470,G0-G0B472	ATG31660.1	Protein phosphatase 2C family protein	NA
Sapur.02G089500.1	0.02724762	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	0.01603842	0.85171953	G0.0G3565,G0-G0B270,G0-G0B275,G0-G0G0700,G0-G0G5515	ATG21175.2	GATA24,TIFY28,ZML1	ZIM-like 1
Sapur.01G179300.1	0.02829534	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	-0.01307271	0.84494803	G0.0G1684,G0-G0B075	ATG17520.1	phosphoglycosamine mutase family protein	phosphoglucosamine mutase/phosphomannomutase alpha/beta/alpha domain protein
Sapur.01G181600.1	0.02803623	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	-0.01512291	0.84893842		ATPEN2;PEN2	PTEN 2	phosphatidylinositol-3H,3C,4H,5C,5-trisphosphate 3-phosphatase
Sapur.01G042300.1	0.02891053	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	-0.01486275	0.85202469	G0.0G5515	ATT36180.1	TRAF-like family protein	NA
Sapur.07G051200.2	0.02117354	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	-0.02361754	0.76873919		ATG51000.1	alpha/beta-Hydrolases superfamily protein	epoxide hydrolase
Sapur.00G413200.1	0.02427348	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	-0.02388139	0.76650456	G0.0G8634,G0-G0G8686,G0-G0G5515	ATTRN1;TRN1	transportin 1	transportin 1 protein
Sapur.01G241700.2	0.01893358	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	-0.07854831	0.32814697	G0.0G4648,G0-G0G5134,G0-G0G4672	ATG53440.1	Leucine-rich repeat transmembrane protein kinase	LRR receptor-like Serine/Threonine-kinase, putative
Sapur.01G205500.2	0.02944212	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	-0.02263798	0.77562132	G0.0G5515	ATS38391.1	ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1
Sapur.01TG031000.1	0.02018486	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	0.03601393	0.70360441	G0.0G1620	ATG25530.2	ATPHB6,PHB6	prohibitin 6
Sapur.01G058800.0	0.01968512	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	0.02347184	0.77042892	G0.0G1592,G0-G0G357,G0-G0G1104	ATG03500.1	Mediator complex, subunit Med7	mediator of RNA polymerase II transcription subunit 7, putative
Sapur.00G007200.1	0.04561732	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	-0.00390368	0.98803961	G0.0G0327			B3 DNA-binding protein
Sapur.01G062700.1	0.02563295	0.09331702	2.90482183	0.030755	0.97546146	NA	grey	0.00898156	0.99027473		ATG45820.1	Remorin family protein	remorin
Sapur.00G102500.5	0.01980434	0.09331701	2.90482183	0.030755	0.97546146	NA	grey	-0.03397005	0.67250032	G0.0G3824,G0-G0B476,G0-G0B472	ATG31660.1	Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.02G176900.2	0.01865457	0.09331701	2.90482183	0.030755	0.97546146	NA	grey	-0.03315321	0.68018312	G0.0G5522,G0-G0B476,G0-G0B468,G0-G0B619	ATG32415.2	Polynucleotidyl transferase, ribonuclease H fold protein with HRDC domain	3'-5' exonuclease
Sapur.00G204200.1	0.02169739	0.07356104	2.41758593	0.03429	0.97574766	NA	grey	-0.06620365	0.23923333				NA
Sapur.01G060400.7	0.03900798	0.07316684	2.61669547	-0.03028	0.97584758	NA	grey	-0.02946867	0.7140065				hypothetical protein
Sapur.00TG011300.2	0.04613343	-0.04624394	1.64173776	-0.02905	0.97610068	NA	grey	-0.11886896	0.13818349	G0.0G0723	ATG01930.1	APO3	Arabidopsis thaliana protein of unknown function (DUF704)
Sapur.02G029000.1	0.03266103	-0.07023629	2.64825214	-0.02992	0.97613082	NA	grey	0.13197904	0.09941558	G0.0G6355,G0-G0B700,G0-G0B775	ATG37752.1	ANT,CXC,CXC1,DRG	integrase-type DNA-binding superfamily protein
Sapur.05G117300.1	0.03925789	0.08297581	2.82278397	0.02954	0.97668623	NA	grey	-0.04026425	0.61559139	G0.0G5114,G0-G0D037,G0-G0.0G7685,G0-G0G5506	ATG09970.1	CYP78A7	cytochrome P450 family 78 protein
Sapur.00G021900.1	0.01869779	0.08297692	2.81910247	-0.02891	0.97671265	NA	grey	-0.04024263	0.63678454		ATG08720.1	GDP81,ZPR1	zinc finger protein 81
Sapur.00G090100.2	0.04361567	-0.05801348	2.03157689	-0.02891	0.97698523	NA	grey	-0.12402142	0.19981802	G0.0G6773,G0-G0B015,G0-G0B854	ATP4H;ALPHA	Phosphatidylinositol 3- and 4-kinase family protein	phosphatidylinositol 4-kinase
Sapur.01TG088700.1	0.03779231	-0.05882406	2.06352428	-0.02884	0.97724318	NA	grey	-0.11216165	0.16194258		ATG66840.1	Plant protein of unknown function (DUF247)	weak movement under blue light protein
Sapur.01TG051000.1	0.04814246	-0.06788767	1.67988779	-0.02856	0.97728326	NA	grey	0.10604707	0.18628621	G0.0G8152,G0-G0B824	ATG23790.1	AAE16	AMP-dependent synthetase and ligase family protein
Sapur.01G257500.1	0.03936046	-0.05882367	2.06758714	-0.02845	0.97733173	NA	grey	-0.13763888	0.08496778				NA
Sapur.02G195800.1	0.03688707	-0.05882142	2.07120517	-0.0284	0.97734325	NA	grey	0.27707181	0.00044092	G0.0G1829,G0-G0B699	ATG47530.1	FUM1	fumarase 1
Sapur.01G026100.1	0.03526183	-0.05882531	2.07773604	-0.02819	0.97744973	NA	grey	-0.14512219	0.08876283				NA
Sapur.01G303500.1	0.03503709	-0.05882203	2.07608014	-0.02829	0.97749702	NA	grey	-0.14654307	0.07404801	G0.0G5515	ATG32660.1	AtRLP22,RLP22	receptor-like protein 22
Sapur.01G081300.1	0.03481008	-0.05881882	2.0803784	-0.02814	0.97754384	NA	grey	-0.11463007	0.15476204		ATG08970.4	NUCLEAR CYCLIN C9	nuclear factor CLF-like protein
Sapur.01G020700.2	0.03053351	-0.06223445	2.35693659	0.028097	0.97756528	NA	grey	-0.03000233	0.70916187	G0.0G5515,G0-G0B764,G0-G0B855	ATG06350.1	EMB3004,MEE32	dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative
Sapur.00G151300.1	0.02272299	-0.05891031	2.06275966	-0.02806	0.97763378	NA	grey	-0.07854831	0.32814697		ATG76730.1		Nga8/Rpk/CoA transferase-like superfamily protein
Sapur.02G062800.1	0.02880934	-0.06224075	2.37953856	0.027931	0.97779047	NA	grey	-0.03387527	0.65161107		ATG02661.1		RING/U-box superfamily protein
Sapur.15WG081300.1	0.04869713	-0.06230226	1.67859372	-0.02754	0.97801679	NA	grey	-0.10381934	0.19567131	G0.0G6983	ATG07530.1	BHLH161,BNQ3	transcription regulator, putative
Sapur.01G098800.2	0.02512739	-0.06224885	2.40993849	-0.02748	0.97807639	NA	grey	-0.20230555	0.05061183		ATG61790.1		Pectinin homology (PH) domain superfamily protein
Sapur.01G080400.7	0.03900798	-0.07316684	2.61669547	-0.03028	0.97584758	NA	grey	-0.03663604	0.64872617	G0.0G5114,G0-G0D661,G0-G0D660,G0-G0D449	ATG21430.1	YUC11	Flavin-binding monooxygenase family protein
Sapur.01G000500.1	0.04561032	-0.04622944	1.64873777	-0.0274	0.97814029	NA	grey	-0.12521665	0.18915426		ATG21220.1		NA
Sapur.01BG042400.5	0.04497387	-0.06229247	1.68405589	-0.02736	0.97819246	NA	grey	-0.0868996	0.27916264	G0.0G6364,G0-G0D4222	ATG25870.1		haloacid dehalogenase-like hydrolase family protein
Sapur.00TG023200.2	0.04423159	-0.06229247	1.70080556	-0.02718	0.97824005	NA	grey	-0.12344145	0.12496943	G0.0G4564,G0-G0D528,G0-G0D662	ATG37200.1	HCF164	Thioredoxin superfamily protein tdx4, putative
Sapur.07G052900.2	0.02805191	0.07349457	2.70779167	0.027137	0.97835076	NA	grey	-0.10126162	0.20691068	G0.0G5515,G0-G0I6773	ATG17930.1		Phosphatidylinositol 3- and 4-kinase family protein with FAT domain
Sapur.01G020300.1	0.04723005	0.04981239	1.83924703	0.027083	0.97839315	NA	grey	0.03288205	0.98845453	G0.0G6281,G0-G0D678,G0-G0D720	ATG31700.1		PIF1 helicase
Sapur.01G284000.1	0.04629718	0.04981437	1.84517724	0.026998	0.97846164	NA	grey	-0.02268754	0.77277766	G0.0G5621	ATG47526.1		Auxin-responsive family protein
Sapur.01G289400.4	0.04205104	0.04981807	1.85218709	0.026897	0.97854201	NA	grey	-0.0391871	0.62657593		ATG32960.1		UDP-Glycosyltransferase superfamily protein
Sapur.15WG010380.1	0.04215868	0.04981812	1.85279831	0.026889	0.97858412	NA	grey	-0.17240604	0.03081218		ATG20960.1	LOB	Lateral organ boundaries (LOB) domain family protein
Sapur.07G008300.2	0.0473292	0.04981826	1.85443571	0.026865	0.97859766	NA	grey	-0.04867338	0.57031645	G0.0G0017,G0-G0T018,G0-G0T0G4,G0-G0T077,G0-G0D5871	ATG10470.1	KAC1,KCA1	kinesin-like protein for actin-based chloroplast movement 1
Sapur.02G029600.2	0.04616733	0.04981833	1.86083301	0.026774	0.97864223	NA	grey	-0.35450368	5.21E-06	G0.0G6432,G0-G0B585,G0-G0G522,G0-G0T375	ATG37620.1	NDL2	Ribosomal protein L6e family protein
Sapur.15WG045100.2	0.04017275	0.04981211	1.86104249	0.026771	0.97864797	NA	grey	-0.06493165	0.42561378	G0.0G5515	ATG48790.1	AMSH1	associated molecule with the SH3 domain of STAM 1
Sapur.01G063100.2	0.03867579	0.04982611	1.87570193	0.02647	0.97887275	NA	grey	-0.03833215	0.63312488		ATG79520.2		cyclin related
Sapur.01G170000.1	0.03676758	0.04982642	1.87579114	0.026563	0.97888369	NA	grey	-0.05370424	0.48834473	G0.0G5114,G0-G0B977,G0-G0B671,G0-G0B665	ATG15710.1		prephenate dehydrogenase family protein
Sapur.02G045800.2	0.03449389	0.04982644	1.88674035	0.026413	0.97892746	NA	grey	-0.27069829	0.00061192	G0.0G2232	ATG25880.1	APUMG,PUM6	pumilio 6
Sapur.05G124200.1	0.03874206	0.04983495	1.90046647	0.026223	0.97907673	NA	grey	-0.07725217	0.13619092	G0.0G5114,G0-G0D037,G0-G0T675,G0-G0T0G6	ATG37370.1	CYP81D8	cytochrome P450 family protein
Sapur.01TG052500.1	0.04795394	0.04795858	1.83850524	0.026091	0.97918109	NA	grey	0.12592903	0.15958415	G0.0G6021,G0-G0B783	ATG14030.4		translocon-associated protein beta (TRAP8) family protein
Sapur.01TG041000.1	0.03869047	0.04050698	1.57638303	0.025688	0.97968037	NA	grey	-0.07867756	0.36037025	G0.0G6326,G0-G0B197	AMC1,ATMC1,ATMCP1L1,G0	metacaspase 1	EC1-like protease 1 conserved peptidase domain protein
Sapur.01G042700.1	0.03104062	0.05960504	2.35463243	0.025313	0.97985054	NA	grey	-0.02850083	0.73209576				NA
Sapur.01G023100.1	0.03421317	0.05839205	2.33640326	-0.02526	0.97986638	NA	grey	-0.13732261	0.0863877	G0.0G5634	ATG35870.1	AHG2,ATPAPA	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Sapur.03G027500.1	0.03404346	-0.05876983	2.32638605	-0.02526	0.97984774	NA	grey	-0.12307805	0.12461589		ATG71260.1	ATWHY2,WHY2	WHIRLY 2
Sapur.01G024500.1	0.02272204	-0.06484848	2.76833823	0.024722	0.98027683	NA	grey	-0.27126229	4.23E-10		ATG71790.1	NDL2	N-MYC downregulated-like 2
Sapur.01BG100200.1	0.04732682	0.04981732	2.02093753	0.024678	0.98031167	NA	grey	-0.07854831	0.32814697	G0.0G5515	ATG15880.1	TPR4,WSIP2	WUS-interacting protein 2
Sapur.01G000100.1	0.02778619	-0.05875947	2.38247656	-0.02427	0.98031527	NA	grey	-0.11894828	0.13708245		ATG20970.1		transmembrane protein, putative
Sapur.01G295600.1	0.04185341	0.04987838	2.04539553	0.024386	0.98054932	NA	grey	-0.05165594	0.50461172				hypothetical protein
Sapur.05G150500.2	0.03789037	0.04987838	2.04539553	0.024386	0.98054932	NA	grey	-0.06885054	0.38185457	G0.0G5114,G0-G0E614,G0-G0D660	ATG19180.1		Long-chain fatty alcohol dehydrogenase family protein
Sapur.03G131200.1	0.03707934	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.04512142	0.23903701	G0.0G1620	ATG33205.1		Serine-domain containing serine and sphingolipid biosynthesis protein
Sapur.09G114400.2	0.06612020	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.18443256	0.03075632	G0.0G6773,G0-G0B015,G0-G0B854	ATP4H;ALPHA	Phosphatidylinositol 3- and 4-kinase family protein	phosphatidylinositol 4-kinase
Sapur.05G192500.3	0.06612020	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.37007248	1.84E-06				brain and reproductive organ-expressed protein
Sapur.09G045600.1	0.07192738	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.67646023	0.40117542	G0.0G5114,G0-G0D037,G0-G0T675,G0-G0T0G6	CYP93D1	cytochrome P450, family 93, subfamily D, polypeptide 1	cytochrome P450 family protein
Sapur.05G286000.1	0.05262674	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.06311763	0.44456891	G0.0G3674			polyadenylate-binding protein family protein, putative
Sapur.07G129400.1	0.07754124	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.06809245	0.39263943		ATG43990.1		hypothetical protein
Sapur.01G005100.1	0.05258688	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.06138862	0.44692752				NA
Sapur.01BG036600.1	0.05258688	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.06138862	0.44692752	G0.0G5515	ATG18230.1		Octicosapeptide/Phox/Bem1p family protein
Sapur.01G260600.1	0.05654703	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.06272649	0.41510631	G0.0G5515,G0-G0B783	ATR8P47C,RBP47C	RNA-binding protein 47C	RNA recognition motif 1 in RNA-binding protein 28 (RBM28)-like protein
Sapur.01G230900.2	0.06680105	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.06614163	0.41049148	G0.0G6020,G0-G0D715,G0-G0D638,G0-G0D422	ATG42632.1		metalloendopeptidase/metallopeptidase/zinc ion binding protein
Sapur.15WG015300.2	0.08799423	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.0691754	0.38942682	G0.0G5515,G0-G0B620,G0-G0B811,G0-G0D216	ATCNGC1,CNGC1	cyclic nucleotide-gated channel 1	cyclic nucleotide-gated ion channel protein
Sapur.15WG094900.1	0.07512186	0.07064775	2.94963918	0.024323	0.98059472	NA	grey	-0.06833092	0.39117087	G0.0G3723,G0-G0B178	ATG21175.1	PA-RG-3 related	NA
Sapur.7I128000.1	0.03767977	0.06834945	2.81917297	0.024272	0.98063598	NA	grey	-0.0643877	0.42308857				NA
Sapur.00G119000.1	0.03508381	0.06849145	2.82954967	0.024187	0.98070155	NA	grey	0.06283181	0.68491945		ATG16385.1		NA
Sapur.01G085600.2	0.05004328	0.04047975	1.67230707	0.024135	0.98076568	NA	grey	-0.04187466	0.60256185	G0.0G6361,G0-G0D630	ATG32905.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Sapur.01G208400.1	0.05688402	-0.04888523	2.07513075	-0.02488	0.98079545	NA	grey	0.10422407	0.19399404	G0.0G3674	ATG36782.1	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif (RRM)2C RBD protein
Sapur.09G083300.1	0.06351254	0.04885581	2.07603541	0.024052	0.98083843	NA	grey	-0.05480003	0.49546214		ATG03150.1		plant/T1D06-60 protein, putative
Sapur.01G146600.1	0.05745022	0.04889493	2.86143544	0.023885	0.98094675	NA	grey	-0.05881325	0.46437563		ATG08060.1		hypothetical protein
Sapur.01G147400.1	0.03477019	0.04986209	2.01200059	0.023857	0.98096932	NA	grey	-0.08557213	0.31564857				NA
Sapur.01G023700.1	0.06152249	0.04985411	1.85273875	0.023375	0.98103771	NA	grey	0.14554834	0.08832064		ATG36932.1	DRB3	double-stranded RNA-binding motif protein
Sapur.01G020600.1	0.06123073	0.06849704	2.88771624	0.023692	0.98108257	NA	grey	-0.16480407	0.04333193		ATG13060.2	ECT5	evolutionally conserved C-terminal region 5
Sapur.01G024800.3	0.05302924	0.06849844	2.92823821	0.023561	0.98120297	NA	grey	-0.03349006	0.68197587	G0.0G0675	ATG18810.1	SCL28	SCL28-like splicing factor 28
Sapur.01G201000.2	0.01558754	0.06849845	2.90482821	0.023561	0.98120297	NA	grey	-0.03544848	0.69388663	G0.0G6468,G0-G0B546,G0-G0B524,G0-G0B472	ATG21580.1	PEPKR1	phosphoenolpyruvate carboxylase-related kinase 1
Sapur.00G039500.1	0.02336313	0.06849845	2.90482821	0.023561	0.98120297	NA	grey	-0.08160864	0.30950942		ATG22550.1		Protein of unknown function (DUF581)
Sapur.01G162700.5	0.08947507	0.05178708	1.28911467	-0.02368	0.98126149	NA	grey	-0.45407558	2.10E-09	G0.0G5597,G0-G0B534,G0-G0B440	ATG2040	ATCOAE	dephospho-CoA kinase
Sapur.01G021600.1	0.04600155	0.05179297	2.10534045	0.023329	0.98216549	NA	grey	0.04080327	0.24155715	G0.0G5114,G0-G0I6491			2-oxoglutarate(2OG) and Fe(II)-dependent dioxygenase, putative
Sapur.01G023400.1	0.03623418	0.05179432	2.12915271	0.023327	0.98218625	NA	grey	-0.02214156	0.97803841		ATG02410.1		hypothetical protein
Sapur.03G131300.1	0.03142308	0.05179499	2.34845281	0.023056	0.98240277	NA	grey	-0.06014228	0.45528612		ATG48655.1		RING/U-box superfamily protein
Sapur.01G027100.1	0.03627747	0.05178824	2.01928215	0.023031	0.98249361	NA	grey	-0.5648143	0.43992016	G0.0G0817,G0-G0T018,G0-G0T0G4,G0-G0T077,G0-G0D5871	ATG20060.1		ATP binding microtubule motor family protein
Sapur.02G044100.4	0.03056201	0.05178956	2.35471284	0.021988	0.98349703	NA	grey	-0.06591557	0.41292521	G0.0G5515	ATG48870.1		Transducin/WD40 repeat family protein
Sapur.06G045800.2	0.08011013	0.05179934	2.35810351	0.021966	0.98357156	NA	grey	-0.03170106	0.69348707	G0.0G1491	ATG18160.1		Aldolase-type TIM barrel family protein
Sapur.01G147400.1	0.02664747	0.05178824	2.01928215	0.021931	0.98369361	NA	grey	-0.5648143	0.43992016		ATG20060.1		ATP binding microtubule motor family protein
Sapur.00G041000.4	0.03056201	0.05178956	2.35471284	0.021988	0.98349703	NA	grey	-0.06591557	0.41292521	G0.0G5515	ATG48870.1		Transducin/WD40 repeat family protein
Sapur.06G045800.2	0.08011013	0.05179934	2.35810351	0.021966	0.98357156	NA	grey	-0.03170106	0.69348707	G0.0G1491	ATG18160.1		Aldolase-type TIM barrel family protein
Sapur.

Sapur.005G014600.10	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.141831729	0.076446592	GO:0008565;GO:0006606;GO:0005737;GO:0005634;GO:0005515	ATSG06730.1	AIMP ALPHA;AT-IMP ATKAP	importin alpha isoform 1	importin subunit alpha
Sapur.005G059200.1	0.006185738	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG39860.1			HN1-like protein
Sapur.005G077700.1	0.004268021	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0008270;GO:0005515	ATSG39950.1	RING/U-box superfamily protein		RING zinc finger protein, putative
Sapur.005G080400.2	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.059152516	0.462074048	GO:0006468;GO:0004672	ATSG35600.2	CONNEXIN 32	Protein kinase superfamily protein	Serine/Threonine-kinase Cx32, putative
Sapur.005G087800.1	0.003680737	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.026810048	0.737752221		ATSG35920.3	MC41	PLACE8 family protein	MD2-complementing activity protein
Sapur.005G104900.2	0.005142252	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG23620.1	ATMES1,MES1	methylesterase 1	polyneuridine-aldehyde esterase, putative
Sapur.005G111500.2	0.004958202	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG01710.1		Chaperone DnaJ-domain superfamily protein	AT hook motif protein
Sapur.005G114500.1	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-1.179204527	0.028281022	GO:0019904	ATSG45430.1	14-3-3EAPPA;GF14 KAPPA;G	general regulatory factor 8	14-3-3like protein GF14 lambda protein
Sapur.005G115500.3	0.007810412	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0009378;GO:0006310;GO:0006281	ATSG50140.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.005G134600.1	0.004268021	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0005515;GO:0008017	ATSG27370.1	ATEB1C,ATEB1H1,EB1C	end binding protein 1c	microtubule-associated protein RP/EB family protein
Sapur.005G129400.2	0.004268371	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG78150.3			HN1-like protein
Sapur.005G141200.1	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.126570203	0.134176361		ATSG31115.2		Protein of unknown function (DUF1997)	plant/FYVE21-30 protein, putative
Sapur.005G143900.2	0.007853997	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006950;GO:0006468;GO:0005524;GO:0004672	ATSG77280.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	adenine nucleotide alpha hydrolase-domain kinase
Sapur.005G173300.2	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.320700000	0.000000000		ATSG45481.1	INDL	Molybdopterin synthase sulfurase protein	MRP-like protein (ATH1G77P-binding protein)
Sapur.005G190600.1	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.249082132	0.001653349		ATSG06300.1		Putative lysine decarboxylase family protein	cytokinin riboside 5'-monophosphate phosphorylohydrolase
Sapur.005G193800.1	0.006185738	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG07551.1		Protein of unknown function (DUF668)	DUF668 family protein
Sapur.005G196400.1	0.006517668	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0055114;GO:0016491	ATSG20735.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	prolyl 4-hydroxylase alpha subunit, putative
Sapur.005G203900.2	0.003303983	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006457	ATSG20810.1		FKBP-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase FKBP18
Sapur.005G205000.1	0.004268021	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG33585.1			transmembrane protein, putative
Sapur.005G206200.1	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.078548531	0.32814487	GO:0003677	ATSG76510.1		ARID/BRIGHT DNA-binding domain-containing protein	ARID/bright DNA-binding domain protein
Sapur.005G205500.1	0.010368291	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG22260.1		oxidoreductase, 2OG-Fe(II) oxygenase family protein	2OG-Fe(II) oxygenase family protein
Sapur.005G208500.1	0.00527888	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.082189299	0.306159904		ATSG09225.1			transmembrane protein, putative
Sapur.005G209100.1	0.006346339	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0000160	ATSG27040.1	ARR9,ATRR4	response regulator 9	type-A response regulator
Sapur.005G042700.1	0.007069729	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006468;GO:0005524;GO:0004672	ATSG20860.1	ATNIK3,NIK3	N1NA-related kinase 5	Serine/Threonine kinase domain protein
Sapur.005G052000.4	0.003749344	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.155584477	0.055484169		ATSG11000.1	ATMAK10,MAK10	NAK10 homologue	NAK10 subunit, N-acetylhydrolase-terminal acetyltransferase
Sapur.005G064600.2	0.006346339	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.401887969	1.82E-07	GO:0006468;GO:0005524;GO:0004672	ATSG07180.2		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.005G089800.1	0.00653968	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0008270	ATSG02310.1	PRT6	proteolysis 6	E3 ubiquitin-protein ligase UBR2
Sapur.005G093600.2	0.004958202	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG27440.1	AtIP5K2	Arabidopsis inositol phosphokinase compatible kinase	phosphatidylinositol ceramide inositolphosphotransferase
Sapur.005G081400.2	0.003831304	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.24312701	0.002153539		ATSG01520.1		RING/U-box superfamily protein	RING finger protein
Sapur.005G099800.2	0.006679921	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG28690.1		Ankyrin-repeat family protein	tankyrase
Sapur.005G106100.4	0.004958722	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.141003174	0.078160559	GO:0008270	ATSG09760.1		RING/U-box superfamily protein	zinc finger protein, putative
Sapur.005G111800.2	0.005144252	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG24317.1		ARM repeat superfamily protein	transmembrane protein, putative
Sapur.005G114300.2	0.004958722	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006457;GO:0005737	ATSG07230.1	ATCPN21,CHCPN 10,CPN 10	chaperonin 20	chaperonin
Sapur.005G116800.1	0.005144252	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006468;GO:0004672	ATSG18800.1		Protein kinase superfamily protein	receptor-like kinase
Sapur.005G138100.2	0.006187019	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.004989952	0.236611024	GO:0055115	ATSG18850.2		SET domain-containing protein	ribulose-bisphosphate carboxylase, lysine N-methyltransferase%2C putative
Sapur.005G156300.2	0.005933709	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.155584477	0.055484169	GO:0016298;GO:0016717;GO:0006629	ATSG21120.2	FAD2	fatty acid desaturase 2	delta-12 fatty acid desaturase
Sapur.005G174100.2	0.00591235	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0005515	ATSG03880.1		Thioredoxin family protein	glutathione S-transferase, amino-terminal domain protein
Sapur.005G207800.2	0.006144922	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006457;GO:0003755;GO:0009412	ATSG24320.3		Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.005G210400.6	0.00947127	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0055114;GO:0030007;GO:0005829;GO:0004601	ATSG23120.1	APX6	ascorbate peroxidase 6	L-ascorbate peroxidase, putative
Sapur.005G217400.1	0.003303983	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0005515;GO:0006355;GO:0005634	ATSG25150.1	TAF5	TBP-associated factor 5	transcription initiation factor TFIID subunit 5
Sapur.005G056400.1	0.006168449	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.084917267	0.278888852		ATSG57462.1		zinc ion binding	NA
Sapur.005G039400.1	0.00578569	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG76300.1			NA
Sapur.005G064400.1	0.006880205	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.105245	0.188432884	GO:0045735	ATSG07750.1		RmlC-like cupins superfamily protein	nutrient reservoir protein, putative
Sapur.005G075100.1	0.00674801	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.23808554	0.002676845	GO:0005634	ATSG64960.1		ARM repeat superfamily protein	condensin-2 complex subunit G2
Sapur.005G053900.1	0.00647127	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0016020;GO:0004970	ATSG14681.1	ATGLR3.6,GLR3.6	glutamate receptor 3.6	glutamate receptor
Sapur.005G071240.1	0.007810412	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG20570.1	ATGAK1,GLK1,GFR11	GAR1's pro-rich region-interacting factor 1	golden-like 1 transcription factor
Sapur.005G020300.3	0.004268021	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0008138;GO:0006470	ATSG21881.1	ATPTP9G1,ATSEB4,DSP4,SE	dual specificity protein phosphatase (DsPTP1) family protein	tyrosine phosphatase, putative
Sapur.005G039800.1	0.005737976	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006412;GO:0005840;GO:0003735	ATSG07735.1	RPS15A	ribosomal protein S15A	40S ribosomal protein S15a
Sapur.005G064300.1	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0003676	ATSG13570.1	SCL30A	SC35-like splicing factor 30A	RNA recognition motif, a.k.a. RRM/RNC RBD protein
Sapur.005G064500.2	0.006346339	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0015757;GO:0016020	ATSG14120.1		Protein of unknown function (DUF804)	transferring glycosyl group transmembrane protein
Sapur.005G059300.2	0.007016761	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG40410.2		Staphylococcal nuclease homologue	Ca(2+)-dependent nuclease
Sapur.005G076600.1	0.004657974	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG76380.1		Ca(2+)-dependent phospholipid-binding protein (Copine) family	E3 ubiquitin-protein ligase RGLG1
Sapur.005G064600.1	0.005674386	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.313819465	6.27E-05		ATSG76380.1		Ca(2+)-dependent phospholipid-binding protein (Copine) family	E3 ubiquitin-protein ligase RGLG1
Sapur.005G087200.2	0.007356884	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG63330.2		DNA binding	hypothetical protein
Sapur.005G078900.1	0.007665737	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0007264;GO:0005525	ATSG10630.1	ARFA1F,ATARFA1F	ADP-ribosylation factor A1F	ADP-ribosylation factor
Sapur.005G078300.1	0.006185738	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.200811063	0.011675554	GO:0016021;GO:0008283;GO:0016020;GO:0005452	ATSG22570.1		HCO3- transporter family	boron transporter
Sapur.005G094900.6	0.00691073	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0030163	ATSG68683.1		Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein	ATP-dependent Clp protease adaptor protein ClpS
Sapur.005G100400.2	0.006144922	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0005515	ATSG68190.1		B-box zinc finger family protein	zinc finger protein, putative
Sapur.005G107300.1	0.005793684	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0005545	ATSG65020.1		EN/ENTH/VHS family protein	clathrin assembly protein, putative
Sapur.005G127000.3	0.005922311	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.133262263	0.095889316		ATSG22810.1		Plant protein of unknown function (DUF828) with plant plecstrin homology-like region	auxin canalization protein
Sapur.005G132000.8	0.00974836	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0003677	ATSG43620.1	TZP	zinc knuckle (CCHC-type) family protein	plus-3 domain protein
Sapur.005G136500.1	0.006517668	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942					hypothetical protein
Sapur.005G146900.1	0.00534877	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0016020	ATSG36085.2		CAAX amino terminal protease family protein	CAAX amino terminal protease family protein
Sapur.005G011800.1	0.005822192	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0005515	ATSG26990.1	ATCSN2,COP12,CSN2,FUS12	proteasome family protein	COP9 signalosome complex subunit
Sapur.005G012700.2	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.309005251	3.38E-07	GO:0005488;GO:0004672	ATSG42620.1	ATNAE1B,DCN1,NEN8	NEDD8 (neural precursor cell expressed, developmentally down-regulated 8) activ	Serine/Threonine-kinase, putative
Sapur.005G017700.5	0.006144922	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG05577.1		Domain of unknown function (DUF966)	DUF966 domain protein
Sapur.005G022400.4	0.006910739	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG40545.1		EN/ENTH/VHS family protein	NA
Sapur.005G071100.3	0.00578569	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0005515	ATSG43740.1		Leucine-rich repeat (LRR) family protein	somatic embryogenesis receptor kinase
Sapur.005G089300.1	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG36800.2	RCE1	RUB1 conjugating enzyme 1	ubiquitin-conjugating enzyme
Sapur.005G100600.7	0.00534877	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.887739268	0.276233973					hypothetical protein
Sapur.005G015500.3	0.005432001	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.229409667	0.003837433		ATSG09020.1	ATSNF4,SNF4	homolog of yeast sucrose nonfermenting 4	AMP-activated kinase, gamma regulatory subunit%2C putative
Sapur.005G022300.2	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.026023939	0.701936289	GO:0005515	ATSG70180.2		Sterile alpha motif (SAM) domain-containing protein	SAM domain (sterile alpha motif) protein
Sapur.005G022500.1	0.00571753	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.110661303	0.167665691		ATSG24120.1	ARL1	ARG2-like 1	chaperone protein DnaJ
Sapur.005G042100.1	0.006806441	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG23570.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif protein
Sapur.005G056400.2	0.003831304	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0007004	ATSG25980.1	MAD2	DNA-binding HORMA family protein	mitotic spindle assembly checkpoint protein MAD2
Sapur.005G079100.1	0.005175753	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.058320734	0.242532383	GO:0015735;GO:0008515;GO:0005887	ATSG02660.1	ATSUC1,ATSUT2,SUC1;SUT1;	sucrose transporter 2	sucrose transport 2
Sapur.005G085900.2	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.354132064	5.36E-06		ATSG70100.1		Chaperone DnaJ-domain superfamily protein	heat shock protein-binding protein, putative
Sapur.005G088700.1	0.005142252	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATSG24910.1	CYP714A1	cytochrome P450, family 714, subfamily A, polypeptide 1	cytochrome P450 family protein
Sapur.005G111900.5	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.342568016	1.12E-05	GO:0005515	ATSG49430.1		WD40/YVTN repeat-like-containing domain;Bromodomain	cytochrome c6; nitrite reductase-like, carboxy-terminal heme protein d1, putative
Sapur.005G119500.1	0.006138519	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG15580.1	APG8B,ATG8I	Ubiquitin-like superfamily	autophagy protein Atg8 ubiquitin-like protein
Sapur.005G122000.1	0.007214977	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.112572674	0.155175564	GO:0008270	ATSG32060.1	TCP2	TBP-associated factor 15	insect RNA-binding protein cabeza-like RNA recognition motif protein
Sapur.005G114100.2	0.006489883	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0016787;GO:0005524;GO:0003677;GO:0005515;GO:0016891;GO:0006396;GO:000452	ATSG03300.1	ATDCL2,DCL2	dicer-like 2	NA
Sapur.005G176500.4	0.003303983	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG39190.2	ATAVH8	Protein kinase superfamily protein	Avr4 domain kinase, putative
Sapur.005G193700.1	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.239892664	0.002476561	GO:0006310;GO:0006281;GO:0006260;GO:0005634;GO:0003677	ATSG18590.1		Nucleic acid-binding, OB-fold-like protein	replication protein A 14 kDa subunit A
Sapur.005G196300.1	0.006520993	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG36230.1		uricase / urate oxidase / uricase 35_kDa_peroxisomal	uricase
Sapur.005G196300.2	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.155454331	0.059834808	GO:0007034	ATSG10640.1	VPS40.1	SNF7 family protein	charged multivesicular body protein
Sapur.005G205600.1	0.007665737	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG61780.1	AtVHP2;2,VHP2;2	pyrophosphate-energized membrane proton pump protein	pyrophosphate-energized membrane proton pump protein
Sapur.005G002700.2	0.007810412	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG66630.1		Protein of unknown function, DUF584	senescence regulator
Sapur.005G028700.2	0.007245688	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG11240.1			nucleolar protein 12, 25 kDa protein
Sapur.005G043900.1	0.006517668	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942					hypothetical protein
Sapur.005G048300.1	0.010368291	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.102475884	0.205177365		ATSG58700.1		Ribosomal L5P family protein	Ribosomal L5P family protein
Sapur.005G053300.1	0.005938202	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.469329276	5.53E-10		ATSG18360.1	TCP2	TCP/BTB/POZ domain-containing protein and PCF transcription factor 2	TCP family transcription factor
Sapur.005G059500.1	0.006346339	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0009378;GO:0006310;GO:0006281	ATSG34560.2		P-loop containing nucleoside triphosphate hydrolases superfamily protein	katanin p60 ATPase subunit A-like protein
Sapur.005G068800.2	0.005876064	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG11110.1			transmembrane protein, putative
Sapur.005G070800.4	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	0.040667229	0.613068887		ATSG78420.2		RING/U-box superfamily protein	RING E3 ubiquitin ligase
Sapur.005G074500.1	0.006185738	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006303;GO:0006403;GO:0003677;GO:0043564;GO:0042162;GO:0005634;GO:0003968	ATKU70;KU70	KU70 homolog	KU70 homolog	ATP-dependent DNA helicase 2 subunit KU70
Sapur.005G091600.2	0.006582233	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0005789	ATSG54130.1	ATMAMR,MAMR	membrane-associated mannitol-induced	vesicle-associated protein
Sapur.005G033000.1	0.005142252	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0008270;GO:0005515	ATSG37730.1	NIP2	NEP-interacting protein 2	RING finger protein
Sapur.005G105800.5	0.006346339	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG12940.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	hypothetical protein
Sapur.005G115500.2	0.00653009	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0006355;GO:0006677	ATSG30660.2	ANAC014,NAC014	NAC 014	NAC transcription factor
Sapur.005G115800.4	0.005413201	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.024891796	0.756980076	GO:0006468;GO:0005524;GO:0004674;GO:0004672	ATSG41550.1		AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	Serine/Threonine-kinase-like protein
Sapur.005G120400.1	0.007214977	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0003677	ATSG21550.1	VAL3	VP1/ABI3-like 3	NA
Sapur.005G029500.1	0.005807273	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.383052191	8.50E-07		ATSG37110.1		Zinc finger domain of monoamine-oxidase A repressor R1	monoamine-oxidase A repressor R1 zf-MCMX-R1: zinc-finger protein
Sapur.005G039800.2	0.010604675	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0003677;GO:0046983	ATSG18560.1		BED zinc finger /MAT family dimerization domain	AC transposase, putative
Sapur.005G046900.3	0.00450009	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG18720.1	NDI6	NDH dependent flow 6	NDH dependent flow 6 protein
Sapur.005G058900.2	0.00627286	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0008270;GO:0005515	ATSG47990.1	SIS3	SUGAR-INSENSITIVE 3	zinc finger, C3HC4 type (RING finger) protein
Sapur.005G061500.1	0.006185738	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0003676				NA
Sapur.005G066100.2	0.005961666	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0016787	ATSG24730.2		Calcineurin-like metallo-phosphoesterase superfamily protein	manganese-dependent ADP-ribose/CDP-alcohol diphosphatase
Sapur.005G003100.1	0.00450009	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942					NA
Sapur.005G042900.1	0.003303983	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG08640.1	CID1	Chlorophyll 2-like domain 1	heat shock protein-binding protein
Sapur.005G043800.5	0.006423571	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.039499011	0.623333202		ATSG10095.1		Protein prenylyltransferase superfamily protein	protein prenyltransferase, alpha subunit
Sapur.005G064800.1	0.006579921	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG39110.1		RmlC-like cupins superfamily protein	germin 1_putative
Sapur.005G067900.2	0.005749346	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.08993023	0.296140004	GO:0003723;GO:0003676;GO:0006402;GO:0004654	ATSG07310.1	PNLP,RIF10	polyribonucleotide nucleotidyltransferase, putative	polyribonucleotide nucleotidyltransferase
Sapur.005G103900.2	0.006947217	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942	GO:0017179;GO:0006396;GO:0003723	ATSG25610.1		Pathogenic and nodulation factor response family protein	tRNA nucleotidyltransferase/polyribonucleotide nucleotidyltransferase family protein
Sapur.005G108100.1	0.00571753	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG34245.1	EPI2	Putative membrane lipoprotein	epidermal patterning factor 2, putative
Sapur.005G118900.1	0.00653968	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942					NA
Sapur.005G136800.4	0.006579915	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG58450.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR repeat protein R12/RL10; putative
Sapur.005G143400.1	0.006185738	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.018018864	0.309590942		ATSG62050.2		oxidoreductase	2OG-Fe(II) oxygenase family protein
Sapur.005G025700.4	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.245139853	0.001972087	GO:0005886;GO:0016020;GO:0006810;GO:0005215	ATSG26510.1	PDE115	Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.005G038000.3	0.005144485	0.055357013	2.904824396	0.01913	0.984737169	NA	NA	grey	-0.113458411

Sapur.004G074700.2	0.16053609	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.21687463B	0.006366827	GO:0008270;GO:0006281	ATSG05055.1	ATGTF2H2,GTF2H2	general transcription factor II H2	general transcription factor IIH subunit
Sapur.008G018300.1	0.01790615	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.06561423	0.41424608		ATSG10030.1		aspartate/glutamate/uridylate kinase family protein	uridylate kinase
Sapur.008G101100.3	0.01780689	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.06503973	0.41834815	GO:0006659	ATSG11110.1		phosphatidyl serine synthase family protein	phosphatidylserine synthase
Sapur.003G113200.6	0.01679436	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.11738802	0.14383	GO:0006281;GO:0003684	ATSG44740.2	PDLH	Y-family DNA polymerase H	DNA polymerase eta
Sapur.015G067300.1	0.01808205	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.06821912	0.38591347		ATSG52605.1		Defensin-like (DEFL) family protein	defensin-like protein
Sapur.002G181300.2	0.01510989	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.05482639	0.51277046	GO:0043195;GO:0006810	ATSG19800.1	TGD1	trigalactosyldiacylglycerol 1	ER-derived-lipid transporter permease subunit
Sapur.004G180900.1	0.01923015	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.07209155	0.37627829		ATSG23282.1		TCP family transcription factor	NA
Sapur.U15W0283.1	0.01508704	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.05758095	0.47374053					NA
Sapur.T047000.1	0.01729625	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.20510482	0.09948465	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATSG05160.1	ATKAO1,CYP88A3,AKO1	cytochrome P450, family 88, subfamily A, polypeptide 3	Ent-kaurenoic acid oxidase
Sapur.T122600.1	0.01559268	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.06641107	0.48284601					NA
Sapur.001G047300.2	0.01474357	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.51728182	4.01E-12		ATKC14140.1		alpha/beta-Hydrolases superfamily protein	alpha/beta fold hydrolase
Sapur.001G179400.1	0.01947943	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.05206904	0.53406745		ATGU7382.1		F-box/RNI-like superfamily protein	cyclin-like F-box protein, putative
Sapur.013G070700.2	0.01445858	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.15671255	0.04998573	GO:0006432;GO:0005524;GO:0000372;GO:0000287;GO:0004826	ATSG72550.1		tRNA synthetase beta subunit family protein	phenylalanyl-tRNA synthetase beta chain, putative
Sapur.003G117200.1	0.01534283	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.07207546	0.28483153	GO:0055114;GO:0006236	ATSG72540.2	AGDH,DCP11	Arginosuccinase family protein	eukaryotic translation initiation factor 2c, putative
Sapur.016G189800.5	0.01802356	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.13018907	0.10414913	GO:0016747	ATSG41120.1		Esterase/lipase/thioesterase family protein	esterase/lipase/thioesterase family protein
Sapur.004G284300.2	0.01492571	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.11485542	0.15231053	GO:0048359;GO:0016020	ATSG28480.1	ATSYNF6,OSM1,SYR6.1	syntaxin of plants 61	syntaxin 61 protein
Sapur.004G142500.2	0.01612862	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.06339051	0.44098627		ATSG22740.1	ATCSLA02,ATCSLA2,CSLA02	cellulose synthase-like A02	glucomannan 4-beta-mannosyltransferase
Sapur.003G092300.3	0.01626972	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.04947234	0.53839767	GO:0046983	ATSG41215.1	G,3,MYC6.2	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Myc-like anthocyanin regulatory protein
Sapur.015G284300.1	0.01504289	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.06139969	0.44998982	GO:0005515	ATSG22681.1	ARR,PTZ,RLP22	receptor like protein 22	receptor-like kinase, putative
Sapur.004G139900.2	0.01800299	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.09324289	0.24543016		ATSG39150.2		DNA/ heat shock N-terminal domain-containing protein	Dnaj heat shock amino-terminal domain protein
Sapur.014G033100.1	0.01317513	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.04150429	0.65760241	GO:0042274	ATSG60120.1		Uncharacterized protein family (UPF0150)	NA
Sapur.014G137300.1	0.01764231	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.15711705	0.04940185		ATSG07700.1		Protein kinase superfamily protein	ABC1 family protein
Sapur.016G115700.1	0.01688931	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.07041676	0.38837015	GO:0055114;GO:0016491	ATSG44190.1		FAD/NAD(P)-binding oxidoreductase family	NA
Sapur.016G042100.2	0.01558108	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.06800285	0.39743337	GO:0030915;GO:0006281;GO:0005634	ATSG51130.1		N-oxal, component of SmcS/C-DNA repair complex	Non-structural maintenance of chromosome element protein, putative
Sapur.004G095200.2	0.01686615	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.05580054	0.48842483	GO:0055114;GO:0016491;GO:0010181	ATSG52520.2		Flavodoxin family protein	NADPH-dependent diflavin oxidoreductase
Sapur.009G021700.1	0.01502331	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.07006913	0.18192026	GO:0006355;GO:0003677	ATSG53570.1	OBP3	DBF-binding protein 3	F-box protein
Sapur.016G219800.1	0.01611298	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.08210152	0.39275795	GO:0006468;GO:0005524;GO:0004672	ATMKK2,MKK3		mitogen-activated protein kinase kinase 3	dual specificity MAP kinase kinase
Sapur.005G146100.1	0.01508539	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.07930246	0.34460328	GO:0055114;GO:0050661;GO:0050660;GO:0004499	ATG14100.1	YUC11	Flavin-binding monooxygenase family protein	flavin-containing monooxygenase family protein
Sapur.017G009500.1	0.01665754	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.08095	0.31868161	GO:0005525;GO:0003924	ATSG46070.1		Guanylate-binding family protein	interferon-induced guanylate-binding protein, putative
Sapur.002G005100.1	0.01395753	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.04446661	0.58027614	GO:0005515	ATSG42150.1		Galactose oxidase/kelch repeat superfamily protein	F-box/kelch-repeat plant protein
Sapur.T123600.1	0.01452546	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.08237861	0.35593374		ATSG54750.1			NA
Sapur.005G131100.1	0.01518865	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.08702827	0.27844584	GO:0016787;GO:0005634;GO:0003677;GO:0006355;GO:0005634	ATSG46520.2	ATBRM,BRM,CHR2,CHR2	transcription regulatory protein SNF2, putative	ATP-dependent helicase BRM
Sapur.013G067900.1	0.01474279	0.35171484	2.904823276	0.0184693	0.98524595	NA	grey	grey	-0.08160864	0.30959042	GO:0003723;GO:0006476;GO:0006402;GO:0004654	ATSG07330.1	PN-RIP10	polyribonucleotide nucleotidyltransferase, putative	polyribonucleotide nucleotidyltransferase
Sapur.004G138300.3	0.08883756	0.20484679	1.5457489	0.0157114	0.98619742	NA	grey	grey	-0.07024326	0.35025429	GO:0072344;GO:0005525	ARFA1E,ATARFA1E	ARFA1E,ATARFA1E	ADP-ribosylation factor A1E	ADP-ribosylation factor/Arf/Sar-like (Arf) small GTPase family protein
Sapur.T082200.1	0.06395369	0.20496073	1.55794365	0.017011	0.98647533	NA	grey	grey	-0.04063455	0.61337786					NA
Sapur.T055600.1	0.03863317	0.20496073	1.57124885	0.016843	0.98651934	NA	grey	grey	-0.09380984	0.21869865		ATSG47550.2			NA
Sapur.T123200.1	0.08612905	0.20498145	1.57331252	0.016842	0.98652432	NA	grey	grey	-0.06546784	0.41528721					NA
Sapur.010G005200.2	0.02834993	0.04541287	2.69939784	0.016823	0.98657755	NA	grey	grey	-0.07568835	0.34611049	GO:0006355;GO:0003700	ATG16770.1	ATERF,ERF27,ERF2.2	ethylene-responsive element binding protein	ethylene response factor 2
Sapur.004G017000.3	0.01547345	0.04796195	2.90483945	0.016821	0.98658766	NA	grey	grey	-0.09573136	0.23003141		ATMG01360.1	B1,BCH1,BETA-CHASE 1,chs	beta-hydroxylase	beta-carotene hydroxylase
Sapur.019G001500.1	0.04757598	0.05274366	1.54800788	-0.01633	0.98697334	NA	grey	grey	-0.08182243	0.28767579		ATSG25320.1	smr (Small MutS Related) domain-containing protein		Smr protein/MutS2 carboxy-terminal protein, putative
Sapur.003G164300.1	0.06035854	0.03878529	1.87770302	0.01351	0.98775238	NA	grey	grey	-0.3233922	3.58E-05		ATSG20330.1			hypothetical protein
Sapur.005G068800.2	0.03571819	0.03730324	1.88072238	0.015276	0.98781188	NA	grey	grey	-0.08603429	0.28602294	GO:0005515	ATSG09660.2	EMB2107,MSA,RPN5A	26S proteasome regulatory subunit, putative (RPN5)	26S proteasome non-ATPase regulatory subunit
Sapur.005G087700.1	0.04446604	0.03730324	1.88687611	0.01527	0.98781188	NA	grey	grey	-0.07023301	0.38210681		ATMG01010.1	ATOMA9,OMA9	mitochondrial 9 kDa protein	NA
Sapur.003G161900.1	0.04332435	0.04179267	2.74634592	-0.01521	0.98786195	NA	grey	grey	-0.11982637	0.13498216	GO:0006355;GO:0003700	ATSG50680.1		AP2/B3 transcription factor family protein	AP2 domain transcription factor
Sapur.001G025400.1	0.04869755	-0.02528132	1.67745637	-0.01502	0.98801402	NA	grey	grey	-0.06488052	0.35667647		ATSG40860.1		Transducin/WD40 repeat-like superfamily protein	DUF2358 family protein
Sapur.003G072100.1	0.03576337	0.02876088	2.07743624	0.01805	0.98861742	NA	grey	grey	-0.35861312	3.96E-06	GO:0005089	ATSG31650.1	ATROPGEF14,ROPGEF14	RHO guanyl-nucleotide exchange factor 14	Rop guanine nucleotide exchange factor, putative
Sapur.004G089400.1	0.03562789	0.02874183	2.06620707	0.01748	0.98863218	NA	grey	grey	-0.06477846	0.42022611		ATSG31881.1			NA
Sapur.016G174600.2	0.02828339	0.02876793	2.09536264	0.01717	0.98905872	NA	grey	grey	-0.17826529	0.02548876	GO:0072364;GO:0005525	ATSG48870.1	ARL4,LC,ATARL4,LC	ADP-ribosylation factor-like A1C	ADP-ribosylation factor-like protein
Sapur.002G043300.1	0.04742904	-0.02531315	1.83684623	-0.01366	0.98910134	NA	grey	grey	-0.08429716	0.28253257					NA
Sapur.005G040400.6	0.02768359	0.02879398	2.14748466	0.01385	0.98920667	NA	grey	grey	-0.30136104	0.00015354					hypothetical protein
Sapur.006G030800.1	0.02663349	0.03059593	2.19115707	0.01248	0.98969516	NA	grey	grey	-0.07016559	0.37678167	GO:0046983;GO:0003677	ATSG58370.1	BHLH038,ORG2	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor ORG2, putative
Sapur.014G051400.4	0.02663364	0.03069944	2.19152088	0.01248	0.98969516	NA	grey	grey	-0.12275564	0.12573476		ATSG52230.1		Protein of unknown function (DUF1232)	DUF1232 family protein
Sapur.008G052400.3	0.02604763	0.03060077	2.3072811	0.012915	0.98985898	NA	grey	grey	-0.0899116	0.3627718	GO:0006508;GO:0004222	ATSG5740.2	ATEGF2,EGV2	ethylene-dependent gravitropism-deficient and yellow-green-like 2	ethylene-dependent gravitropism-deficient and yellow-green-like protein
Sapur.003G081800.1	0.02605005	0.03060092	2.30793187	0.012911	0.98986864	NA	grey	grey	-0.06016497	0.44383264					NA
Sapur.005G111700.2	0.02466879	0.03060419	2.41238745	0.01284	0.98990285	NA	grey	grey	-0.0619812	0.44107469					PWWP domain protein
Sapur.005G085500.1	0.02388184	0.03060618	2.43132263	0.012787	0.98993804	NA	grey	grey	0.06405611	0.42546856		ATSG18900.2		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.001G066100.1	0.02378544	0.03060642	2.42248213	0.012781	0.98992735	NA	grey	grey	-0.09202789	0.25162887	GO:0008270;GO:0005515	ATSG07100.2		RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.007G026400.1	0.02241271	0.03060783	2.42890526	0.012747	0.98982794	NA	grey	grey	-0.09127839	0.25584472					NA
Sapur.003G051400.1	0.02240591	0.03060984	2.43132469	0.012731	0.98984722	NA	grey	grey	-0.08488558	0.29684129	GO:0006468;GO:0005524;GO:0004672	ATSG53050.1		Protein kinase superfamily protein	cyclin-dependent kinase-like Serine/Threonine kinase family protein
Sapur.017G042900.1	0.02261028	0.03061004	2.43912884	0.012693	0.98987226	NA	grey	grey	-0.1024719	0.20305136	GO:0006355;GO:0003700	ATSG80580.1		Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.010G097400.1	0.04072771	0.03061256	2.83907958	0.01042	0.99053192	NA	grey	grey	-0.03267062	0.83471798		ATSG39150.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	hypothetical protein
Sapur.010G012300.2	0.02193849	0.03061274	2.45193938	0.012627	0.98995134	NA	grey	grey	-0.23778546	0.00271151	GO:0006468;GO:0005524;GO:0004672	ATSG19010.1	MPK16	mitogen-activated protein kinase 16	MAP kinase
Sapur.005G134700.1	0.02117822	0.03061339	2.45492575	0.012612	0.98997399	NA	grey	grey	-0.09927637	0.21581337		ATSG56320.1	ARFA1F,ATARFA1F	ADP-ribosylation factor A1F	Arf ADP-ribosylation factor, putative
Sapur.014G136900.1	0.04193789	0.02370289	1.85362534	-0.01255	0.98983673	NA	grey	grey	-0.09239413	0.24549278	GO:0016020;GO:0015979;GO:0009539;GO:0009523	ATCG00680.1		photosystem II reaction center protein I	photosystem II reaction center protein I
Sapur.010G077300.1	0.04050818	0.02368228	1.85041329	-0.01251	0.98985746	NA	grey	grey	-0.13152147	0.09648059					NA
Sapur.004G044600.5	0.04042172	-0.02368228	1.85975976	-0.01251	0.98001737	NA	grey	grey	-0.10131709	0.20674879	GO:0006468;GO:0004672	ATSG29730.1		Leucine-rich repeat transmembrane protein kinase	tyrosine kinase domain protein
Sapur.006G180300.10	0.03708677	-0.02328284	1.8627649	-0.01249	0.98004205	NA	grey	grey	-0.07919325	0.32087533		ATSG57260.1	RIP3	ROP interactive peptide 3	Interactor of constitutive active ROPs protein
Sapur.001G133300.1	0.03964784	-0.02366956	1.86201547	-0.01249	0.99003573	NA	grey	grey	-0.08283576	0.3023691	GO:0043565;GO:0006355;GO:0003700	ATSG28735.2	AtbZIP62,BZO2H3	bZIP transcription factor family protein	bZIP transcription factor
Sapur.005G138500.2	0.03947348	-0.02366893	1.86750388	-0.01248	0.99003695	NA	grey	grey	-0.21808415	0.00275845		ATCRY1,BLU1,CRY1,HYH,OC	cryptochrome 1	cryptochrome 1	cryptochrome protein
Sapur.009G058400.2	0.03899984	-0.02366582	1.86407744	-0.01248	0.99004424	NA	grey	grey	-0.10757412	0.17989269	GO:0006357;GO:0043565;GO:0006355;GO:0003700	ATHB6,HB6		homeobox protein 6	homeobox leucine zipper protein
Sapur.002G164500.2	0.03775674	-0.02364066	1.87127928	-0.01243	0.99008817	NA	grey	grey	-0.0934922	0.24443041	GO:0006396;GO:0004526	ATSG47300.3		ribonuclease P/MRP protein subunit POP1, putative	ribonuclease P/MRP protein subunit POP1, putative
Sapur.006G230700.4	0.03600749	-0.02361279	1.87936107	-0.01238	0.99014498	NA	grey	grey	-0.07504546	0.34631319	GO:0006468;GO:0004672	ATSG31730.1		Protein kinase superfamily protein	Serine/Threonine/tyrosine kinase, putative
Sapur.003G131900.1	0.03042163	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.0619817	0.41407469		ATSG61490.2		Pectin lyase-like superfamily protein	glycosyl hydrolase family 28 protein
Sapur.004G156400.1	0.03037317	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	0.06445766	0.23935218	GO:0032012;GO:0005886	ATSG38020.1		SCF1-like guanine nucleotide exchange factor family protein	brefeldin A-inhibited guanine nucleotide-exchange protein
Sapur.005G184800.2	0.03012617	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.3193206	0.19524321	GO:0004457;GO:0003755;GO:0000413	ATSG57530.1	ATPUB48,PUB48	plant U-box 49	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.003G180500.1	0.03002706	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.17981102	0.02422583	GO:0005515	ATSG50680.1		GET domain-containing protein	ribulose-1%2C5-bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, putative
Sapur.009G025900.1	0.01252257	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.35897963	3.90E-06	GO:0003723	ATPUM2,PUM2	pumilio 2	pumilio 2	pumilio protein, putative
Sapur.006G081300.1	0.00957761	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.07391646	0.37074597					hypothetical protein
Sapur.015G148800.1	0.01602188	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.10591629	0.18675947		ATSG40095.1		Alpha/beta hydrolase related protein	alpha/beta hydrolase-like protein
Sapur.015G012300.2	0.01353275	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.07864531	0.3261497		ATSG24010.1	HT1	Protein kinase superfamily protein	Serine/Threonine-kinase HT1
Sapur.U12G018500.4	0.01667934	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.10708622	0.16584767	GO:0055085;GO:0016021	ATSTR6.1,PIN1	Auxin efflux carrier family protein	auxin efflux carrier PIN protein	cysteine-rich secretory family protein
Sapur.016G175500.1	0.01430383	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.10491454	0.19098301		ATSR8G1,PR8E1	basic pathogenesis-related protein 1		multidrug resistance protein, putative
Sapur.010G096000.3	0.01328167	0.03318256	2.90483918	0.01243	0.99085729	NA	grey	grey	-0.10700394	0.18169794	GO:0055085;GO:0016020;GO:0015297;GO:0015238;GO:0008855	ATSG26120.1		MATE efflux family protein	multidrug resistance protein, putative
Sapur.016G058900.1	0.04249882	0.03221203	2.04285022	-0.01137	0.99039159	NA	grey	grey	-0.0929291	0.24707135	GO:0006281;GO:0003678;GO:0000723	ATSG28780.1		PIF1 helicase	ATP-dependent DNA helicase PIF1, putative
Sapur.004G129600.1	0.04164833	0.03221203	2.06066095	-0.01126	0.99101268	NA	grey	grey	-0.07231502	0.38914082					NA
Sapur.004G039400.2	0.03857032	0.02307097	2.06192052	-0.01126	0.99103851	NA	grey	grey	-0.12441287	0.13054846		ATSG42632.2	LSH10	Protein of unknown function (DUF640)	DUF640 family protein
Sapur.007G095600.1	0.03750158	0.02307097	2.06192052	-0.01126	0.99103851	NA	grey	grey	-0.11451024	0.15125252					NA
Sapur.003G045200.2	0.02301166	0.00966302	2.76638757	0.011194	0.99188852	NA	grey	grey	-0.36030275	3.57E-06	GO:0008168;GO:0006479	ATSG16570.1	ATPRMT7,PRMT7	protein arginine methyltransferase 7	arginine N-methyltransferase
Sapur.007G100500.2	0.04655577	-0.02301382	2.08457088	-0.01113	0.99119696	NA	grey	grey	-0.35828832	4.73E-06		ATSG16880.1	PEPKR2	phosphoenolpyruvate carboxylase-related kinase 2	transcription factor jumonji (jmj) domain-containing protein
Sapur.012G088200.2	0.03545746	-0.02338163	2.0978971	-0.01106	0.99137577	NA	grey	grey	-0.02895736	0.78442189		ATSG29120.1		transcription factor jumonji (jmj) domain-containing protein	trans-specific dimethylase 34-8, putative
Sapur.008G161100.2	0.02022618	0.00966858	2.81784889	0.011005	0.99129136	NA	grey	grey	-0.07287871	0.36436761	GO:0055114;GO:0016491;GO:0006633;GO:0003857	ATMFP2,MFP2	multifunctional protein 2	multifunctional protein 2	glycosomal fatty acid beta-oxidation MFP-A protein
Sapur.009G029200.1	0.04292934	0.01947434	1.85898139	0.01057	0.99164481	NA	grey	grey	-0.0914138	0.26432603		ATSG36570.1		Tetratricopeptide repeat (TPR)-like superfamily protein	plant/FYVE02-22 protein, putative
Sapur.010G126600.1	0.03717248	0.02315783	2.31001826	-0.01002	0.99200752	NA	grey	grey	-0.11824138	0.14261887	GO:0055114;GO:0003676	ATSG69440.1	AGOT,ZIP	Argonaute family protein	argonaute protein
Sapur.006G173200.2	0.03503138	0.02315138	2.12378634	-0.00996	0.99205975	NA	grey	grey	-0.10232471	0.19826429		ATSG26220.1		transmembrane protein family protein	transmembrane protein, putative
Sapur.017G112400.1	0.03181708	0.02314871	2.34200708	-0.00988	0.99211192	NA	grey	grey	0.26784757	0.00096239	GO:0043531	ATSG14470.1	NB-ARC domain-containing disease resistance protein	NB-ARC domain-containing protein	CC-NBS-LRR resistance protein
Sapur.003G117300.2	0.04257451	-0.02180709	2.20054828	-0.00939	0.99239171	NA	grey	grey	-0.06827944	0.91801042					hypothetical protein
Sapur.015G184800.1	0.03462946	-0.02129793	2.32158625	-0.00917	0.99268152	NA	grey	grey	-0.1294781	0.10605579		ATSG52480.1			hypothetical protein
Sapur.006G140300.1	0.03483352	-0.02129793	2.32688926	-0.00916	0.99269042	NA	grey	grey	-0.07517329	0.34642655	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATKA,CYP83B1,AKD1,RNT1,1	cytochrome P450, family 83, subfamily B, polypeptide 1	cytochrome P450, family 83, subfamily B, polypeptide 1	NA
Sapur.007G089400.4	0.03167821	-0.02129821	2.34467278	-0.00908	0.99275381	NA	grey	grey	-0.29355164	0.00019459	GO:0055114;GO:0016491	ATSG08740.1	NDC1	NAD(P)H dehydrogenase C1	NAD(P)H dehydrogenase
Sapur.T171500.1	0.03164959	-0.02129772	2.34696346	-0.00908	0.99275795	NA	grey	grey	-0.12404872	0.12627522					NA
Sapur.003G134100.1	0.02946562	-0.02126629	2.36387764	-0.00901	0.99281824	NA	grey	grey	-0.1248171	0.19189995		ATSG42040.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	haloacid dehalogenase-like hydrolase
Sapur.016G108200.2	0.02027562	-0.02126081	2.36607581	-0.009	0.99283613	NA	grey	grey	-0.03261829	0.68690674	GO:0043565	ATSG03780.1		Transfin family protein	transfin-associated factor X
Sapur.005G091200.2	0.02782684	-0.02118764	2.38136868	-0.00884	0.99286715	NA	grey	grey	-0.1166025	0.14563676	GO:0006355;GO:0003677	ATSR6G0.1	ANACS37,VND1	vascular related NAC-domain protein 1	NAC transcription factor
Sapur.016G043900.2	0.02696606	-0.02128679	2.38786173	-0.00891	0.99288047	NA	grey	grey	-0.3059141	9.94E-05	GO:0005515	ATSG7880.1		Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein	anthranilate phosphoribosyltransferase-like protein
Sapur.018G064300.1	0.02854501	-0.02134589	2.69545868	-0.00788	0.99370383	NA	grey	grey	-0.10270649	0.19585285					NA
Sapur.007G021200.1	0.02729376	-0.02145463	2.70635007	-0.00785	0.99373576	NA	grey	grey	-0.10860898	0.17793191	GO:0005524	ATSG18330.1		AAA-type ATPase family protein	AAA-type ATPase family protein
Sapur.015G060700.4	0.02368609	-0.02224423	2.71778025	-0.00762	0.99379522	NA	grey	grey	-0.13631229	0.08908134	GO:0006810	ATSG43150.1			neurotransmitter-amino acid transporter protein
Sapur.016G124900.3	0.02595289	-0.02243684	2.72032854	-0.0078	0.99377583	NA	grey	grey	-0.11269333	0.15892273		ATSG51180.1	AXR1	NAD(P)-binding Rossmann-fold superfamily protein	NEDD8-activating enzyme E1 regulatory subunit
Sapur.010G088500.1	0.02823355	-0.02263447	2.72532816	-0.00779	0.99378581	NA	grey	grey	0.00904758	0.94194347	GO:0006468;GO:0005524;GO:0004672	ATSG10730.1		Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.015G000900.2	0.02508933	-0.02342277	2.73579266	-0.00776	0.99389706	NA	grey	grey	0.07536637	0.34817671	GO:0005515;GO:0006508	ATSG68610.1	CYP98A6	Ribosomal protein S7 family protein	ATP-dependent Clp protease adaptor protein ClpS family protein
Sapur.008G137000.1	0.02418611	-0.02416104	2.74922936	-0.00773	0.99383453	NA	grey	grey	-0.05659188	0.48171452	GO:0016020;GO:0005509;GO:0004571	ATSG43710.1		Glycosyl hydrolase family 47 protein	alpha-mannosidase, putative
Sapur.013G017800.1	0.02418352	-0.02429733	2.75239878	-0.00772	0.99384134	NA	grey	grey	-0.43943848	8.52E-09	GO:0008386;GO:0000077;GO:0006281	ATSG45480.1	ATRAD9,RAD9	cell cycle checkpoint control protein family	Rad9 protein
Sapur.004G180900.4	0.01617821	-0.02495218	2.43434185	-0.00767	0.99388277	NA	grey	grey	-0.11489862	0.15321367		ATSG21800.1	QDT2	Protein kinase superfamily protein	GPN-loop GTPase-like protein
Sapur.008G184700.1	0.01767230	-0.02512625	2.30483276	-0.00762	0.99391578	NA	grey	grey	-0.09224006	0.24309894	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATSG49490.1	CYP98A6	Ribosomal protein S7, subfamily A, polypeptide 6	cytochrome P450 family protein
Sapur.013G058500.10	0.02496298	-0.02512625	2.30483276	-0.00731	0.99419578	NA	grey	grey	-0.02278792	0.77752542	GO:0005085;GO:0016020;GO:0006810;GO:0005215	ATSG42890.1		Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.004G180200.1	0.02617205	-0.02512625	2.30483276	-0.00731	0.99419578	NA	grey	grey	-0.14407215	0.07870172	GO:0016556;GO:0005759	ATSG42740.3	PEX11D	peroxin 11D	peroxisomal biogenesis factor 11
Sapur.012G036800.5	0.02184005	-0.02512625	2.30483276	-0.00731	0.99419578	NA	grey	grey	-0.05838243	0.46763247		ATSG15060.1		Uncharacterised conserved protein UCP031088, alpha/beta hydrolase	alpha/beta hydrolase family protein
Sapur.015G090600.1	0.02012469	-0.02512625	2.30483276	-0.00731	0.99419578	NA	grey	grey	-0.0684542	0.3642521	GO:0046872	ATSG68830.1		Zinc finger C-x8-C-x5-C-x3-H type family protein	zinc finger protein, putative
Sapur.007G039000.1	0.02019368	-0.02512625	2.30483276	-0.00731	0.99419578	NA	grey	grey	-0.4887384E5	8.37E-11		ATSG67620.1			DUF4228 domain protein
Sapur.018G028800.2	0.04685648	0.02172719	1.68075937	0.007382	0.99417429	NA	grey	grey	-0.08117705	0.31216645		ATSG07950.1			stellacyanin, putative
Sapur.T186800.1	0.04568713	0.02172719	1.68451284	0.007367	0.99418082	NA	grey	grey	-0.06019266	0.41723872					NA
Sapur.001G047300.1	0.06326751	0.01227511	1.68557828	0.007282	0.99418949	NA	grey	grey	-0.07176605	0.33670377		ATSG08391.1		Protein of un

Sapur.006G026100.3	0.01157923	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.042937042	0.593378396	GO:0006508,GO:0004185		CAZ28110.2	SCP1/45	serine carboxypeptidase
Sapur.006G026100.2	0.01006764	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115527053	0.149483227	GO:0006508,GO:0004185		CAZ28110.1	SCP1/45	serine carboxypeptidase
Sapur.006G089100.2	0.01349681	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.018108864	0.309509042			CAZ26830.1	emb1187	Protein kinase superfamily protein
Sapur.006G103900.1	0.010228969	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	0.359768118	3.706-06			CAZ37025.2	TRF1B	Myb-like DNA-binding domain protein
Sapur.006G140000.1	0.010228969	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.118808279	0.140328469			CAZ28303.2		metal-dependent phosphohydrolase HD domain protein
Sapur.006G164200.2	0.013769757	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.081608864	0.309509042			CAZ06448.2		START domain protein, putative
Sapur.006G196200.1	0.01271707	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115452803	0.149091668	GO:0003677,GO:0008289		CAZ32880.1	ATHB-8,ATHB8,HB-8	homeobox leucine zipper protein ATHB-15
Sapur.006Z100001.1	0.011101	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115234412	0.155575689			CAZ12700.1		ATP binding;nucleic acid binding;helicases
Sapur.006G230400.2	0.011915702	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.114565646	0.153111207	GO:0006468,GO:0004672		CAZ01170.3		Protein kinase superfamily protein
Sapur.007G025900.1	0.010847212	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.114755974	0.15225121	GO:0003824		CAZ56720.1		Protein phosphatase 2C family protein
Sapur.007G059500.1	0.010190027	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.114402204	0.153606373					
Sapur.008G086000.4	0.013157574	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.112791919	0.155929692			CAZ16146.1		cAMP-regulated phosphoprotein 19-related protein
Sapur.008G155100.2	0.009469188	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.00785256	0.922436686	GO:0008168,GO:0008033,GO:0006364,GO:0003723		CAZ52470.1	ATFIB8,LATFIB3,FIB3,FIB1.5	fibrillarin 1
Sapur.008G165200.1	0.010452214	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.231226497	0.05017516	GO:0005515		CAZ70180.2		Sterile alpha motif (SAM) domain-containing protein
Sapur.008G156700.1	0.009705285	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.46070893	1.27E-09			CAZ70703.1		5'(-AMP-activated kinase-like protein, putative
Sapur.009G261100.2	0.013545319	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.081608864	0.309509042	GO:0003676		CAZ19192.1		RNA-binding(RRM/RBD/RNP motifs) family protein
Sapur.009G048000.4	0.010293188	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.109368324	0.172717359	GO:0008270,GO:0005515		CAZ63530.2	BB,BB2	RING/U-box superfamily protein
Sapur.009G068800.3	0.010014341	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115461726	0.149869966	GO:0005975,GO:0004553		CAZ33840.1		Glycosyl hydrolase family protein
Sapur.009G094000.2	0.013560345	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115634412	0.15575689			CAZ21520.1		Sec14-like phosphatidylinositol transfer protein
Sapur.009G119000.2	0.010228969	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.081608864	0.309509042	GO:0030131,GO:0016192,GO:0006886,GO:0030117		CAZ32780.1		Adaptor protein complex AP-2, alpha subunit
Sapur.010G004600.1	0.009600581	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.081608864	0.309509042			CAZ61600.1		hypothetical protein
Sapur.010G013100.2	0.012344827	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.062583606	0.436178848			CAZ61470.1		transmembrane BAX inhibitor motif protein
Sapur.010G019600.1	0.01003829	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.223882826	0.05195723			CAZ60302.1	CIPK-L	CIPK1-interacting protein 4.1
Sapur.010G028000.7	0.01203369	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.061583729	0.443353354	GO:0005975,GO:0004650		CAZ60590.1		Pectin lyase-like superfamily protein
Sapur.010G076200.2	0.011562606	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.01913437	0.88227386			CAZ17960.1		Threonyl-tRNA synthetase
Sapur.010G124700.7	0.01102181	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.0194217	0.809230847	GO:0005515,GO:0003677		CAZ03390.1		uvrB/uvrC-motif-containing protein
Sapur.010G138200.2	0.012710002	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115263537	0.148807802			CAZ79270.1	ECT8	evolutionarily conserved C-terminal region 8
Sapur.010G149000.1	0.010687277	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.28697312	5.54E-07	GO:0055114,GO:0020037,GO:0016705,GO:0005506		CAZ05690.1	CBB1,CPD,CYP80,CYP80A,C	Cytochrome P450 family 90 monooxygenase, putative
Sapur.010G149100.3	0.009387076	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.335157456	1.96E-05	GO:0006355,GO:0005634,GO:0003700,GO:0003677		CAZ51880.2	HMGB1,NFD1	High mobility group B1
Sapur.010G157601.1	0.010488311	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.11923677	0.160389922					
Sapur.010G202000.4	0.011568711	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.113866778	0.15251865			CAZ11430.1		plastid developmental protein DAG, putative
Sapur.010G231200.2	0.011197	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115263412	0.155575689	ATSOT16,ATSTSA,COR-7,SC		CAZ76100.1		flavonol 3-sulfotransferase, putative
Sapur.011G107500.2	0.013644416	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115757568	0.148832535	GO:0003677		CAZ17430.1		ARID/BRIGHT DNA-binding domain-containing protein
Sapur.011G122100.2	0.009600581	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.081608864	0.309509042			CAZ32820.1		Protein of unknown function (DUF1269)
Sapur.011G014900.1	0.01156928	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115771364	0.148770084					
Sapur.011G031300.1	0.011012547	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.05008079	0.486760065	GO:0008270		CAZ80550.1		Cytidine/deoxycytidylate deaminase family protein
Sapur.011G043800.1	0.009915734	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.113630327	0.163952367			CAZ10095.1		Protein prenylhistidine transferase family protein
Sapur.011G056100.1	0.009261533	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.118895546	0.166762385	GO:0006491	PSL4	CAZ56360.1		calmodulin-binding protein
Sapur.011G088100.7	0.013877503	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.112948014	0.159030478			CAZ12820.1		Uncharacterized conserved protein (DUF2358)
Sapur.011G115500.1	0.009458292	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115725778	0.148935603			CAZ59670.1		
Sapur.011G140800.2	0.009895522	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.113455607	0.157125575			CAZ77924.1		nucleic acid binding
Sapur.011G149400.1	0.01322836	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.00970801	0.903948123			CAZ57870.1	AHUS5,ATSCE1,EMB1627.5(	sumo conjugation enzyme 1
Sapur.011G201100.2	0.011712934	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.054503506	0.497775651	GO:0005515		CAZ75060.2		
Sapur.011G104600.2	0.011650325	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115647657	0.149210581	GO:0006396		CAZ77230.1	emb1644	Small nuclear ribonucleoprotein family protein
Sapur.011G014200.1	0.01412244	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.251510433	0.050485658	GO:0008471,GO:0000160		CAZ02430.1	AHP5	histidine-containing phosphotransfer factor 5
Sapur.011G020800.1	0.016889073	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.112945243	0.159012168			CAZ02630.1		
Sapur.011G028900.2	0.010228794	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.113809654	0.15622864	GO:0005515		CAZ66600.2	UBP12	ubiquitin-specific protease 12
Sapur.011G063400.4	0.012124214	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.453840671	2.46E-09	GO:0016888		CAZ52390.2		Tat/D related DNA ase
Sapur.011G068800.1	0.012068088	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115782304	0.148748925					
Sapur.011G080400.1	0.010228969	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.07854831	0.32814497			CAZ01520.1		RING/U-box superfamily protein
Sapur.011G104100.3	0.00042273	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115172369	0.166172724	GO:0016021,GO:0004659		CAZ51820.1	ATGA,CHLG,G4	LSbA prenyltransferase family protein
Sapur.011G133300.1	0.010848231	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.114829699	0.151772207	GO:0008152,GO:0004807		CAZ55440.1	CTT,TMC,CYT07PL,TPI	triosephosphate isomerase
Sapur.011G218300.2	0.011741262	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115725212	0.148837219	GO:0005515		CAZ57640.1		Transducin/WD40 repeat-like superfamily protein
Sapur.011G221300.1	0.011877316	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.117717167	0.153742586	GO:0006355,GO:0005634		CAZ59710.1	AtVIP2,VIP2	VIH2 interacting protein 2
Sapur.011G231100.1	0.012276656	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115678846	0.149101959	GO:0006412,GO:0005840,GO:0003735		CAZ13120.1		Ribosomal protein S10p/S20e family protein
Sapur.011G270300.1	0.014700714	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.040360535	0.615754108	GO:0003824,GO:0000029,GO:0000026		CAZ20488.1		tetracyclidinosylhexose-6'-kinase family protein
Sapur.011G282700.1	0.01073159	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.11485008	0.152054637	GO:0005515		CAZ33060.1	AtRLP27,RLP27	receptor-like protein 27
Sapur.012G011100.1	0.011922931	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.081608864	0.309509042					
Sapur.012G058200.1	0.012668482	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.112778959	0.159632409			CAZ07705.1		NOT2 / NOT3 / NOT5 family
Sapur.012G096700.1	0.011878286	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.44089703	7.51E-09	GO:0005525		CAZ02030.1		Avirulence induced gene (AIG2) family protein
Sapur.012G116100.1	0.010327808	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115182788	0.150863317			CAZ04645.1		Plant self-incompatibility protein S1 family
Sapur.012G019400.1	0.011455505	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115278886	0.148738853					
Sapur.012G051500.1	0.014167577	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.11484699	0.151721245					hypothetical protein
Sapur.012G094900.2	0.010228969	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.22682786	0.006434916			CAZ10040.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.012G148400.1	0.009667454	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.218770016	0.005932576	GO:0008234,GO:0006508		CAZ68480.1		Cysteine proteinase superfamily protein; putative; cysteine protease, putative
Sapur.013G116700.3	0.008943995	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115718897	0.148954982			CAZ63540.1	ATRM1,BLAP75,RIM1	Domain of unknown function (DUF1767)
Sapur.013G000100.1	0.009327813	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115415637	0.156758777	GO:0005515		CAZ40840.2	ARAD2,L1-5,YK2	Rad21/Rec8-like family protein
Sapur.T166000.1	0.011652771	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115569076	0.149488994					
Sapur.T187700.1	0.01156584	0.018008013	2.904824395	0.00623	0.995028949	NA	NA	grey	-0.115782293	0.148738013					
Sapur.003G082100.3	-0.046924628	0.012338819	2.018716	0.00148	0.995028949	NA	NA	grey	-0.042830496	0.586888753	GO:0006506,GO:0005789		CAZ46850.2		PIG-K/PBN1 family protein
Sapur.006G093900.2	0.02661248	0.018223439	2.675505205	0.00606	0.995019594	NA	NA	grey	-0.08781283	0.274126675	GO:0043565,GO:0006355,GO:0003700		CAZ19490.1		Basic-leucine zipper (bZIP) transcription factor family protein
Sapur.006G112900.1	0.028251587	0.018223473	2.664038789	0.00622	0.995019506	NA	NA	grey	-0.082341608	0.306286628					
Sapur.006L029700.2	0.027313007	0.01622663	2.703208236	0.006003	0.995210505	NA	NA	grey	-0.062692096	0.431706348	GO:0005515		CAZ32950.1	ATCOP1,COP1,DET340,EMB	Transducin/WD40 repeat-like superfamily protein
Sapur.006G164500.1	0.025445413	0.016228709	2.725161313	0.005965	0.995248483	NA	NA	grey	-0.07092368	0.377021668					
Sapur.013G134000.2	0.025469571	0.016228958	2.72756219	0.00595	0.995252626	NA	NA	grey	-0.28102657	0.00036347	GO:0006950		CAZ11360.1		Adenine nucleotide alpha hydrolases-like superfamily protein
Sapur.013G146000.2	0.025169667	0.016229472	2.732579693	0.005939	0.995261193	NA	NA	grey	-0.104192137	0.194068654					
Sapur.013G110400.1	0.024834654	0.016229869	2.736477585	0.005931	0.995267827	NA	NA	grey	-0.092496655	0.249253226			CAZ06930.1		hypothetical protein
Sapur.15W6G058700.1	0.024758286	0.016229991	2.737675609	0.005928	0.995268862	NA	NA	grey	-0.085646675	0.286181783	GO:0006355,GO:0003700		CAZ68550.1		Integrase-type DNA-binding superfamily protein
Sapur.009G018200.2	0.024605355	0.016230202	2.739763826	0.005924	0.995274406	NA	NA	grey	-0.115498057	0.164643199			CAZ45680.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.013G111700.1	0.02442171	0.016230475	2.742463754	0.005918	0.995277198	NA	NA	grey	-0.095093836	0.231184103			CAZ06890.1		nodulin MtN21 /EamA-like transporter family protein
Sapur.T089600.1	0.024369893	0.016230511	2.742632977	0.005917	0.995278589	NA	NA	grey	-0.050647752	0.530392368			CAZ29570.1		Exonuclease family protein
Sapur.013G049300.2	0.024281955	0.016230681	2.744506557	0.005914	0.995281434	NA	NA	grey	-0.081608864	0.309509042			CAZ58700.1		Ribosomal L5P family protein
Sapur.013G061200.1	0.023953384	0.016231168	2.749367822	0.005904	0.995289636	NA	NA	grey	-0.103311143	0.197889141			CAZ16172.1		hypothetical protein
Sapur.008G090000.2	0.023625238	0.016231661	2.754368838	0.005893	0.995297994	NA	NA	grey	-0.224549427	0.006469077	GO:0008725,GO:0006284		CAZ13635.2		DNA 3-methyladenine glycosylase I
Sapur.013G000100.10	0.023569489	0.016231765	2.755154471	0.005892	0.995299162	NA	NA	grey	-0.113448229	0.16277786	GO:0005634,GO:0003677	SPL2	CAZ42275.1		squamosa promoter-binding-like protein
Sapur.013G170500.5	0.02334138	0.016232092	2.758649089	0.005884	0.995305216	NA	NA	grey	-0.051052018	0.525439858			CAZ63690.1		plant/T16L1-18D protein, putative
Sapur.013G242500.1	0.023007249	0.016232934	2.767002072	0.005867	0.995319152	NA	NA	grey	-0.095768252	0.23403078			CAZ69180.1		Copper transport protein family
Sapur.013G027500.1	0.022760145	0.016232987	2.767750446	0.005865	0.995320396	NA	NA	grey	-0.081839216	0.308227711			CAZ58490.1		Protein of unknown function (DUF3677)
Sapur.013G102700.2	0.022633842	0.016233185	2.769789862	0.005861	0.995323751	NA	NA	grey	-0.100874221	0.208732246	GO:0006629,GO:0055114,GO:0016717		CAZ05580.1	FAD8	fatty acid desaturase 8
Sapur.006G175000.2	0.021948376	0.016234227	2.780661222	0.005838	0.995352258	NA	NA	grey	-0.081819714	0.308489203					
Sapur.018G001600.1	0.021895408	0.016234355	2.781844465	0.005836	0.995354710	NA	NA	grey	-0.113621037	0.163988404	GO:0009733		CAZ69530.1		SAUR-like auxin-responsive family protein
Sapur.018G004300.1	0.021844583	0.016234437	2.782694506	0.005834	0.995356111	NA	NA	grey	-0.067684743	0.401842376	GO:0006508,GO:0008233		CAZ52740.1		ATP-dependent protease La (LON) domain protein
Sapur.018G039100.2	0.021775875	0.016234547	2.783847583	0.005832	0.995357008	NA	NA	grey	-0.109276954	0.17207856	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810		CAZ69040.1	ALS1,ATTAP2,TAP2	transporter associated with antigen processing protein 2
Sapur.012G080100.2	0.020238739	0.016237337	2.810065581	0.005776	0.995650722	NA	NA	grey	-0.08827417	0.230981207			CAZ56160.1		Root hair defective 3 GTP-binding protein (RHD3)
Sapur.012G050800.2	0.020063692	0.016237484	2.814150292	0.00577	0.9953963	NA	NA	grey	-0.00414857	0.959282615	GO:0055085,GO:0016020,GO:0008810,GO:0005215		CAZ62890.3		Xanthine/uracil permease family protein
Sapur.008G020800.1	0.020024884	0.016237472	2.814874429	0.005768	0.995396466	NA	NA	grey	-0.066074004	0.439494656	GO:0003677,GO:0006310,GO:0005634		CAZ70510.1	ATKU,KNAT2	KN/TEX1-like homeobox gene 2
Sapur.001G165500.4	0.020000166	0.016237514	2.815336633	0.005768	0.995398209	NA	NA	grey	-0.230975345	0.003609128	GO:0008270,GO:0003676,GO:0016787,GO:0005524,GO:0003677		CAZ51280.1		DEAD-box protein abstrakt, putative
Sapur.001G046800.1	0.01927384	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.121406228	0.055249858	GO:0016020,GO:0008233,GO:0006465		CAZ62600.1		Peptidase S24/S26A/S26C family protein
Sapur.001G092500.1	0.023152291	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.085419551	0.287456221			CAZ62890.4	PGR5-LIKE A	PGR5-like protein 1A
Sapur.001G031100.1	0.022804153	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.11578276	0.148729298			CAZ65470.1		Bax inhibitor-1 family protein
Sapur.017G064300.2	0.022773375	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.073479006	0.36041086	GO:0016020		CAZ27461.1	ATHIR1,HIR1	SPFH/Band 7/PHB domain-containing membrane-associated protein family
Sapur.008G021300.2	0.022782794	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.13092592	0.10203366			CAZ04440.1		Protein of unknown function (DUF3997)
Sapur.002G034900.1	0.022813652	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.067741105	0.23228652			CAZ25520.1		Sec14p-like phosphatidylcholine transfer family protein
Sapur.015G031100.4	0.01759675	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.01060679	0.85078985			CAZ61150.1		Lsh and RanBPM domains containing protein
Sapur.015G058800.2	0.015659504	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.00902079	0.93272085			CAZ62640.1		Protein of unknown function (DUF641)
Sapur.018G063500.1	0.021692094	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.086850331	0.279438966			CAZ19950.2	GC1	golgin candidate 1
Sapur.016G239000.1	0.020270674	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.088579229	0.272679617					hypothetical protein
Sapur.005G149900.1	0.02247819	0.016236387	2.904823276	0.005623	0.995237815	NA	NA	grey	-0.091138641	0.256290426					NA
Sapur.006L039800.2	0.037418258	0.014362264	2.603632092	0.005516	0.995588772	NA	NA	grey	-0.064786126	0.430168897	GO:0008017,GO:0007010		CAZ24756.1	ATMAP70-2,MAP70-2	microtubule-associated proteins 70-2
Sapur.004G061050.2	-0.045617559	-0.008756658	1.691073614	-0.00858	0.995898438	NA	NA	grey	-0.06293494	0.404324568			CAZ17681.1		hypothetical protein
Sapur.006G061100.1	0.040883104	-0.008755854	1.699495247	-0.00515	0.995890938	NA	NA	grey	-0.24806259	0.001733497	GO:0005515		CAZ24481.1	LRK2	leucine-rich repeat/extensin 2
Sapur.15W6G110000.1	0.030049897	-0.014362777	2.918423183	0.004955	0.990846468	NA	NA	grey	-0.077365564	0.335880603	GO:0005515,GO:0006468,GO:0004672		CAZ42192.1		Leucine-rich repeat protein kinase family protein
Sapur.014G014400.1	0.04223439	-0.008764022	1.851228677	-0.00472	0.993226137	NA	NA	grey	-0.075238709	0.345846157			CAZ46630.1		Protein of unknown function (DUF2223)
Sapur.001G155600.1	0.036355546	-0.008783871	1.851406353	-0.00472	0.993226425	NA	NA	grey	-0.091844229	0.252611824					hypothetical protein
Sapur.T045600.2	0.037542917	-0.008742392	1.875802304	-0.00466	0.992361381	NA	NA	grey	-0.100073603	0.212385968	GO:0055114,GO:0046877,GO:0016702		CAZ24000.1	LOX5	PLAT/LH2 domain-containing lipoxygenase family protein
Sapur.016G246200.4	0.029424314	-0.014819842	2.316648208	-0.00643	0.990461628	NA	NA	grey	-0.112050224	0.162432621	GO:0016491,GO:0008610		CAZ76580.1	ATTPS1,TPS1	trehalose-6-phosphate synthase
Sapur.016G246200.3	0.028398877	-0.008002353	2.126246837	-0.00374	0.994907085	NA	NA	grey	-0.4004449	2.03E-07	GO:0005992,GO:0008824		CAZ76580.1	ATTPS1,TPS1	trehalose-6-phosphate synthase
Sapur.005G139000.1	0.017861139	0.004849274	2.904823455	0.00363	0.995718857	NA	NA	grey	-0.058167406	0.48039617			CAZ21830.1		
Sapur.007G087900.1	0.03607898	-0.006521763	2.084838837	-0.00313	0.995704081	NA	NA	grey	-0.119777201	0.135124188					
Sapur.010G098900.2	0.028616218	-0.006320027	2.121669171	-0.00307	0.995748287	NA	NA	grey	-0.085127277	0.287739722			CAZ13677.2		hypothetical protein
Sapur.014G029100.1	0.02729272	-0.00601995	2.132251419	-0.00306	0.995750251	NA	NA	grey	-0.109401226	0.175576611			CAZ18210.2		Calcium-binding EF-hand family protein
Sapur.014G049400.3	0.026593001	-0.006319765	2.137931389	-0.00305	0.995768809	NA	NA	grey	-0.17523476	0.028044435			CAZ45280.2	ATRADS1C,RAD51C	RAS associated with diabetes protein 51C
Sapur.005G087100.1	0.026029974	-0.006316042	2.139952246	-0.00305	0.995775975	NA	NA	grey	-0.099915276	0.21286543			CAZ33752.2		Remorin family protein
Sapur.006G185300.5	0.024766687	-0.006511814	2.413893693	-0.0027	0.995784758	NA	NA	grey	-0.010692613	0.884440273	GO:0017069,GO:0000398				RNA recognition motif, a.k.a. RRM/RZC R8D protein
Sapur.006L000400.1	0.044913884	0.005463787	2.052561609	-0.00182	0.997876378	NA	NA	grey	-0.077705605	0.358604658			CAZ17165.1		NA
Sapur.002G188200.1	0.029473205	-0.006506611	2.707608861	-0.0024	0.998802682	NA	NA	grey	-0.081608864	0.309509042			CAZ61630.1		zein-binding protein
Sapur.015G039900.4	0.025639904	-0.006506392	2.730719995	-0.00237	0.998852208	NA	NA	grey	-0.276667227	0.008185825	GO:0016567,GO:0006462	ABI17,ATABI7	CAZ42150.1		IBR domain-containing protein
Sapur.006G073600.5	0.048169752	0.003004549	1.685157892	0.001783	0.998577414	NA	NA	grey	-0.118823674	0.181150443			CAZ53830.1		Regulator of chromosome condensation (RCC1) family protein
Sapur.016G264100.1	0.030910584	0.004296382	2.788727256	-0.00153	0.998576935	NA	NA	grey	-0.134823674	0.09434316	GO:0003677		CAZ01500.1	NGA4	AP2/B3-like transcriptional factor family protein
Sapur.T187700.1	0.03762248	-0.004289687	2.875888556	-0.00149	0.998809042	NA	NA	grey	-0.132242008	0.088741928	GO:0005515		CAZ42150.1		Glutathione S-transferase family protein
Sapur.001G035700.2	0 NA	NA	NA	NA	NA	NA	NA	grey	-0.01661039	5.72E-08			CAZ15860.1		NA
Sapur.001G185700.1	0 NA	NA	NA	NA	NA	NA	NA	grey	-0.103817129	0.19562667	GO:0005515		CAZ46660.1		SH3 domain-containing protein
Sapur.001G110300.2	0 NA	NA	NA	NA	NA	NA	NA	grey	0.033167705	0.695172862	GO:0016020		CAZ32060.1		early-responsive to dehydration stress protein (ERD4)
Sapur.001G147800.2	0 NA	NA	NA	NA	NA	NA	NA	grey	0.043475864	0.642842274	GO:0006352,GO:0005669		CAZ17440.2	EER4,TAF12B	Transcription initiation factor TFIID subunit A
Sapur.001G125600.2	0 NA	NA	NA	NA	NA	NA	NA	grey	-0.014351597	0.658377755	GO:0005515		CAZ60755.2		F-box family protein
Sapur.001G130100.4	0 NA	NA	NA	NA	NA	NA	NA	grey	-0.048762627	0.549232148			CAZ20450.1	CCT,CRP	RNA polymerase II transcription mediators
Sapur.002G171200.2	0 NA	NA	NA	NA	NA	NA	NA	grey	-0.055420615	0.490572059			CAZ48160.2	OBE2	Protein of unknown function (DUF4423)
Sapur.002G075000.2	0 NA	NA	NA	NA	NA	NA	NA	grey	-0.055282315	0.512060471	GO:0005515,GO:0006468,GO:0004672		CAZ60550.1		Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain
Sapur.003G127300.2	0 NA	NA	NA	NA	NA	NA	NA	grey	-0.316161932	5.46E-05			CAZ72760.2		transmembrane protein, putative
Sapur.004G027500.2	0 NA	NA	NA	NA	NA	NA	NA	grey	-0.26499743	0.008915526	GO:0006289,GO:0005634,GO:0004003,GO:0000439		CAZ17020.3		transcription factor–related
Sapur.005G185000.1	0 NA	NA

Sapur.T075700.1	1.984043962	1.321129376	0.364200623	3.627477	0.000286204	0.000466644	grey60	0.33117623	5.81E-05		ATSG42280.1	GM61	gamma-irradiation and mitomycin c induced 1		NA
Sapur.T178200.1	0.387569963	1.626814089	0.452738832	3.593274	0.000326549	0.000350752	grey60	0.348832981	7.56E-06		ATSG42280.1	GM61	gamma-irradiation and mitomycin c induced 1		NA
Sapur.T123100.1	0.355618879	1.54583884	0.445392912	3.482484	0.000469785	0.000760031	grey60	0.370936587	1.75E-06		ATSG42280.1	GM61	gamma-irradiation and mitomycin c induced 1		NA
Sapur.T055900.1	0.015663251	0.620196756	0.186209364	3.42109	0.000623708	0.000995296	grey60	0.244648343	0.002023904		ATSG54750.3				NA
Sapur.Scf1926230.1	92.10564019	0.605461174	0.182928212	3.31165	0.000931267	0.001444653	grey60	0.344828809	0.000396807						NA
Sapur.Scf1926210.1	68.82774913	0.560236318	0.192386968	2.912059	0.003585052	0.005423285	grey60	0.221420471	0.005321511	GO:0006468;GO:0005634;GO:0004672	ATSG10940.2	AGI1;SNRK2-4;SNRK2-4;SRK	Protein kinase superfamily protein		NA
Sapur.T137100.1	0.321499886	1.362071287	0.473759748	2.832889	0.004614088	0.006811207	grey60	0.292857567	0.000197456		ATSG42280.1	GM61	gamma-irradiation and mitomycin c induced 1		NA
Sapur.T174900.1	0.24656106	1.128800319	0.492538072	2.291852	0.021916646	0.030762857	grey60	0.335167007	1.78E-05		ATSG42280.1	GM61	gamma-irradiation and mitomycin c induced 1		NA
Sapur.T118300.1	0.243911187	1.165895691	0.508775179	2.291561	0.021930962	0.030777929	grey60	0.333887104	1.91E-05		ATSG42280.1	GM61	gamma-irradiation and mitomycin c induced 1		NA
Sapur.Scf1926040.1	11.43679792	0.468860968	0.132062025	2.842667646	0.018415681	0.029257645	grey60	0.231231965	0.002788425		ATSG42280.1	GM61	gamma-irradiation and mitomycin c induced 1		NA
Sapur.Scf1926060.1	11.33582713	0.445801469	0.132591742	-1.91667	0.055279959	0.074388856	grey60	-0.196926365	0.012421361		ATSG42280.1	GM61	gamma-irradiation and mitomycin c induced 1		NA
Sapur.Scf1926250.1	37.48853843	0.263461609	0.151151148	2.088502732	0.037264615	0.051724021	grey60	0.155723821	0.015472027		ATSG10940.2	AGI1;SNRK2-4;SNRK2-4;SRK	Protein kinase superfamily protein		NA
Sapur.Scf1926730.1	4651.011511	12.1396533	0.257663328	47.11404	0	0	lightyellow	0.615457749	9.74E-18		ATSG18730.1		Late embryogenesis abundant protein (LEA) family protein		pollen coat-like protein
Sapur.Scf1926110.1	14.61196334	0.458890327	0.241823117	16.42352	2.47E-42	1.65E-41	lightyellow	0.601179222	8.45E-17	GO:0005515	ATSG18950.1		Transducin/WD40 repeat-like superfamily protein		F-box and WD40 domain protein, putative
Sapur.Scf1926900.1	166.2758157	1.153149972	0.129897923	16.57567	1.04E-61	6.93E-61	lightyellow	0.588823496	6.67E-16	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATSG34500.1	CYP710A1	cytochrome P450, family 710, subfamily A, polypeptide 1		cytochrome P450 family 710 protein
Sapur.T067800.1	8.69953664	0.617559059	0.246445138	15.95941	5.45E-57	3.25E-56	lightyellow	0.581342162	1.23E-15	GO:0005515	ATSG43851.1		ARM-repeat superfamily protein		NA
Sapur.T068400.1	3.82694627	0.337978053	0.299702162	14.4743	1.76E-47	9.24E-47	lightyellow	0.608133355	2.99E-17	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T156900.1	3.237776625	0.196164889	0.304887529	13.76299	4.28E-43	2.07E-42	lightyellow	0.574168338	3.79E-15	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1928830.3	8.708815005	0.475182827	0.129149757	13.70544	9.42E-43	5.01E-42	lightyellow	0.356426188	4.61E-06		ATSG48740.1		PLC-like phosphodiesterases superfamily protein		MAPEM kinase-like protein
Sapur.Scf1929500.1	0.046286313	1.205461034	0.386830986	13.45663	2.81E-41	1.33E-40	lightyellow	0.50884284	2.39E-11		ATSG19190.1		alpha/beta-Hydrolases superfamily protein		CXE carboxylesterase
Sapur.T135400.1	2.584271478	0.1855	0.263185432	13.25001	8.74E-40	3.29E-39	lightyellow	0.705258656	6.21E-25	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T156200.1	8.814622555	1.118558641	0.238320985	13.08554	3.98E-39	1.81E-38	lightyellow	0.602321693	7.13E-17	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T135600.1	2.118128318	0.344795543	0.262127748	12.62554	1.53E-36	6.98E-36	lightyellow	0.604574533	6.22E-24	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T020600.1	9.564134164	2.292137847	0.184879863	12.3982	2.67E-35	1.12E-34	lightyellow	0.57308892	5.92E-15	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T068200.1	1.464613863	0.238489027	0.262700181	12.2352	2.02E-34	8.12E-34	lightyellow	0.643329954	1.03E-19	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1927000.1	4.448104832	2.653861894	0.225140735	11.97911	4.57E-33	1.84E-32	lightyellow	0.585642572	7.87E-16	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926940.0	1.60748779	1.467635763	0.300285671	11.54779	7.57E-31	2.90E-30	lightyellow	0.596696525	1.62E-16	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T135800.1	1.564138369	0.503441133	0.231782084	11.51329	1.13E-30	4.01E-30	lightyellow	0.567338661	9.40E-15	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926930.1	2.310602268	2.358077217	0.284050698	11.47006	1.87E-30	7.09E-30	lightyellow	0.607284571	3.40E-17	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926790.1	1.633670571	2.422317826	0.3045315	11.46778	1.92E-30	7.30E-30	lightyellow	0.583692217	1.16E-15	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926190.1	10.39728908	1.475660045	0.129008491	11.43125	2.92E-30	1.10E-29	lightyellow	0.55811539	3.10E-14		ATSG06160.1	ATO	splicing factor-related		NA
Sapur.T077500.1	4.875023875	2.020720188	0.187193869	10.7948	1.64E-27	5.26E-26	lightyellow	0.603457276	6.01E-17	GO:0005515	ATSG62762.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T077200.1	11.22686756	0.488658193	0.130239672	10.28376	8.34E-25	2.76E-24	lightyellow	0.501865319	2.15E-11	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T077700.1	6.388656643	2.846095482	0.276888185	10.2821	8.48E-25	2.84E-24	lightyellow	0.524751246	1.78E-12	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T181400.1	1.177839633	2.280395075	0.321152768	10.11522	3.27E-24	1.08E-23	lightyellow	0.516817108	4.23E-12		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T077500.1	6.717954569	2.312307422	0.301223607	10.11276	3.35E-24	1.08E-23	lightyellow	0.494267214	7.72E-11	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T098200.1	1.033704872	0.074196189	0.103311498	9.906887	3.88E-23	1.25E-22	lightyellow	0.55102091	7.13E-14		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T120800.1	9.458229565	1.667385544	0.166444846	9.89629	4.32E-23	1.38E-22	lightyellow	0.554392848	4.97E-14		ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T156400.1	1.858668361	0.877397179	0.192544674	9.878304	5.18E-23	1.66E-22	lightyellow	0.454532215	2.34E-09		ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T135300.1	8.19818876	2.665131954	0.274740631	9.700473	3.03E-22	9.42E-22	lightyellow	0.496230646	3.87E-11		ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926710.1	2.193496219	1.560763799	0.268604554	9.531588	1.55E-21	4.78E-21	lightyellow	0.565415253	1.21E-14	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T098400.1	0.699412268	2.742438628	0.289928415	9.461814	3.03E-21	9.27E-21	lightyellow	0.605288729	4.59E-17	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T020500.1	1.260218738	2.192062041	0.272245563	9.46069	3.64E-21	1.11E-20	lightyellow	0.594716121	1.16E-16	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926930.1	3.871009926	2.899097881	0.308547504	9.395953	5.67E-21	1.72E-20	lightyellow	0.459235539	7.18E-11	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1927500.1	4.002813435	3.646887249	0.196512271	9.302223	3.51E-20	1.04E-19	lightyellow	0.483892918	2.81E-10	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T135100.1	3.468006527	2.631135391	0.28628817	9.190513	3.91E-20	1.16E-19	lightyellow	0.483202092	1.48E-10	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926890.1	1.886292104	2.16941524	0.236922886	9.156628	5.15E-20	1.58E-19	lightyellow	0.5842225	9.59E-16	GO:0005681;GO:0000398;GO:0000387	ATSG43185.2		ARM-repeat superfamily protein		NA
Sapur.T185000.1	2.496745954	2.026126155	0.227873916	9.153433	6.64E-20	2.03E-19	lightyellow	0.521317619	2.60E-12	GO:0005681;GO:0000398;GO:0000387	ATSG43185.2		ARM-repeat superfamily protein		NA
Sapur.T020000.1	7.432919971	3.187239907	0.162531618	8.791592	1.47E-18	4.21E-18	lightyellow	0.48022288	1.96E-10	GO:0005681;GO:0000398;GO:0000387	ATSG43185.2		ARM-repeat superfamily protein		NA
Sapur.T076600.1	1.600313374	3.502884451	0.38909571	8.783161	1.60E-18	4.57E-18	lightyellow	0.463317957	9.93E-10	GO:0005681;GO:0000398;GO:0000387	ATSG43185.2		ARM-repeat superfamily protein		NA
Sapur.Scf1926200.1	0.646686164	2.708898848	0.317539786	8.625564	6.37E-18	1.79E-17	lightyellow	0.554509848	4.89E-14	GO:0005681;GO:0000398;GO:0000387	ATSG43185.2		ARM-repeat superfamily protein		NA
Sapur.Scf1926900.1	1.88316721	1.881436722	0.223151347	8.425375	3.68E-17	1.01E-16	lightyellow	0.49844034	7.21E-11		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T077900.1	2.149611327	1.368157779	0.28166634	8.407734	4.18E-17	1.15E-16	lightyellow	0.472617277	4.47E-10	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T068800.1	5.610327791	3.386469771	0.290235856	8.22185	2.00E-16	5.37E-16	lightyellow	0.393719485	1.37E-07		ATSG43240.1		Actin binding Calponin homology (CH) domain-containing protein		NA
Sapur.T021400.1	1.17689673	2.420145601	0.311776956	7.762426	8.33E-15	2.13E-14	lightyellow	0.469716086	5.43E-10		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.Scf1926810.1	2.140678079	1.867456129	0.345625976	7.684426	1.54E-14	3.88E-14	lightyellow	0.480401383	3.91E-10		ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T067200.1	1.641109636	1.774791836	0.230972924	7.683663	1.55E-14	3.92E-14	lightyellow	0.513583036	6.05E-12						NA
Sapur.T020300.1	1.044957915	2.199024006	0.28828265	7.629566	2.16E-14	5.95E-14	lightyellow	0.48599677	1.10E-10	GO:0005515	ATSG55400.1		Actin binding Calponin homology (CH) domain-containing protein		NA
Sapur.Scf1926600.1	1.554562469	2.060581974	0.28083315	7.443679	9.79E-14	2.42E-13	lightyellow	0.442856001	2.10E-09	GO:0005515	ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.Scf1926300.1	120.3797025	0.542482163	0.07353408	7.377289	1.62E-13	3.97E-13	lightyellow	0.452335833	2.75E-09	GO:0016491	ATSG36750.1		Quinone reductase family protein		minor allergen AN protein A, putative
Sapur.T069000.1	2.349631918	2.000277187	0.310588208	7.36466	1.79E-13	4.36E-13	lightyellow	0.409472723	1.01E-07		ATSG51120.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T135200.1	2.712208877	1.822162265	0.24815168	7.332184	2.26E-13	5.54E-13	lightyellow	0.443117344	6.16E-09	GO:0005515	ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T077300.1	4.416404674	3.342078831	0.185068588	7.216756	3.13E-13	7.26E-13	lightyellow	0.452831661	6.02E-09		ATSG51120.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T067000.1	0.775456134	2.053020355	0.285117506	7.200611	5.99E-13	1.44E-12	lightyellow	0.514823232	5.27E-12	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926490.1	1.617745679	2.124824279	0.280792218	7.090248	6.05E-13	1.46E-12	lightyellow	0.4166676	5.70E-08	GO:0005515	ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T021100.1	1.945592254	1.888951265	0.268094526	7.045706	1.88E-12	4.37E-12	lightyellow	0.411507784	8.60E-08	GO:0005515	ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T181000.1	0.665144835	1.624838284	0.377094851	6.967576	3.76E-12	8.81E-12	lightyellow	0.44858724	2.04E-08		ATSG51120.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.Scf1927000.1	1.452645919	1.967109964	0.282211807	6.94572	3.77E-12	8.82E-12	lightyellow	0.403864698	1.56E-07	GO:0005515	ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T067900.1	0.922326242	2.292763090	0.332227211	6.901191	5.16E-12	1.20E-11	lightyellow	0.513380845	6.19E-12		ATSG51120.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T097500.1	0.728645462	2.985488518	0.432931343	6.896236	5.34E-12	1.25E-11	lightyellow	0.445863607	4.82E-09	GO:0005681;GO:0000398;GO:0000387	ATSG43185.2		ARM-repeat superfamily protein		NA
Sapur.Scf1926520.1	4.66863032	1.86879666	0.272450071	6.858219	6.97E-12	1.62E-11	lightyellow	0.41521806	6.40E-08		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T067600.1	0.563087231	2.532446801	0.370335666	6.83767	8.03E-12	1.86E-11	lightyellow	0.49057702	7.11E-11		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T127000.1	1.060039737	2.487063057	0.366219758	6.791177	1.11E-11	2.56E-11	lightyellow	0.424935658	2.91E-08	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926910.1	1.554926152	1.693555264	0.258333372	6.555687	1.54E-11	1.24E-10	lightyellow	0.453479121	2.46E-08	GO:0005515	ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T186900.1	0.760888015	1.887162901	0.288831163	6.532763	6.41E-11	1.44E-10	lightyellow	0.479547588	2.09E-10						NA
Sapur.T022700.1	2.524656613	3.349283921	0.210626126	6.405757	1.50E-10	3.30E-10	lightyellow	0.393240793	6.02E-07						NA
Sapur.Scf1926200.1	2.218644151	1.290231397	0.205076621	6.29196	3.13E-10	6.83E-10	lightyellow	0.363288577	2.37E-06		ATSG51130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T067700.1	0.441904887	2.143351593	0.341631166	6.274128	3.52E-10	7.64E-10	lightyellow	0.49191324	3.52E-11		ATSG51131.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.Scf1918700.1	220.8050724	0.470606068	0.076057986	6.256439	3.94E-10	8.51E-10	lightyellow	0.432174864	1.59E-08		ATSG45188.1	CPU8R2	conserved peptide upstream open reading frame 2		NA
Sapur.Scf1926400.1	2.228663212	2.102620011	0.33791882	6.22416	4.84E-10	1.05E-09	lightyellow	0.37038041	1.80E-06	GO:0005515	ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T020300.1	1.509180849	1.223383866	0.197362864	6.165186	5.88E-10	1.27E-09	lightyellow	0.352841481	2.45E-05		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T193300.1	0.485573851	2.006951166	0.329847561	6.084473	1.17E-09	2.49E-09	lightyellow	0.467080607	6.98E-10						NA
Sapur.T077400.1	14.24287051	1.84961227	0.104518826	6.074303	1.25E-09	2.65E-09	lightyellow	0.437122134	1.04E-08	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T119700.1	0.59254899	2.351872276	0.390392246	6.024383	1.70E-09	3.59E-09	lightyellow	0.439018864	8.82E-09						NA
Sapur.T068800.1	0.606649623	1.812872585	0.306328921	5.908415	3.45E-09	7.21E-09	lightyellow	0.42972757	1.71E-08	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.Scf1926920.1	2.262877012	2.216683232	0.208100237	5.846621	5.02E-09	1.04E-08	lightyellow	0.348808569	7.93E-06		ATSG51130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T068900.1	1.113161661	2.966229665	0.40425364	5.834061	5.74E-09	1.19E-08	lightyellow	0.33331177	1.96E-05		ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T020400.1	15.53097297	1.005035367	0.173167275	5.668024	1.44E-08	2.94E-08	lightyellow	0.34030451	1.20E-05		ATSG06160.1	ATO	splicing factor-related		NA
Sapur.T067400.1	0.430988054	2.364657952	0.400750931	5.651036	1.59E-08	3.24E-08	lightyellow	0.454529312	2.21E-09		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.Scf1927000.1	1.965581973	1.165365637	0.207103172	5.62703	1.81E-08	3.71E-08	lightyellow	0.375222262	1.29E-06		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T176200.1	3.340420592	2.986942555	0.358857534	5.583762	3.08E-08	6.19E-08	lightyellow	0.387374539	5.38E-07	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T020100.1	2.174562314	1.355874279	0.246963789	5.489521	4.03E-08	8.05E-08	lightyellow	0.309398556	8.14E-05		ATSG51131.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T170300.1	2.673347889	1.829202023	0.331925711	5.478823	4.28E-08	8.55E-08	lightyellow	0.39117476	4.07E-07	GO:0005515	ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T078100.1	1.585192964	0.418409025	0.260705567	5.446027	5.31E-08	1.06E-07	lightyellow	0.373487681	1.45E-06		ATSG51131.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T097400.1	0.411084952	2.103585324	0.40464793	5.198557	2.01E-07	3.90E-07	lightyellow	0.433429062	1.41E-08		ATSG51130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T021200.1	0.438600044	2.008887294	0.39114623	5.135702	2.81E-07	5.42E-07	lightyellow	0.442790606	1.81E-08	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T126900.1	2.250091157	2.272898185	0.445661168	5.100256	3.39E-07	6.50E-07	lightyellow	0.324769	3.32E-05						NA
Sapur.Scf1926950.1	1.109651522	1.085378966	0.313570123	5.078132	3.81E-07	7.29E-07	lightyellow	0.290501964	0.001232557		ATSG51130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.Scf1927200.1	0.49303852	1.52985437	0.30210274	5.06402	4.11E-07	7.84E-07	lightyellow	0.42224738	3.62E-08	GO:0005515	ATSG55400.1		Actin binding Calponin homology (CH) domain-containing protein		NA
Sapur.T135900.1	2.182775782	0.815425149	0.188142063	4.84962	1.24E-06	2.31E-06	lightyellow	0.356851916	4.54E-06		ATSG06160.1	ATO	splicing factor-related		NA
Sapur.Scf1926910.1	0.519245136	1.774997544	0.370661416	4.79316	1.68E-06	3.07E-06	lightyellow	0.363030409	2.60E-06	GO:0005515	ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.Scf1926920.1	1.563886756	0.924009318	0.306751808	4.473525	7.69E-06	1.38E-05	lightyellow	0.325733374	3.14E-05						NA
Sapur.Scf1926910.1	0.677500727	1.101931338	0.261387	4.215626	2.49E-05	4.10E-05	lightyellow	0.363950338	2.56E-06						NA
Sapur.Scf1927100.1	0.959463524	1.415664306	0.337345795	4.196478	2.71E-05	4.71E-05	lightyellow	0.286318945	0.00027765						NA
Sapur.T076200.1	0.273816017	1.802159234	0.444384576	4.122897	3.74E-05	6.45E-05	lightyellow	0.480930266	1.81E-10	GO:0005681;GO:0000398;GO:0000387	ATSG43185.2		ARM-repeat superfamily protein		NA
Sapur.Scf1926800.1	0.930261419	1.220861179	0.298428836	4.091376	4.28E-05	7.36E-05	lightyellow	0.265212665	0.000788303						NA
Sapur.T097700.1	0.336303681	1.882685089	0.461308861	4.080189	4.48E-05	7.68E-05	lightyellow	0.455707086	3.91E-07		ATSG51130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T021000.1	0.366780669	1.533311987	0.384016061	3.982833	6.53E-05	0.00011005	lightyellow	0.339439041	1.37E-05		ATSG62700.2	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T146200.1	0.387284832	1.689276719	0.427433676	3.95284	7.73E-05	0.001326	lightyellow	0.439053609	8.81E-09	GO:0005681;GO:0000398;GO:0000387	ATSG43185.1		ARM-repeat superfamily protein		NA
Sapur.T056400.1	11.28408982	1.426773232	0.385166559	3.75047	0.000232135	0.000365454	lightyellow	0.310819215	0.000396758		ATSG51130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.Scf1926910.1	0.978931994	0.929860014	0.26068325	3.563832	0.00036548	0.000502253	lightyellow	0.243058825	0.002159913		ATSG51131.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T017500.1	7.740804084	1.356073234	0.356826775	3.548827	0.000385494	0.000623641	lightyellow	0.32673564	2.96E-05						NA
Sapur.T022300.1	0.331748767	1.258089811	0.358089938	3.514784	0.000440111	0.000709299	lightyellow	0.309758125	7.89E-05	GO:0005515	ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T021600.1	0.343643423	1.365452173	0.419080871	3.260884	0.000970556	0.001526765	lightyellow	0.286662421	0.000277184		ATSG62700.1	ATFIM1;FIM1	fimbrin 1		NA
Sapur.T181500.1	0.191463839	1.334445486	0.550958348	2.432045	0.015433457	0.02169251	lightyellow	0.374363735	1.37E-06		ATSG51130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.Scf1927000.1	0.366813601	1.308448147	0.358426927	2.249597	0.024476549	0.034326161	lightyellow	0.143243703	0.072888008		ATSG51131.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T195001.1	0.162865848	0.917691395	0.576163594	2.004134	0.045055661	0.061220612	lightyellow	0.373372762	1.46E-06		ATSG51130.1	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3		NA
Sapur.T145500.1	0.168614938	1.100340895	0.705401596	1.559452	0.118889362	0.153720189	lightyellow	0.374469432	2.02E-06		ATSG49963.1		HIT-type Zinc finger family protein		NA
Sapur.Scf1923800.3	0.005114885	0.055357653	2.904824396	0.01913	0.984737169	NA	lightyellow	0.432048853	1.60E-08	GO:0006355	ATSG45600.1	GASA1;TAR1A6	YEATS family protein		NA
Sapur.Scf1926750.1	95.02269074	0.928897732	0.073702099	8.523663	1.55E-17	4.29E-17	lightgreen	0.581476128	1.40E-15		ATSG67140.3	SWEETIE	HEAT repeat-containing protein		NA
Sapur.T097700.1	484.2279456	0.481936517	0.054387928	7.504658	6.17E-14	1.54E-13	lightgreen	0.572488711	4.75E-15		ATSG67140.3	SWEETIE	HEAT repeat-containing protein		NA
Sapur.T070100.1	407.3494696	0.489362016	0.065123839	7.468544	8.11E-14	2.01E-13	lightgreen	0.517588836	3.88E-12		ATSG67140.3	SWEETIE	HEAT repeat-containing protein		NA
Sapur.T069900.1	173.4363352	0.479126184	0.095652349	7.046568	1.83E-12	4.28E-12	lightgreen	0.487938977	9.76E-11		ATSG67140.3	SWEETIE	HEAT repeat-containing protein		NA
Sapur.Scf1926500.1	108.5805821	0.411557154	0.063613855	6.469015	9.83E-11	2.19E-10	lightgreen	0.50925973	9.70E-12		ATSG67140.3	SWEETIE	HEAT repeat-containing protein		NA
Sapur.T126200.1	151.6415681	0.458207395	0.072228899	6.277246	3.51E-10

Sapur.T101900.1	10.3313696	0.986009029	0.100730912	9.788545	1.26E-22	4.00E-22	tightyellow	0.614178165	1.59E-17	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T101200.1	24.34143448	1.048845287	0.107733108	9.735633	2.12E-22	6.70E-22	lightyellow	0.607391687	1.34E-17	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T075257400.1	11.81618621	1.114849413	0.115511133	9.651305	4.85E-22	1.52E-21	lightyellow	0.579173708	1.93E-15	ATSG21660.1	EDA10	SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T099800.1	48.6305556	0.962797009	0.100988624	9.533717	1.52E-21	4.68E-21	lightyellow	0.576889095	2.62E-15	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T141600.1	19.05469624	1.221667143	0.128756217	9.485386	2.41E-21	7.41E-21	lightyellow	0.567809334	1.38E-16	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T152400.1	17.76797158	1.185828374	0.127249581	9.317346	1.19E-20	3.60E-20	lightyellow	0.551409696	3.48E-16	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T174000.1	4.471076422	1.216794534	0.132418188	9.189029	3.96E-20	1.18E-19	lightyellow	0.614018849	1.10E-17	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T164200.1	52.16229793	0.812889164	0.088727072	9.162337	5.08E-20	1.50E-19	lightyellow	0.594118186	2.36E-16	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T152200.1	10.92604017	0.92114284	0.101097307	9.111448	8.13E-20	2.40E-19	lightyellow	0.571387045	5.92E-15	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T093600.1	32.74217529	0.908114028	0.099748846	9.09595	9.38E-20	2.76E-19	lightyellow	0.56601785	1.80E-16	ATSG61291.1		Leucine-rich receptor-like serine/threonine-protein kinase	NA
Sapur.T141500.1	14.32523384	0.888205142	0.097882115	9.064408	1.25E-19	3.67E-19	lightyellow	0.571146749	5.68E-15	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T170700.1	28.96192924	1.143839176	0.126367025	9.046125	1.51E-19	4.41E-19	lightyellow	0.59236824	2.53E-16	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T187900.1	5.700180134	1.113692174	0.126390304	8.811532	1.23E-18	3.53E-18	lightyellow	0.602394328	7.06E-17	ATSG01960.1	EDA10	Helicase/SANT-associated, DNA binding protein	NA
Sapur.T146022300.1	23.48216578	0.908114028	0.103384329	8.783866	1.56E-18	4.50E-18	lightyellow	0.553702184	5.56E-14	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T170500.1	6.842758844	0.92071824	0.107137051	8.677945	4.03E-18	1.14E-17	lightyellow	0.576614005	6.10E-15	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T075257500.1	17.04953866	0.854027664	0.101573667	8.406003	5.68E-18	1.92E-17	lightyellow	0.511155963	1.90E-12	GO:0003012;GO:0005086	EDA10	SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T188200.1	6.243303956	0.917225501	0.114827453	7.987859	1.37E-15	3.59E-15	lightyellow	0.58528645	8.27E-16	ATSG01960.1	EDA10	SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T146021500.1	6.727215625	0.88012843	0.115136846	7.722354	1.14E-14	2.91E-14	lightyellow	0.518162683	3.64E-12	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T162800.1	12.93993048	0.928247394	0.120406557	7.712403	1.21E-14	3.14E-14	lightyellow	0.492219716	9.61E-11	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T075257000.1	19.9053497	0.849582879	0.11089998	7.660622	1.85E-14	4.68E-14	lightyellow	0.509973541	8.98E-12	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T102200.1	6.487097693	0.91128	0.119078659	7.591148	3.07E-14	7.87E-14	lightyellow	0.555450203	1.37E-14	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T188400.1	15.93570923	0.911811695	0.12053035	7.564997	3.88E-14	9.72E-14	lightyellow	0.47828648	2.27E-10	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T101800.1	4.142501736	1.089139825	0.144159596	7.545447	4.58E-14	1.14E-13	lightyellow	0.492091832	5.35E-11	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T176200.1	3.066756339	1.367950289	0.168799278	7.511042	5.87E-14	1.46E-13	lightyellow	0.523415837	2.26E-12	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T170600.1	3.857161556	1.777564368	0.104281714	7.449237	9.35E-14	2.32E-13	lightyellow	0.49692041	2.12E-11	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T166400.1	11.89606216	1.121267043	0.151539734	7.399162	1.37E-13	3.37E-13	lightyellow	0.472932226	3.99E-10	GO:0003012;GO:0005086	EDA10	SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T103100.1	17.70059129	0.825026817	0.113244475	7.290659	3.08E-13	7.51E-13	lightyellow	0.482043816	1.64E-10	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T101000.1	11.85723859	0.902648871	0.104457563	7.281699	3.38E-13	8.01E-13	lightyellow	0.526799326	1.27E-11	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T146021600.1	7.28365166	1.075272289	0.148683322	7.212012	4.76E-13	1.15E-12	lightyellow	0.47292775	4.05E-10	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T099500.1	12.54424869	0.875894337	0.175158143	7.219158	5.23E-13	1.26E-12	lightyellow	0.45730651	1.73E-09	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T163900.1	6.08210845	0.814936087	0.115054447	7.083047	1.41E-12	3.36E-12	lightyellow	0.526240927	1.46E-12	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T188600.1	17.38516522	0.887605529	0.108001823	7.06764	1.54E-12	3.76E-12	lightyellow	0.44616653	7.07E-09	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T170400.1	10.03425027	0.764392616	0.1085678	6.854477	7.06E-12	1.64E-11	lightyellow	0.465737835	7.90E-10	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T176100.1	10.16480042	1.000399431	0.162609662	6.72142	1.80E-11	4.11E-11	lightyellow	0.427382643	9.83E-09	GO:0003012;GO:0005086	EDA10	SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T188900.1	2.077810702	1.254154509	0.197616378	6.346364	2.20E-10	4.83E-10	lightyellow	0.481886657	1.66E-10	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T164300.1	1.852465584	0.977532275	0.113158239	6.305776	2.87E-10	6.26E-10	lightyellow	0.508793606	1.02E-11	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T182500.1	3.953478389	0.864867862	0.135561124	6.229567	4.68E-10	1.01E-09	lightyellow	0.45090521	1.48E-09	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T099600.1	2.521993905	1.193023922	0.191779374	6.220884	4.94E-10	1.07E-09	lightyellow	0.459073127	1.47E-09	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T075269300.1	17.45112887	0.843508552	0.151750181	5.560315	2.68E-08	5.42E-08	lightyellow	0.383052614	6.37E-07				NA
Sapur.T152500.1	5.502329824	0.610330886	1.103347391	5.529183	3.23E-08	6.45E-08	lightyellow	0.457395338	1.72E-09	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T102500.1	4.613613465	0.703139403	0.143774384	5.321604	1.03E-07	2.02E-07	lightyellow	0.383874186	8.02E-07	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T027700.1	221.4762207	0.369695507	0.07916559	4.673123	2.97E-06	5.43E-06	lightyellow	0.394812934	3.11E-07				NA
Sapur.T130900.1	5.017041981	0.568849779	0.117652526	4.663463	3.12E-06	5.68E-06	lightyellow	0.40247611	3.25E-07	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T075257500.2	3.353671583	0.584689701	0.138170376	4.561816	5.07E-06	9.18E-06	lightyellow	0.33835388	4.06E-06	GO:0003012;GO:0005086		SEC7-like guanine nucleotide exchange family protein	NA
Sapur.T075257600.1	3.143378609	0.556442274	0.135131308	4.205588	0.000039966	0.062270564	lightyellow	0.274976966	0.000129279	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T100400.1	3.583253339	0.218561927	0.126289005	1.730649	0.083544406	0.109827255	lightyellow	0.192898154	0.015500451	ATSG26880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T002149800.1	63.84850133	1.032132837	0.119392364	-9.46658	2.89E-23	8.86E-23	midnightblue	-0.534527597	5.55E-13	GO:0004565;GO:0006355;GO:0003700		WRKY family transcription factor	NA
Sapur.T014608800.1	249.8692498	0.913864402	0.092466518	-8.45084	2.89E-17	7.86E-17	midnightblue	-0.51682044	4.24E-12	ATSG42070.1		hypothetical protein	NA
Sapur.T012609500.1	57.56491125	-0.759253389	0.093900396	-8.08537	6.20E-16	1.64E-15	midnightblue	-0.474898345	1.27E-10	ATSG75020.2	LPAT4	lysophosphatidyl acyltransferase 4	NA
Sapur.T002649800.1	287.7843137	-0.768000153	0.108069938	-7.49403	6.68E-14	1.66E-13	midnightblue	-0.45872671	1.52E-09	GO:0016757	ATSG1250.1	galactosyltransferase-like 3	NA
Sapur.T017121700.1	26.42610513	-0.767427809	0.159410556	-7.32605	2.37E-13	5.79E-13	midnightblue	-0.399345887	2.21E-07	GO:0046872;GO:0030001	ATSG1490.1	Heavy metal transport/detoxification superfamily protein	NA
Sapur.T015622500.1	6.527709994	-1.261765782	0.195688113	-6.39668	1.54E-10	3.10E-10	midnightblue	-0.35587976	4.78E-06	GO:0004869;GO:0006472	CRK42	cysteine-rich RLK (RECEPTOR-LIKE KINASE) 42	NA
Sapur.T001627900.1	38.77566516	-0.798816666	0.126882113	-6.29574	3.06E-10	6.67E-10	midnightblue	-0.378518161	1.02E-06	GO:0006355;GO:0003700	ATERF-5;ATERF5;ERF5	ethylene response element binding factor 5	NA
Sapur.T002614200.1	165.2779009	-0.728006479	0.117652526	-6.66343	3.11E-10	6.86E-10	midnightblue	-0.40247611	3.25E-07				NA
Sapur.T007028300.1	104.1818428	-0.208036336	0.035152113	-5.91857	3.24E-09	6.80E-09	midnightblue	-0.423268292	3.32E-08	ATSG26830.1		Protein of unknown function (DUF677)	NA
Sapur.T015272300.1	33.61889713	-0.205709965	0.18039655	-5.69129	6.05E-09	1.25E-08	midnightblue	-0.298152042	0.000347684	GO:0006629	PLA-I(beta)2	alpha/beta-hydrolases superfamily protein	NA
Sapur.T017112200.1	130.6113224	-0.489960343	0.086334878	-5.67511	1.39E-08	2.82E-08	midnightblue	-0.339254134	1.38E-05	GO:0043531		NB-ARC domain-containing disease resistance protein	NA
Sapur.T012610800.1	122.3886727	-0.431095527	0.076386442	-5.64517	1.65E-08	3.35E-08	midnightblue	-0.363877092	2.45E-06		ATSG35880.1	ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2)	NA
Sapur.T014620105.1	75.96639797	-0.432857173	0.11814121	-5.38641	7.19E-08	1.42E-07	midnightblue	-0.37214035	9.68E-07	ATMYB73;MYB73	ATMYB73;MYB73	myb domain protein 73	NA
Sapur.T012608800.1	4.303847422	-1.469083821	0.272822406	-5.31446	1.07E-07	2.10E-07	midnightblue	-0.264172134	0.000281812	GO:0006355;GO:0003700	ATG2193.1	Integrase-type DNA-binding superfamily protein	NA
Sapur.T010688800.1	54.4146124	-0.298197109	0.11365882	-5.31053	1.06E-07	2.14E-07	midnightblue	-0.372628208	1.34E-06		ATSC71.1.1		NA
Sapur.T009615700.1	105.9993569	-0.82668769	0.157698757	-5.24869	1.53E-07	2.99E-07	midnightblue	-0.296836697	0.000105969	GO:0005509	CML42	calmodulin like 42	NA
Sapur.T015273800.1	94.08005604	-0.515462943	0.10060475	-5.12543	2.97E-07	5.71E-07	midnightblue	-0.31243148	6.75E-05		SCL5	scarecrow-like 5	NA
Sapur.T016112300.1	23.79248837	-0.874082214	0.171610188	-5.094978	3.49E-07	6.68E-07	midnightblue	-0.283673385	0.000318483		ATSG32280.1		NA
Sapur.T016279000.1	252.46588	-0.657107	0.079016329	-5.06687	4.01E-07	7.67E-07	midnightblue	-0.336167602	1.64E-05		PAT1	GRAS family transcription factor	NA
Sapur.T015039300.1	212.0128202	-0.405162761	0.080265152	-5.047813	4.47E-07	8.52E-07	midnightblue	-0.335434144	1.97E-05	GO:0006355;GO:0003700	ATERF-5;ATERF5;ERF5	erf domain protein 9	NA
Sapur.T003619100.1	12.50543242	-1.18649661	0.243482929	-4.8642	1.15E-06	2.15E-06	midnightblue	-0.31835575	0.001120075				NA
Sapur.T006179900.1	51.05992238	-1.184737418	0.24477457	-4.84052	1.30E-06	2.42E-06	midnightblue	-0.274683555	0.000486642	GO:0006355;GO:0003700	ATG2193.1	Integrase-type DNA-binding superfamily protein	NA
Sapur.T002063300.1	362.4532996	-0.670082928	0.140857701	-4.76355	1.90E-06	3.52E-06	midnightblue	-0.288883721	0.000241932		ATG77380.1	amino acid permease 2	NA
Sapur.T006203400.1	223.1239211	-0.603889389	0.128308404	-4.73709	2.18E-06	3.99E-06	midnightblue	-0.293945055	0.000207271	GO:0004869	CSA57510.1	Cysteine/cystatin protease inhibitor	NA
Sapur.T005202000.1	57.46534626	-0.576206768	0.132999953	-4.33464	1.46E-05	2.57E-05	midnightblue	-0.235271184	0.002957663	GO005515	GO09070.1	(AT)SRC2;SRC2	soybean gene regulated by cold-2
Sapur.T017121800.1	19.26823967	-0.864137725	0.209662585	-4.11167	3.86E-05	6.65E-05	midnightblue	-0.248869307	0.001672318	GO:0046872;GO:0030001	ATSG1491.1	Heavy metal transport/detoxification superfamily protein	NA
Sapur.T018076300.1	1319.594229	-0.411319113	0.100637422	-4.086145	4.39E-05	7.53E-05	midnightblue	-0.272802074	0.000517649	GO:0055114;GO:0016614;GO:0006694;GO:0003854	GAE1	UDP-glucuronic acid 4-epimerase 1	NA
Sapur.T015242401.1	339.7330207	-0.255719188	0.06317948	-4.0485	4.83E-05	8.27E-05	midnightblue	-0.275815151	0.000470604	GO:0043531	ATG3449.1	LRR and NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.T002679100.1	50.81314752	-0.967664026	0.241417301	-4.00827	6.12E-05	1.03E-04	midnightblue	-0.203645513	0.01052321		ATG8950.1	Phosphate-responsive 1 family protein	phosphate-induced protein 1 motif protein
Sapur.T006149300.1	138.7154513	-0.267936759	0.066851382	-3.76741	0.000165129	0.000273023	midnightblue	-0.200328258	0.018369195		ATWRKY40;WRKY40	WRKY DNA-binding protein 40	WRKY transcription factor
Sapur.T012697100.1	287.1253389	-0.173963237	0.046459348	-3.74166	0.000182812	0.000302414	midnightblue	-0.198478312	0.010374664	GO005524	SCL5	scarecrow-like 5	GRAS family transcription factor
Sapur.T001885500.1	5.423218013	-0.914301423	0.25329273	-3.60326	0.000314249	0.000511163	midnightblue	-0.198143566	0.010381615		ATG4159.1	Protein of unknown function (DUF567)	tubby C 2 protein
Sapur.T013618600.1	43.43920572	-0.513444529	0.144561499	-3.56047	0.000369149	0.000592537	midnightblue	-0.224690945	0.003063121		ATG4599.1	pinoid-binding protein 2	AvrRPT2-induced gene 4
Sapur.T008155000.1	108.8444990	-0.343821131	0.09700173	-3.54448	0.000393182	0.000630034	midnightblue	-0.224441404	0.004714581	GO:0016757	PBP1	GATA;UGT8	galactosyltransferase family 8
Sapur.T008155000.2	46.47499465	-0.556881122	0.159101241	-3.5025	0.000479486	0.000727105	midnightblue	-0.06209382	0.42792072		ATG2193.1		NA
Sapur.T010618300.1	171.181624	-0.244798946	0.070192071	-3.48756	0.000487453	0.000739134	midnightblue	-0.242675512	0.010335666	GO0046685;GO006472	ATG3910.1	Protein kinase superfamily protein	tyrosine kinase
Sapur.T010688500.1	188.6506329	-0.570754799	0.164178876	-3.47688	0.000509152	0.000771845	midnightblue	-0.224371461	0.020107376		ATG2193.1		NA
Sapur.T002689800.1	27.37125542	-0.339116163	0.100057196	-3.38918	0.000700105	0.00011459	midnightblue	-0.217870756	0.016612274	GO:0006355;GO:0003677	ANC02;ATAF1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NA
Sapur.T003628800.1	92.83697421	-0.595176197	0.175503668	-3.38309	0.000716738	0.001190027	midnightblue	-0.181934976	0.023133622	GO:0006270;GO005515	ATL2;TL2	RING-H2 finger protein ATL2	RING-H2 finger protein ATL2
Sapur.T014620700.1	20.97893959	-0.457063836	0.137995829	-3.31216	0.000929796	0.001458849	midnightblue	-0.184786587	0.030511567	GO:0043565;GO006355;GO:0003700	ATG1570.1	AtWRKY41;WRKY41	WRKY transcription factor; putative
Sapur.T005338300.1	478.4038816	-0.267129906	0.082327421	-3.24435	0.001180147	0.001852665	midnightblue	-0.217172157	0.016192226	GO:0043565;GO006355;GO:0003700	ATG8040.1	ATWRKY40;WRKY40	WRKY transcription factor
Sapur.T007016800.1	175.9488853	-0.282864404	0.09611864	-3.15029	0.001630196	0.002527486	midnightblue	-0.198442853	0.012722604	GO005524	ATG4393.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	AAA family ATPase
Sapur.T007123400.1	403.2384514	-0.281525815	0.089738943	-3.13723	0.001705498	0.002639984	midnightblue	-0.21821621	0.006041423	GO:0006355;GO:0003700	ATERF-5;ATERF5;ERF9	erf domain protein 9	NA
Sapur.T005161005.1	227.9192058	-0.247949416	0.079617222	-3.11269	0.001849015	0.002860695	midnightblue	-0.224990945	0.010260269		ATG8950.1	Phosphate-responsive 1 family protein	phosphate-induced protein 1 motif protein
Sapur.T012690500.1	27.20065788	-0.493875839	0.159142469	-3.09079	0.001996255	0.003073606	midnightblue	-0.208387006	0.008819027		ATG5300.1		hypothetical protein
Sapur.T006207100.1	14.39681533	-0.587665555	0.188813305	-3.09565	0.002739189	0.004170693	midnightblue	-0.148847948	0.066841151		ATG4374.1	Leucine-rich repeat (LRR) family protein	somatic embryogenesis receptor kinase
Sapur.T015W0292600.1	77.07427548	-0.467153066	0.16119921	-2.897986	0.003755174	0.005662259	midnightblue	-0.159545879	0.045941307	GO:0016567;GO:0006842	ATG6190.1	ARM-repeat superfamily protein	spotted leaf protein; putative
Sapur.T015W0241900.1	6.072605924	-1.0694	0.38968859	-2.80576	0.005032802	0.007494171	midnightblue	-0.16913242	0.042121594	GO:0006355;GO:0003700	ATG8910.1	C-repeat/DRE binding factor 3	CBF transcription factor 3
Sapur.T012610100.1	61.39181685	-0.920001695	0.330346221	-2.78496	0.005323398	0.007868779	midnightblue	-0.158295013	0.047694145	GO:0006355;GO:0003700	ATG8910.1	C-repeat/DRE binding factor 4	CBF transcription factor 1
Sapur.T012027600.1	214.6147219	-0.601718836	0.220026271	-2.72647	0.006456553	0.009356621	midnightblue	-0.16696968	0.03722427		ATG8950.1	Phosphate-responsive 1 family protein	phosphate-induced protein 1 motif protein
Sapur.T006211700.1	8.824420883	-0.664570248	0.246027617	-2.72334	0.006462545	0.009364193	midnightblue	-0.16762683	0.042966651		ATG17230.1	SCL13	GRAS family transcription factor
Sapur.T007670.1	251.8299812	-0.123185468	0.045605566	-2.67052	0.007539428	0.011008621	midnightblue	-0.200533363	0.013765515		ATG17230.1	SCL13	SCARECROW-like 13
Sapur.T015W0292500.1	85.37225837	-0.365407558	0.143911391	-2.539115	0.011113332	0.016060601	midnightblue	-0.155165628	0.080490118	GO:0016567;GO:0006842	ATG6190.1	ARM-repeat superfamily protein	NA
Sapur.T016049400.1	873.5259021	-0.164519966	0.060886517	-2.697066	0.012521556	0.018080272	midnightblue	0.1580434	0.048053399	GO:0051861;GO:0046838;GO:0017089;GO:0005737	ATG3660.1	ACD11	Glycolipid transfer protein (GLTP) family protein
Sapur.T006286300.1	5.796039514	-0.429256721	0.175676449	-2.44345	0.014547542	0.020782949	midnightblue	-0.134152628	0.093193387	GO:0003824;GO:0006755;GO:0004722	ATG8420.1	Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.T017111500.1	73.98743318	-0.427449056	0.178519209	-2.39451	0.016645141	0.023619782	midnightblue	-0.14515114	0.088988996	GO:0016567;GO:0006842	ATCMPG1;CMPG1	CYS, MET, PRO, and GLY protein 1	AvrRPT-R rapidly elicited protein
Sapur.T015027800.1	41.29753964	-0.342907816	0.145137169	-2.35737	0.018614149	0.026287709	midnightblue	-0.131125166	0.09318869	GO005319	ATG4174.1	SAUR-like auxin-responsive family protein	auxin-responsive family protein
Sapur.T009279700.1	20.08728527	-0.742631883	0.315474739	-2.35395	0.018575257	0.026253486	midnightblue	-0.13375739	0.09495441	GO:0006355;GO:0003700	ATG4343.1	RRTF1	redox responsive transcription factor 1
Sapur.T006254800.1	948.9730919	-0.187994815	0.085411175	-2.20106	0.027731977	0.038152634	midnightblue	-0.149723016	0.061262739	GO0046872	ATG4914.2	AT1G72;ZF1;SZF2;ZFAR1	zinc finger (CCCH type) family protein
Sapur.T009203300.1	20.80273847	0.363671352	0.165589231	2.196226	0.028075781	0.03901262	midnightblue	0.115880747	0.146387054		ATG5982.0.1	RHA1;AT1G2	C3H2-type zinc finger family protein
Sapur.T005686700.1	6.271504368	0.524067183	0.238854745	2.195999	0.028155448	0.039152245	midnightblue	0.131836663	0.056332815		ATG4495.0.1		pathogenic type III effector avirulence factor Avr AvrRpt-cleavage; cleavage site protein
Sapur.T017006700.2	4.81861775	-0.480991301	0.224884344	-2.13884	0.032448747	0.044780517	midnightblue	-0.121147236	0.130683322	GO:0018424;GO:0006470;GO:0004722	ATG8240.0.1	Protein phosphatase 2C family protein	protein phosphatase 2C
Sapur.T017005500.1	13.68342883	0.320118167	0.151605697	2.111518	0.034737807	0.047784145	midnightblue	-0.13649372	0.08839165		ATG0150.1	zinc ion binding;nucleic acid binding	RHA2B;RHA2B protein
Sapur.T010200900.1	158.6569163	-0.243356078	0.115409052	-2.11083	0.034891119	0.048150827	midnightblue	-0.125897273	0.152868082				NA
Sapur.T006137300.1	43.00886675	-0.325054903	0.154663259	-2.10169	0.035580056	0.04890391	midnightblue	-0.120968464	0.131256396		ATG3680.1	ATNHL10;NHL10;YLS9	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Sapur.T014608700.1	22.75830804	-0.275207006	0.130924713	-2.10069	0.035677322	0.051251148	midnightblue	-0.104521788	0.192616602	GO005516;GO:0046872;GO:0000166	ATCAL;KAL	autoinhibited Ca2+/ATPase 2, plasma membrane-type protein	calcium-transporting ATPase 2, plasma membrane-type protein
Sapur.T008151100.1	92.58501553	-0.149378269	0.072208311	-2.07428	0.038052942	0.052116568	midnightblue	-0.185916768	0.01973872		ATG4748.4	alpha/beta-hydrolases superfamily protein	hypothetical protein
Sapur.T006236200.1	341.3888722	-0.253664323	0.12853617	-1.97321	0.048528977	0.065362702	midnightblue	-0.123421241	0.09171287	GO005634	ATG2720.1	Polynucleotide adenylyltransferase, ribonuclease H-like superfamily protein	CCR4-associated factor-like protein, putative
Sapur.T009025800.1	133.7050847	-0.127935542	0.065457021	-1.94854	0.051930001	0.069345375	midnightblue	-0.140002432	0.080302252	GO008270;GO005515	ATG4630.1	zinc finger (C3HC4-type RING finger) family protein	zinc-finger protein
Sapur.T015280.1	156.0936008	-0.127935542	0.065457021	-1.94854	0.051930001	0.072156471	midnightblue	-0.140002432	0.132238654		ATG8820.1	Phosphate-responsive 1 family protein	NA
Sapur.T125900.1	156.0885031	-0.307483508	0.205954609	-1.92974	0.053639032	0.072265972	midnightblue	-0.11471281	0.152213307		ATG6950.1	Phosphate-responsive 1 family protein	NA
Sapur.T016283300.1	203.1152177	-0.323018302	0.169000363	-1.91288	0.055769399	0.075353287	midnightblue	-0.120429767	0.110008815	GO008270;GO005515	ATG4626.1	zinc finger (C3HC4-type RING finger) family protein	RING zinc finger protein, putative
Sapur.T009600.1	127.805856	0.399428652	0.204071361	1.865867	0.062059999	0.082905277	midnightblue	-0.112208023	0.161768015		ATG8950.1	Phosphate-responsive 1 family protein	NA
Sapur.T005158400.1	10.10726231	-0.460376387	0.247354117	-1.8612	0.062715423	0.08385174	midnightblue	-0.080768808	0.354906578	GO:0004904;GO:0016762;GO:0006073;GO:0005618;GO:0005975;GO:0004553	ATG4130.1	XTH15;XTR7	xyloglucan endotransglucosylase/hydrolase 15
Sapur.T005258800.1	57.99725868	-0.295248082	0.159796777	-1.75293	0.078722	0.105826044	midnightblue	-0.111876221	0.183977656	GO:0006355;GO:0003700	ATG4299.1	2-AZAPROPANOL;BZIP40	bZIP transcription factor family protein; putative
Sapur.T016139800.1	54.92045862	-0.307167886	0.175845722	-1.7468	0.080675445	0.106295687	midnightblue	-0.09789769	0.225456992	GO0008887;GO000145	ATG3918B0.1	ATEXO70H2;EXO70H2	exo70 subunit exo70 family protein H2
Sapur.T006114400.1	77.17624993	-0.307167886	0.175845722	-1.7468	0.080675445	0.106295687	midnightblue	-0.124692778	0.138910059	GO0003700;GO005515	ATG8950.1	Integrase-type DNA-binding superfamily protein	NA
Sapur.T005137400.1	44.09278879	-0.305744468	0.180388748	-1.694883	0.090097581	0.117977964	midnightblue	-0.104013337	0.196841839	GO:0006355;GO:0003700	ATG2193.1	Integrase-type DNA-binding superfamily protein	AP2 domain transcription factor
Sapur.T015650.1	73.04414243	-0.189587644	0.113283929	-1.67368	0.094195223	0.121574168	midnightblue	-0.108408608	0.230230054	GO:0016491;GO:0016628	ATG4160.1	ATFaxo 11-12 type flavoprotein ribosomal dehydrogenase-like hydrolase family protein	autoinhibited calcium ATPase 11
Sapur.T006165300.1	263.3236616	0.099103095	0.060356645	1.642421	0.105028276	0.132795314	midnightblue	-0.099015471	0.217284761	GO005515;GO:0016020	ATG11820.1	AT-SYR1;ATSYP121;ATSYR1.	syntaxin of plants 121
Sapur.T008155800.1	80.42746663	-0.152051222	0.092667229	1.638678829	0.101491102	0.131491102	midnightblue	-0.05

Sapur.002G080400.1	154.7016615	-0.43791675	0.23177234	-1.88942	0.05883498	0.07890305	pseluropsoe	-0.13519243	0.09137859		ATMG00900.1	structural constituent of ribosome;protein binding	ribosomal protein S1,psaluter
Sapur.010G089500.1	31.51426168	-0.45926303	0.25247845	-1.81947	0.06869382	0.09155573	pseluropsoe	-0.14641824	0.06728844	GO:0005114;GO:0016020	ATMG01275.1	NADH dehydrogenase 1A	NA
Sapur.006G201800.1	4.96021274	-0.53601133	0.32263174	-1.66091	0.0967	0.13511394	pseluropsoe	-0.14261184	0.07968343				NA
Sapur.012G051000.1	77.35148654	-0.30128707	0.26944211	-1.11816	0.26349077	0.32197762	pseluropsoe	-0.08776454	0.27439324	GO:0016020;GO:0005507;GO:0004129	ATMG00160.1	cytochrome oxidase 2	NA
Sapur.001G055100.1	133.3143763	-0.10907038	0.10746612	-1.01495	0.31031612	0.37431284	pseluropsoe	-0.07626853	0.34243926	GO:0022900;GO:0016021	ATCG16630.1	calmodulin-binding family protein	cytochrome C oxidase subunit II, transmembrane domain protein
Sapur.012G042700.1	2.15960193	-0.20725336	0.29191951	-0.70998	0.47771983	0.51280349	pseluropsoe	-0.07885225	0.13625401				NA
Sapur.003G181000.1	37.58684866	-0.09079214	0.25420595	-29.9801	7.24E-127	1.14E-125	pseu	-0.33275882	2.06E-05		ATCG02645.1	Plant protein of unknown function (DUF247)	transmembrane protein, putative
Sapur.016G194900.1	135.0620869	3.64385457	0.38075085	20.15884	2.25E-90	2.26E-89	pseu	-0.53843005	3.51E-13	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP707A2	cytochrome P450, family 707, subfamily A, polypeptide 2	cytochrome P450 family 707 ABA 8'-hydroxylase
Sapur.006G118800.1	498.1969645	-2.00410986	0.10055718	-19.9309	2.20E-88	2.15E-87	pseu	-0.15124016	0.05802561	GO:0045735	ATG02630.1	ATG8F3;G8F3;G8_F3;G_F3A1	germin 3	auxin-binding protein ABP19a, putative
Sapur.003G131100.1	19.24978885	-0.38229109	0.17343697	-18.6809	5.87E-78	4.86E-77	pseu	-0.05145455	0.15728307	GO:0016747	ATG86050.1	HXXXD-type acyl-transferase family protein	anthocyanin 5-O-glucoside-6-O-malonyltransferase, putative
Sapur.009G097000.1	62.60195811	-2.47476282	0.13597673	18.20017	5.14E-76	4.10E-73	pseu	-0.56352876	1.55E-14		ATG28680.1	Protein of unknown function (DUF3633)	UPA23, putative
Sapur.016G114200.1	18.08932	-0.47127077	0.1462975	-3.2196	5.99E-04	4.41E-04	pseu	-0.13407055	1.90E-05		ATG22090.1	Protein of unknown function (DUF3246)	DUF3246 family protein
Sapur.009G085500.1	14.3761885	-0.81320809	0.16090201	-17.4875	1.79E-68	1.31E-67	pseu	-0.42241274	3.57E-08	GO:0009512	ATG26500.1	cytochrome b6f complex subunit (petM), putative	plastoquinol-plastocyanin reductase, putative
Sapur.003G052000.1	15.54715486	-0.29204202	0.09614476	-17.2512	1.93E-67	1.39E-66	pseu	-0.52647009	1.32E-05		ATG26950.1	GRAS family transcriptor	NA
Sapur.002G064000.1	17.10626	-2.33475658	0.13499853	-17.2953	5.11E-67	3.67E-66	pseu	-0.21581817	0.00463674	GO:0006355;GO:0003676	AtDD12;DD12	indeterminate(ID)-domain 12	nucleic acid-binding protein, putative
Sapur.001G087400.1	23.88860211	-0.35377537	0.12463586	17.13125	6.52E-66	6.01E-65	pseu	-0.21355284	2.18E-05		ATG25128.1	Family of unknown function (DUF736)	proteinase inhibitor I4, serpin
Sapur.008G106000.1	9.85517839	-2.49475377	0.1516868	-16.4457	9.01E-61	5.89E-60	pseu	-0.39260754	3.72E-07	GO:0016868;GO:0005975	ATG70820.1	phosphoglucomutase, putative / glucose phosphomutase, putative	phosphoglucomutase/phosphomannomutase alpha/beta/alpha domain protein
Sapur.003G082700.1	435.9425396	-2.11201429	0.13006326	-16.1568	8.94E-59	5.65E-58	pseu	-0.83137641	1.75E-10		ATG02610.1	germin-like protein 1	auxin-binding protein ABP19a, putative
Sapur.009G037700.1	25.28017868	-2.50247889	0.14180606	-16.0968	3.54E-57	2.32E-56	pseu	-0.52809331	3.1E-11		ATG27400.1	HXXXD-like acyltransferase family protein	class I small heat shock protein
Sapur.018G071600.1	10.73943229	-3.38609814	0.21303813	-15.8943	6.94E-57	4.20E-56	pseu	-0.23129675	0.00731467		ATKC25780.1	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein	cysteine-rich secretory family protein
Sapur.007G007700.1	11.10215475	-2.75625158	0.14180606	-15.8879	7.56E-57	4.58E-56	pseu	-0.31327621	1.45E-07	GO:0005885;GO:0016020;GO:0015297;GO:0015238;GO:0006855	ATCG01180.1	MATE efflux family protein	MATE efflux family protein
Sapur.001G149900.1	87.66140847	-2.45786636	0.15480795	15.80734	2.77E-56	1.68E-55	pseu	0.44341799	6.03E-09	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATCG07990.1	CYP75B1;D501;T7	Cytochrome P450 superfamily protein	cytochrome P450 family 92 protein
Sapur.009G037600.1	8.79018322	-2.92189525	0.24879944	-15.7785	4.38E-56	2.65E-55	pseu	0.00568112	0.93461571				NA	ricin-type beta-trefoil lectin domain protein
Sapur.010G119800.1	29.23808896	-2.36800868	0.15085334	15.47051	5.48E-54	3.32E-53	pseu	0.61933835	5.31E-18	GO:0016747	ATG39980.1	HXXXD-type acyl-transferase family protein	BAHD acyltransferase
Sapur.010G119600.1	6.87664658	-2.98377618	0.19307665	15.36106565	1.57E-53	9.56E-53	pseu	0.61933835	5.31E-18	GO:0005515;GO:0005635	ATG42660.1	RmlC-like cupins superfamily protein	NA
Sapur.010G202000.1	22.81086176	-3.04625608	0.20300781	15.00133	7.20E-51	4.01E-50	pseu	0.45180832	2.86E-09	GO:0016758;GO:0008152	AtUGT85A1;UGT85A1	UDP-glucosyltransferase 85A1	UDP-glucosyltransferase family protein
Sapur.002G011900.1	59.40457892	3.37125739	0.23024521	14.64233	1.51E-48	8.08E-48	pseu	0.28889826	0.00024306		ATG68420.1	DC1 domain-containing protein	nucleosomain, putative
Sapur.012G000500.1	170.6452525	2.11047405	0.14721168	14.61697	2.07E-48	1.10E-47	pseu	0.21775888	0.05610344	GO:0051082;GO:0006950;GO:0006457;GO:0005524	ATHSP1;Arthsp90-1;ATHSP90	heat shock protein90-1	heat shock protein
Sapur.013G132800.1	41.7889968	-1.38233601	0.09745032	-14.2293	6.03E-46	3.08E-45	pseu	-0.37942218	9.55E-07	GO:0055114;GO:0015137;GO:0016491;GO:0042651;GO:0009496;GO:0016679	ATCG02380.1	PETC;PGR1	photosynthetic electron transfer C	cytochrome b6-f complex iron-sulfur subunit
Sapur.005G061000.1	15.94443884	-2.86641798	0.20694925	13.98742	1.86E-44	9.28E-44	pseu	0.49110656	6.53E-11	GO:0055114;GO:0020037;GO:0004670;GO:0004601	ATG49570.1	Peroxidase superfamily protein	peroxidase
Sapur.010G080800.2	3.89242636	2.96982726	0.28388714	13.91349	5.25E-44	2.59E-43	pseu	0.27867404	0.00040536		ATG01230.1	SQD2	glycosyltransferase group 1 protein	glycosyltransferase group 1 protein
Sapur.005G139800.1	65.91864501	3.46338015	0.10746961	13.81628	6.96E-43	3.32E-42	pseu	0.50255656			ATG47920.1		NA	plastid/NAK;12-16 protein; putative
Sapur.001G194000.1	3.90895201	-2.55729768	0.18484522	-13.8347	1.57E-43	7.71E-43	pseu	-0.29303917	0.00016479		ATG58840.1	myb-like transcription factor family protein	MYB transcription factor, putative
Sapur.008G102600.1	105.9362361	1.65466095	0.12008838	-13.7684	3.95E-43	1.92E-42	pseu	-0.61452786	5.94E-08		ATG41660.1	Auxin-responsive family protein	indole-3-acetic acid inducible/responsive GH3-3 protein, putative
Sapur.010G162300.1	105.9495701	1.70162049	0.12400622	13.72205	7.49E-43	3.63E-42	pseu	-0.28232782	0.00277522		ATG12580.1	ATHSP70;HSP70	heat shock protein 70	heat shock cognate 70 kDa protein
Sapur.010G027500.1	5.95248562	-3.08189207	0.22964659	-13.4209	2.38E-42	1.06E-39	pseu	-0.3817792	0.054-07		ATG25880.1		NA	hypothetical protein
Sapur.015G043800.1	108.3689441	1.25885649	0.09594194	13.13102	2.53E-39	1.14E-38	pseu	0.56688746	1.02E-14	GO:0016887;GO:0005524;GO:0019538	ATG74310.1	ATHSP10;HOT1;HSP10I	heat shock protein 10I	NA
Sapur.009G037600.1	106.4408937	1.62637574	0.12660749	13.05022	6.34E-39	2.86E-38	pseu	0.38254063	7.64E-07				NA	dehydration-responsive element-binding protein 2F
Sapur.016G047500.1	2.14751989	-3.62458381	0.27880619	-13.0073	1.13E-38	5.00E-38	pseu	-0.47003127	2.21E-02	GO:0006355;GO:0003700	ATG57600.1	Integrase-type DNA-binding superfamily protein	hypothetical protein
Sapur.016G081100.1	152.4308883	1.46771373	0.11408591	12.86475	7.11E-38	3.15E-37	pseu	0.49284746	5.46E-11	GO:0045735;GO:0006355;GO:0003700;GO:0003677	ATG46680.1	ATHB-7;ATHB7;HB-7	homeobox 7	homeobox leucine zipper protein ATHB-7
Sapur.013G091100.1	5.77965155	-3.56156107	0.14997725	-12.7223	2.34E-37	1.03E-36	pseu	-0.35192288	4.77E-06	GO:0006508;GO:0004185	ATG35540.1	serine carboxypeptidase-like 18	NA	NA
Sapur.013G141000.1	32.07112068	-1.58272182	0.12617515	-12.5488	4.04E-36	1.73E-35	pseu	-0.42277463	3.62E-08	GO:0016887;GO:0005524	ATG71960.1	ABCG25;ATABCG25	ATP-binding cassette family G25	white-brown-complex ABC transporter family protein, putative
Sapur.008G099500.1	10.18812093	-3.29187215	0.16074609	12.51741	4.66E-36	1.96E-35	pseu	0.44113767	7.32E-08	GO:0016020;GO:0008375	ATG68390.1		NA	core 12-branching enzyme
Sapur.014G119900.1	13.1359936	-2.05345575	0.16398209	12.52161	5.69E-36	2.42E-35	pseu	-0.4837676	1.38E-10		ATG68280.1	ARAC10;ATRAC10;ATRGP11	RAC-like 10	serine carboxypeptidase-like 18
Sapur.003G001600.1	4.93976797	-3.96288882	0.1601681	-12.4472	1.45E-35	6.12E-35	pseu	-0.19304545	0.01145931	GO:0006508;GO:0004185	ATG35145.1	serine carboxypeptidase-like 18	NA	NA
Sapur.019G071600.1	127.7597653	1.92760729	0.15130721	12.40403	2.48E-35	1.06E-34	pseu	-0.3579478	4.17E-06	GO:0010031;GO:0008270;GO:0006538;GO:0004222	ATG24140.1	Matrixin family protein	NA	NA
Sapur.009G049800.1	47.70667348	1.91968968	0.16267578	11.8765	2.48E-35	1.11E-34	pseu	-0.36491616	0.03861887		ATHSP70;HSP70	heat shock protein 70	cell autonomous heat shock cognate protein
Sapur.012G261800.1	446.9293332	1.06008027	0.08495224	12.26205	1.45E-34	5.96E-34	pseu	-0.54790329	1.11E-13	GO:0006355;GO:0003677	ATG27433.2	AtNAC072;RD26	NAC (No Apical Meristem) domain transmembrane protein	NAC transcription factor
Sapur.013G122300.1	302.9091004	1.17796512	0.09609579	12.25805	1.52E-34	6.29E-34	pseu	-0.48020629	1.10E-10		ATRMA1;RMA1	RING-membrane-anchor 1	E3 ubiquitin-protein ligase RMA1, putative	E3 ubiquitin-protein ligase RMA1, putative
Sapur.005G137700.1	50.13994954	1.42038461	0.11664823	12.17675	1.59E-34	6.70E-34	pseu	-0.51983058	2.98E-12				NA	hypothetical protein
Sapur.019G071500.1	761.2403408	1.58720204	0.13199374	12.08496	1.32E-33	5.35E-33	pseu	-0.52641658	1.63E-12	GO:0010012;GO:0008270;GO:0006355;GO:0003700	ATG26140.1	Matrixin family protein	matrix metalloproteinase
Sapur.009G044300.1	218.5573123	1.62208207	0.13427224	12.05175	1.68E-33	6.25E-33	pseu	-0.37737566	1.12E-06	GO:0016758;GO:0008152	IAGLU	indole-3-acetate beta-D-glucosyltransferase	UDP-glucose:flavonoid 7-O-glucosyltransferase	UDP-glucose:flavonoid 7-O-glucosyltransferase
Sapur.005G147700.1	11.58434965	2.85562782	0.23856544	11.96848	5.20E-33	2.09E-32	pseu	-0.42391401	1.37E-08	GO:0055114;GO:0016491	ATG77330.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1-aminocyclopropane-1-carboxylate oxidase	NA
Sapur.019G144000.1	6.45839377	2.71883992	0.2367657	11.7552	4.79E-32	1.86E-31	pseu	-0.31369597	1.4E-05	GO:0007010;GO:0005634;GO:0081	ATCG01160.1	Plant protein of unknown function (DUF247)	Golgi transfer protein, putative	Golgi transfer protein, putative
Sapur.004G051400.1	16.75287937	1.35375685	0.18709203	11.42097	3.29E-30	1.24E-29	pseu	-0.21674634	0.06398743	GO:0016887;GO:0005524	ATG52640.1	ATHSB1;Arthsp90-1;ATHSP90	heat shock protein 90-1	heat shock protein
Sapur.004G141300.1	8.59443668	1.93183281	0.17148333	11.26791	6.04E-30	2.27E-29	pseu	-0.47268557	1.82E-10		ATG74810.1	HXXXD-like acyltransferase family protein	NA	NA
Sapur.012G092700.1	4.60615741	3.15839813	0.30144893	11.08023	1.56E-28	5.71E-28	pseu	-0.38841931	4.96E-07	GO:0055114;GO:0016491	ATG24030.1	ATGA2OX4;ATGA2OX6;OLTA	gibberellin 2-oxidase 6	gibberellin 2-oxidase
Sapur.008G136100.1	5.09518895	2.33127545	0.21147813	11.05921	1.98E-28	7.20E-28	pseu	-0.21204098	0.07340486		ATG22740.1	HMT3	homocysteine S-methyltransferase 3	homocysteine S-methyltransferase
Sapur.004G042200.1	1.22860322	-2.18287786	0.28079851	-11.0391	2.48E-28	8.98E-28	pseu	-0.29926018	0.00037631				NA	hypothetical protein
Sapur.016G085000.1	5.49663665	-2.00862468	0.18208361	-11.0313	2.70E-28	9.80E-28	pseu	-0.03507916	0.66275162		ATG68620.1	alpha/beta-Hydrolases superfamily protein		CXE carboxylesterase
Sapur.017G031200.1	6.57796329	-2.19187109	0.30056216	-10.976	4.98E-28	1.77E-27	pseu	-0.45781627	1.46E-09	GO:0016829;GO:0010333;GO:0008152;GO:0000287	ATTPS03;TPS03	terpene synthase 03	terpene synthase	isoprene synthase
Sapur.016G184700.1	108.7388679	1.20315550	0.11004072	10.90764	1.06E-27	3.80E-27	pseu	-0.40125236	3.91E-07	GO:0055114;GO:0016491	ATG53200.1	FAD/NAD(P)-binding oxidoreductase family protein	monooxygenase, putative	monooxygenase, putative
Sapur.012G000100.1	9.26567852	3.15329918	0.14026512	-10.7694	1.46E-27	2.20E-26	pseu	-0.13946688	0.08159443		ATG56880.2	Transducin/WD40 repeat-like superfamily protein	transducin-like protein, putative	transducin-like protein, putative
Sapur.010G080600.1	107.8702278	0.98204596	0.09123278	10.76489	5.04E-27	1.78E-26	pseu	-0.44547891	4.95E-09	GO:0005515	ATG34930.1	disease resistance family protein / LRR family protein	LRR receptor-like Serine/Threonine-kinase GSO1, putative	LRR receptor-like Serine/Threonine-kinase GSO1, putative
Sapur.002G117800.1	2.10167977	-2.50264383	0.23187784	-10.7437	6.12E-27	2.15E-26	pseu	-0.23197906	0.00481887	GO:0006260	UNE10	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	helix loop helix DNA-binding domain protein, putative	helix loop helix DNA-binding domain protein, putative
Sapur.012G161600.1	89.0275462	-2.86293288	0.17078894	-10.7244	7.82E-27	2.74E-26	pseu	-0.00877971	0.91309769		ATHSL;HS1	heat stable protein 1	stress responsive A/B barrel domain protein	stress responsive A/B barrel domain protein
Sapur.003G093700.1	11.86513886	2.56231599	0.15140926	10.7201	8.16E-27	2.87E-26	pseu	-0.23787738	0.00235867	GO:0003824;GO:0006470;GO:0004722	HA12	highly ABA-induced PP2C gene 2	protein phosphatase 2C	protein phosphatase 2C
Sapur.007G129500.1	31.48043848	1.08891112	0.10192618	10.67643	1.31E-26	4.58E-26	pseu	-0.54784018	1.18E-13				NA	hypothetical protein
Sapur.018G117800.1	5.20212974	3.31767845	0.31430085	10.55214	4.97E-26	1.71E-25	pseu	-0.38299855	7.72E-07	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP716A1	cytochrome P450, family 716, subfamily A, polypeptide 1	cytochrome P450 family protein	cytochrome P450 family protein
Sapur.007G027400.1	19.45737893	-2.95184734	0.16677526	10.5045	8.24E-26	2.82E-25	pseu	-0.50618557	1.36E-11	GO:0016758;GO:0008152		UDP-glucosyl transferase family protein	UDP-glucosyl transferase	UDP-glucosyl transferase
Sapur.001G089000.2	36.2025801	1.17160124	0.11005387	10.36767	3.48E-25	1.17E-24	pseu	-0.00479743	0.95247521	GO:0045165;GO:0006355;GO:0005634;GO:0003700	ATG11660.1	AT-HSFB2B;HSFB2B	winged-helix DNA-binding transcription factor family protein	heat shock transcription factor
Sapur.005G107000.1	188.3595764	0.72362668	0.08074734	10.16412	3.62E-24	1.21E-23	pseu	-0.45902001	1.46E-09	GO:0007010;GO:0005634;GO:0081	ATG39150.1	KIP-related protein 5	cyclin-dependent kinase inhibitor protein	cyclin-dependent kinase inhibitor protein
Sapur.006G096800.1	3.02863671	-3.36264744	0.32724949	-10.2757	9.06E-25	3.03E-24	pseu	-0.45743356	1.76E-09	GO:0045165;GO:0006355;GO:0003700;GO:0003677	ATG03790.1	ATHB51;HB51;LMI1	homeobox 51	homeobox leucine zipper protein ATHB-22
Sapur.008G155800.1	4.00602263	3.93328393	0.48118821	10.25399	1.14E-24	3.76E-24	pseu	-0.23029725	0.00541058		ATG68150.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	NA
Sapur.012G092000.1	129.8998634	0.78581447	0.07606769	10.21055	1.78E-24	5.90E-24	pseu	-0.46824263	3.14E-11	GO:0008270;GO:0005515	ATG47630.1	RING/U-box superfamily protein	RING-U box protein	RING-H2 zinc finger protein
Sapur.012G000300.1	42.30575157	-0.66366213	0.09062818	-10.1233	4.65E-24	1.46E-23	pseu	-0.62457594	3.41E-17	GO:0004252;GO:0004175	ATG44620.1	Peptidase family C1A (papain) protein	low molecular weight tyrosine-phosphatase, putative	low molecular weight tyrosine-phosphatase, putative
Sapur.012G092500.1	4.97769471	-2.12545793	0.21054284	-10.0952	5.80E-24	1.90E-23	pseu	-0.09243125	0.24957932		ATG02480.1	Pectin lyase-like superfamily protein	pectin lyase/curtovirus	polygalacturonase
Sapur.006G073100.1	15.8083204	1.69668179	0.16953609	10.00764	1.41E-23	4.57E-23	pseu	-0.35737369	4.31E-06	GO:0015753;GO:0016020	ATG37730.1	Protein of unknown function (DUF684)	fringe-like protein	fringe-like protein
Sapur.017G123800.1	9.62831	2.40748399	0.24007229	9.8649	5.05E-23	1.66E-22	pseu	-0.40597616	9.99E-08	GO:0043531	ATG44970.1	NB-ARC domain-containing disease resistance protein	NA	NA
Sapur.013G047200.1	5.80216804	1.78937353	0.18205333	9.828515	8.49E-23	2.70E-22	pseu	-0.51639032	4.46E-12	GO:0055515;GO:0006468;GO:0005524;GO:0004672	ATG62930.1	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase	LRR receptor-like kinase
Sapur.006G184300.1	85.01601097	2.27438328	0.13053365	9.76168	1.65E-22	5.21E-22	pseu	-0.31601835	1.5E-07		ATG10520.1	Leucine-rich repeat protein family	17.5 kDa class I heat shock protein	NA
Sapur.016G091900.1	1.94776273	3.26482086	0.33024205	9.623859	6.34E-22	1.97E-21	pseu	-0.39973983	2.14E-07	GO:0016758;GO:0008152	ATG22380.1	AtUGT85A1;UGT85A1	UDP-glucosyl transferase 85A3	UDP-glucosyl transferase 85A3
Sapur.006G116600.1	5.97417518	2.49109382	0.26287132	9.47438	6.42E-21	1.98E-20	pseu	-0.4631356	9.92E-10		ATG27420.1		NA	18.5 kDa class I heat shock protein
Sapur.001G169000.1	605.3452577	1.46818962	0.12052162	9.526788	1.62E-21	5.00E-21	pseu	-0.47254303	1.4E-10	GO:0016021;GO:0015116;GO:0008272;GO:0055085;GO:0016020;GO:0008271;GO:0009560	ATS1;ERS1;ATR1;ERS1	sulfate transporter 3.1	sulfate transporter 3.1	sulfate/bicarbonate/oxalate exchanger and transporter-sat-1
Sapur.012G161300.1	2.34785868	3.01597195	0.31721617	9.46931	2.23E-21	6.84E-21	pseu	-0.39320018	1.8E-07	GO:0005515	ATGB1930.1	AtRLP18;RLP8	receptor like protein	receptor like protein
Sapur.003G117600.1	26.84019606	1.47364776	0.15458829	9.478115	2.58E-21	7.94E-21	pseu	-0.24360763	0.02109497		ATG12710.1	ATHSL;HS1	heat stable protein 1	stress responsive A/B barrel domain protein
Sapur.019G078800.1	14.94422	1.68833015	0.19662818	9.163504	5.81E-21	1.77E-20	pseu	-0.4732632	4.3E-10		ATG46220.1	HXXXD-like acyltransferase family protein	HXXXD-like acyltransferase family protein	NA
Sapur.018G081700.1	4.44622434	2.02869932	0.21732015	9.342763	9.38E-21	2.86E-20	pseu	-0.47466914	3.46E-10	GO:0006508;GO:0004190	ATG23945.1	Eukaryotic aspartyl protease family protein	Eukaryotic aspartyl protease family protein	NA
Sapur.010G073800.1	23.56487481	0.81217789	0.08764956	9.266191	1.93E-20	5.78E-20	pseu	-0.52188441	2.45E-12		ATG48260.1	Homeodomain-like superfamily protein	myb-like DNA-binding domain protein	NA
Sapur.008G139500.1	1.98428652	3.07329325	0.39107618	9.08135	1.04E-20	2.88E-20	pseu	-0.3775146	2.06E-06	GO:0016884;GO:0009058	ATG63110.1	strictosidine synthase 3	strictosidine synthase 3	NA
Sapur.008G120500.1	71.95388369	1.57369559	0.17230591	9.133423	6.64E-20	1.96E-19	pseu	-0.20654793	0.09847569		ATG54870.1	NAD(P)-binding Rossmann-fold superfamily protein	NA	short chain dehydrogenase
Sapur.008G067700.1	8.80667571	2.38282859	0.24108083	9.107969	1.09E-19	2.94E-19	pseu	-0.19192216	0.01533307	GO:0055515;GO:0006468;GO:0005524;GO:0004672	ATEMB1396;EG42	Leucine-rich repeat protein kinase family protein	NA	NA
Sapur.016G192500.1	2.31104182	2.64325273	0.29406866	8.99232	2.42E-19	7.05E-19	pseu	-0.29027849	0.00166563	GO:0006355	ATG15520.1	SIN1-like 2	SIN3-like 2	paired amphipathic helix protein Sin3, putative
Sapur.004G253000.1	121.0119449	1.97466467	0.15402679	8.95642	2.53E-19	9.50E-19	pseu	-0.64884922	3.73E-09	GO:0005515	ATG32170.2	Adenine nucleotide alpha hydrolases-like superfamily protein	universal stress family protein	universal stress family protein
Sapur.015G151400.1	7.12627574	2.05637049	0.23039698	8.925335	4.44E-19	1.38E-18	pseu	-0.35124596	6.47E-06	GO:0006629	ATG30370.1	alpha/beta-Hydrolases superfamily protein	NA	triacylglycerol lipase
Sapur.008G118600.1	1.15146174	3.51648822	0.39460481	8.92085	4.62E-19	1.34E-18	pseu	-0.36238906	2.54E-06		ATEMB1396;EG42	Stress induced protein	NA	late embryogenesis abundant protein
Sapur.002G012800.1	431.4587261	-1.05486527	0.11980764	-8.80984	1.25E-18	3.58E-18	pseu	-0.43562871	1.18E-08	GO:0055114;GO:0016491;GO:0008270	ATCAD6;CAD9	cinnamyl alcohol dehydrogenase 9	NA	NA
Sapur.003G181300.1	34.8058183	-1.76277569	0.20108847	8.66873	4.44E-18	1.25E-17	pseu	-0.32439486	0.00887779	GO:0008233	AECYS2;CYS2	PHYTOCYSTATIN 2	cysteine proteinase inhibitor, putative	NA
Sapur.008G087700.1	-0.03826795	2.41816614	0.27902271	8.628384	5.70E-18	1.60E-17	pseu	-0.24300761	0.02180015		ATG13480.1	Protein of unknown function (DUF1262)	NA	NA
Sapur.006G031300.1	8.92994621	-2.23887993	0.14516277	-8.53447	1.41E-17	3.91E-17	pseu	-0.15593256	0.05155738	GO:0016758;GO:0008152	ATG24040.1	UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase family	NA
Sapur.006G124400.1	5.71165925	-1.96139262	0.23014008	-8.51595	1.65E-17	4.58E-17	pseu	-0.01211046	0.87874555		ATG68570.1	galactinol synthase 4	AtGolS4;GolS4	galactinol synthase
Sapur.005G142600.1	256.7185573	0.85769442	0.10228508	8.390321	4.77E-17	1.30E-16	pseu	-0.50470645	1.58E-11		ATG77180.1	AAT3;ATAAT3	amino acid permease 3	amino acid permease
Sapur.019G142800.1	-2.68024419	3.54080426	0.38031755	8.14086	3.56E-16	8.93E-16	pseu	-0.07200163	0.38221108	GO:0016758;GO:0008152	ATG81610.1	AT2G31;AT5GA20OX2;GA20D	gibberellin 20-oxidase 2	gibberellin 20-oxidase
Sapur.006G075900.2	41.5673322	0.76728842	0.09431037	8.132917	4.16E-16	1.10E-15	pseu	-0.41461935	6.71E-08		ATG02030.1		NA	plant/TTM20-70 protein, putative
Sapur.005G145900.1	10.98327741	-2.63920982	0.17840071	-8.06721	7.16E-16	1.86E-15	pseu	-0.68420304	1.32E-10		ATG02100.1	Homeodomain-like superfamily protein	transcription factor MYB63	transcription factor MYB63
Sapur.019G095900.1	16.85910006	3.31556123	0.51222663	8.059988	7.64E-16	2.02E-15	pseu	-0.49066419	6.86E-11		ATG82680.1		NA	monothiol glutaredoxin-S11, putative	monothiol glutaredoxin-S11, putative
Sapur.003G138800.1	24.36686137	1.19545853	0.14800343	8.076971	6.91E-16	1.83E-15	pseu	-0.40580609	6.01E-07	GO:0016887;GO:0005524;GO:0016020	ATG15530.1	ABCG40;ATABCG40;ATPDR1	pleiotropic drug resistance 12	pleiotropic drug resistance; ABC transporter family protein, putative
Sapur.001G024000.1	4.01305665	1.77875967	0.22131435	8.037057	9.20E-16	2.42E-15	pseu	-0.38548729	6.21E-07		ATG12580.1	ATHSP70;HSP70	heat shock protein 70	heat shock 70 kDa protein
Sapur.001G035200.1	205.2363701	0.45730471	0.05820112	8.032765	9.78E-16	2.57E-15	pseu	-0.48048289	1.91E-10		ATMES1;MES1	methyl esterase 1	methyl esterase 1	NA
Sapur.001G073000.1	1.91158694	-0.52467052	0.06513579	-8.03765	9.94E-16	2.57E-15	pseu	-0.18589013	0.03756105		ATG29370.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	protease inhibitor/seed storage/lipid transfer family protein
Sapur.003G149700.1	1.21519109	2.80287028	0.35157121	7.975922	1.51E-15	3.95E-15	pseu	-0.39352427	3.42E-07	GO:0008146	ATG07010.1	ATST2A;ST2A	sulfotransferase 2A	flavonol 4'-sulfotransferase, putative
Sapur.009G088000.1	11.90691377	-1.06230174	0.13754653	-7.91888	2.56E-15	6.14E-15	pseu	-0.38168159	1.5E-07	GO:0055114;GO:0047134	ATG16050.1	Cysteine/Histidine-rich C1 domain family protein	cysteine/histidine-rich C1 domain family protein	cysteine/histidine-rich C1 domain family protein
Sapur.012G286600.1	2.31532801	-1.68452921	0.21904208	-7.90509	2.68E-15	6.95E-15	pseu	-0.32006262	4.27E-05	GO:0006468;GO:0006672	ATG21960.1	S-locus lectin protein kinase family protein	B120	S-locus lectin protein kinase family
Sapur.012G000200.1	1.87988763	3.06545463	0.39419652	7.7684	7.44E-15	1.91E-14	pse

Sapur.006G129900.1	337.42408	-0.39996045	0.08674071	-3.91969	8.87E-05	0.000149353	pink	-0.24766507	0.00174078	GO:0016747,GO:0008610,GO:0016020,GO:0006633	ACS4G6230.1	KCS2	3-ketoacyl-CoA synthase 2
Sapur.006G133400.1	2.60915902	2.23227949	0.31534894	3.909128	9.26E-05	0.00155855	pink	0.23771359	0.00271655		ACS26650.1		NA
Sapur.006G257500.1	5.46263811	1.03897263	0.26629392	3.901729	9.51E-05	0.00160675	pink	0.6831725	0.29805022	GO:0008152,GO:0003824	ACS26880.1	BZO1	benzoylsuccinoylacetate 1
Sapur.013G110700.1	3.38529805	-1.68162908	0.43371845	-3.87722	0.00010567	0.00177322	pink	0.01391291	1.86293484	GO:0016747,GO:0008610,GO:0016020,GO:0006633	ACS04530.1	KCS19	3-ketoacyl-CoA synthase 19
Sapur.005G081000.1	9.47650525	1.09237617	0.28362546	3.851474	0.00011749	0.00196547	pink	0.18885257	0.01784748	GO:0015114,GO:0048038,GO:0009698,GO:0008031,GO:0005507	ACS21710.1		amine oxidase [copper-containing] protein, putative
Sapur.015G212700.1	0.40042909	1.88838477	0.49368125	3.825109	0.00130714	0.00218235	pink	0.26613486	0.00075473		ACS29290.1		hypothetical protein
Sapur.004G266400.1	0.82758943	-1.50620483	0.39507669	-3.812	0.00013947	0.00229819	pink	0.07202892	1.36891128	GO:0016747	ACS39080.1		HXXXD-type acyl-transferase family protein
Sapur.014G188000.1	27.0068793	0.57688466	0.15167746	-3.80348	0.00014297	0.00237674	pink	-2.22623916	0.00433108	GO:0015114,GO:0004764,GO:0003854	ACS26350.1		dehydroquinate dehydratase/shikimate dehydrogenase
Sapur.018G076000.1	0.77886879	-1.40799692	0.3731844	-3.7728	0.00016427	0.00267997	pink	-1.14284109	0.07431126				NA
Sapur.010G121400.1	309.16971	-0.37015024	0.10184265	-3.72481	0.00019459	0.00322268	pink	-0.22015148	0.00032268	GO:0007165	ACS13740.1	AFP2	ABI five binding protein 2
Sapur.005G191800.1	53.69659053	0.40112181	0.10800372	3.713035	0.00020789	0.00337512	pink	0.23813048	0.02592132		ACS75750.2	GAS41	GAST protein homolog 1
Sapur.018G111900.1	1.05889188	2.59450284	0.70127924	3.698509	0.00023194	0.00382724	pink	-0.04591677	0.92922684	GO:0003824,GO:0008376,GO:0004722	ACS27420.1	HAL2	3'(2'),5'-bisphosphate nucleotidase 1
Sapur.006G070100.1	0.46702878	2.07124249	0.56483695	3.66769	0.00024526	0.00404076	pink	0.33135872	2.245-05		ACS26650.1		NA
Sapur.015G161300.1	0.81464554	1.23232407	0.33680085	3.6567	0.00025131	0.00414784	pink	-0.25225161	0.01884828	GO:0016788	ACS26630.1		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.009G009300.1	0.69150571	-0.65109785	0.49529416	-3.64635	0.00026592	0.00439587	pink	-0.37589261	1.23E-06		ACS20490.1	FLA12	FASCICLIN-like arabinogalactan protein 12
Sapur.002G208500.1	0.40056832	-1.24383623	0.37007519	-3.61652	0.00028938	0.00469013	pink	-0.17630904	0.03477725		ACS20465.1	ATMYB12,MYB3	myb domain protein 3
Sapur.018G074200.1	10.47739614	0.50948483	0.14071208	3.620763	0.00029736	0.00487572	pink	0.17365466	0.02963401	GO:0008270,GO:0005515	ACS18635.1		RING/U-box superfamily protein
Sapur.013G178700.1	12.68603395	0.41639182	0.11520887	3.614237	0.00030124	0.00496045	pink	0.21461199	0.00699369		ACS26625.1	ZFP7	zinc finger protein 7
Sapur.010G098000.1	0.92368213	1.34869532	0.37554692	3.591284	0.00031093	0.00506179	pink	0.92349246	0.01494646	GO:0015114,GO:0005654,GO:0050660,GO:0050662,GO:0004499	ACS26410.1	YUCA	flavine containing monooxygenase
Sapur.001G070000.1	0.55409126	-2.32753293	0.36823579	-3.55221	0.00037889	0.00531852	pink	0.06615825	0.40336966		ACS31180.1	ATMYB14,MYB14,MYB14A7	myb domain protein 14
Sapur.015G171900.1	0.45168204	-1.79877508	0.48802837	-3.58646	0.00037536	0.00527007	pink	0.24227316	0.02020481				hypothetical protein
Sapur.002G057500.1	3099.60884	0.32875762	0.09200224	-3.57313	0.00032742	0.00570288	pink	-0.21858652	0.05993473	GO:0055114,GO:0016491,GO:0008270	ACS17120.1	ADH,ADH1,ATADH,ATADH1	alcohol dehydrogenase 1
Sapur.011G158400.1	1340.59136	0.71386441	0.20117538	3.551303	0.00040219	0.00703128	pink	0.25001652	0.05538653	GO:0016491,GO:0055114,GO:0016491	ACS14120.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.019G228900.1	197.4970001	0.12534742	0.09356463	3.477069	0.00050938	0.00891029	pink	0.23950506	0.00251825	GO:0005524	ACS40032.1	AATP1	AAA-ATPase 1
Sapur.006G170700.1	7.80376842	0.89969157	0.26067067	3.451471	0.00055704	0.00973722	pink	0.19609578	0.01842668	GO:0005509			NA
Sapur.008G111900.1	41.30229027	-0.37170984	0.10947752	-3.39147	0.00069179	0.01105561	pink	-0.20933752	0.03807209	GO:0007165,GO:0000155,GO:0000160	ACS02180.2	AHK4,ATCRE1,CRE1,WOL,W	CHASE domain containing histidine kinase protein
Sapur.015G077100.1	126.2779878	0.43062229	0.12608161	3.39123	0.00069798	0.01106498	pink	0.13492678	0.09578795		ACS14440.1	ATNCED3,NCED3,SDT,STO1	nine-cis-epoxycarotenoid dioxygenase 3
Sapur.006G077400.1	1.76894002	0.39891424	0.26747478	3.35925	0.00078153	0.01238124	pink	-0.03843666	0.63087851	GO:0005507,GO:0055114,GO:0016491	ACS20220.1	LACT	laccase 7
Sapur.004G136700.1	14.02808445	-0.65169785	0.19388162	-3.35852	0.00078734	0.01242962	pink	-0.25385967	0.00133589	GO:0009733	ACS29480.1		SAUR-like auxin-responsive protein family
Sapur.013G268000.1	41.83495949	0.32663674	0.09658274	3.381084	0.00091602	0.01467983	pink	0.19321871	0.01337557	GO:0016788	ACS18311.1		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.002G081200.1	22.58727942	0.45318402	0.13713242	3.305049	0.00094599	0.01495075	pink	0.17845471	0.02534369	GO:0005085,GO:0016020,GO:0051297,GO:0051328,GO:0006855	ACS18340.1	ZF14	MATE efflux family protein
Sapur.T044600.1	12.70761114	0.10982681	0.33893131	-3.274	0.00106035	0.01664251	pink	0.24277536	0.02020481	GO:0005515	ACS29550.1	ATMYB123,ATTT2,MYB123	Duplicated homeodomain-like superfamily protein
Sapur.003G121700.1	9.96801041	0.42045528	0.13074687	3.240191	0.00114497	0.01807668	pink	0.22039129	0.00540172		ACS45420.1	LBD18	LOB domain-containing protein 18
Sapur.002G202800.1	11.23818025	0.42035365	0.13006239	3.231462	0.00119015	0.01859119	pink	0.20968568	0.03845809		ACS31160.1	LSH3	Protein of unknown function (DUF640)
Sapur.015G222800.1	6.11394768	0.79053738	0.24672016	3.204186	0.00135445	0.02110083	pink	0.21850948	0.00568586	GO:0048544,GO:0006468,GO:0004672	ACS11340.1		S-locus lectin protein kinase family protein
Sapur.008G208500.1	1398.462869	0.19157001	0.06000355	3.192266	0.00140306	0.02191597	pink	0.12533307	0.00458169	GO:0006950	ACS29370.1		stress-induced protein
Sapur.15WG134600.2	1.24620854	1.24279479	0.39135561	3.17809	0.00158599	0.02464925	pink	0.19156532	0.01601528	GO:0005515,GO:0006468,GO:0055114,GO:0004672	ACS08550.1		Leucine-rich repeat receptor-like protein kinase family protein
Sapur.006G138800.1	2.86349029	0.78345447	0.24854203	3.152245	0.0016202	0.02514126	pink	0.17591707	0.02753348		ACS42760.1		NA
Sapur.15WG141600.1	2.70380327	0.60605076	0.19651991	3.11327	0.00185156	0.02869722	pink	0.17291194	0.03032382	GO:0005515,GO:0006468,GO:0055114,GO:0004672	ACS08850.1		Leucine-rich repeat receptor-like protein kinase family protein
Sapur.009G047400.1	1.86698849	-0.83827147	0.27004152	-3.07159	0.00215921	0.03372886	pink	-2.24935866	0.02427763		ACS08490.1		transmembrane protein, putative
Sapur.014G307800.1	3.85175852	0.75541242	0.24587545	3.072418	0.00216121	0.03382563	pink	-0.18760617	0.01863024	GO:0045454,GO:0015035,GO:0009055	ACS47080.1		Glutaredoxin family protein
Sapur.015G077700.1	26.60722399	0.41885679	0.13758356	3.043153	0.00234133	0.03588406	pink	0.13034039	0.10374966		ACS14440.1	ATNCED3,NCED3,SDT,STO1	nine-cis-epoxycarotenoid dioxygenase 3
Sapur.005G195000.1	0.58824448	0.82237974	0.27080628	3.038668	0.00238792	0.03652508	pink	0.19859717	0.01882045				NA
Sapur.002G051300.1	3.37075139	-1.55847239	0.52330653	-2.98398	0.00284257	0.04334184	pink	-0.15475583	0.05297741				NA
Sapur.015G204700.1	25.35769173	0.32000396	0.10734692	2.980126	0.00287422	0.04399504	pink	0.20588142	0.00668982	GO:0005515,GO:0006468,GO:0055114,GO:0004672	ACS47570.1		Leucine-rich repeat protein kinase family protein
Sapur.015G191200.1	16.03873887	0.32033516	0.10798835	-2.96634	0.00301679	0.0458521	pink	-0.22816549	0.00652366	GO:0006281	ACS24140.1	FMA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.001G125600.1	210.2353383	0.07477529	0.02523148	2.963167	0.00304313	0.04771015	pink	0.17668679	0.02837489	GO:0006413,GO:0003743	ACS54940.1		Translation initiation factor SUI1 family protein
Sapur.002G215400.1	0.02823323	1.14578305	0.38853854	2.948954	0.00318518	0.04836593	pink	1.20637872	0.00958148				transmembrane protein, putative
Sapur.001G035500.1	99.04712821	-0.32522151	0.10739734	-2.93065	0.00328552	0.04975211	pink	-0.13227831	0.01586144	GO:0005516	ACS38800.1		plant calmodulin-binding domain protein
Sapur.003G097900.1	1369.73082	0.15226231	0.04329132	2.91875	0.00353407	0.05351122	pink	-0.24068254	0.03296366		ACS44841.1		transcription factor, putative
Sapur.002G026500.1	7.15311665	0.45165953	0.15503853	2.913177	0.00357775	0.05404659	pink	0.19395859	0.01493993				NA
Sapur.002G170300.1	0.51178208	-1.13195164	0.39157325	-2.87752	0.00400624	0.06024629	pink	-0.10549901	0.18756241	GO:0007275	ACS45190.1	AFO,FIL,YAB1	Plant-specific transcription factor YABBY family protein
Sapur.008G119000.1	0.53104559	1.05719176	0.36764137	2.875608	0.00402503	0.06066454	pink	0.07854831	0.3261487		ACS14780.1		MAC/Perforin domain-containing protein
Sapur.004G207400.1	20.2797964	0.50205102	0.17463167	2.87456	0.00404207	0.06095994	pink	0.26204881	0.00108489		ACS45380.1	CLPR4,NCLPR4	CLP protease R4
Sapur.007G080900.1	2.37124692	0.68338109	0.24028591	2.774551	0.00552798	0.08219594	pink	0.13926982	0.08192841		ACS06920.1	FLA21	FASCICLIN-like arabinogalactan protein 21 precursor
Sapur.015G130300.1	0.56832878	0.73188828	0.27611519	2.651388	0.00798152	0.11822553	pink	0.13264331	0.12278938		ACS26110.1	MPL1	Myosin penetration-induced kinase 1
Sapur.T044600.1	1.47148433	1.19296784	0.43074204	2.769569	0.00561056	0.08332789	pink	0.1728879	0.03054569	GO:0005515,GO:0006468,GO:0055114,GO:0004672	ACS08850.1		Leucine-rich repeat receptor-like protein kinase family protein
Sapur.018G095600.1	0.37891091	1.79514196	0.64897029	2.76613	0.00567586	0.08481842	pink	0.11202517	0.15858768		ACS29550.1	ATMYB123,ATTT2,MYB123	Duplicated homeodomain-like superfamily protein
Sapur.013G071300.1	0.36360960	1.02326063	0.37010384	2.76447	0.00568605	0.08492945	pink	-0.05632468	0.45312759	GO:0010312,GO:0008270,GO:0005509,GO:0005622	ACS24140.1		Matrixin family protein
Sapur.014G048200.1	2.08894818	0.67428313	0.24510872	2.752362	0.00595704	0.08767039	pink	0.15074205	0.06050229	GO:0006281	ACS08550.1	UNI10	helix loop helix DNA-binding domain protein
Sapur.001G125600.1	0.39457153	0.84969453	0.31000257	2.740993	0.00605943	0.08928024	pink	0.19882604	0.01520467	GO:0006508,GO:0004252	ACS19170.1	SBT1.7	subtilisin-like serine protease 1.7
Sapur.005G151300.1	6.27908859	0.38467948	0.14087591	-2.73073	0.00633431	0.09360343	pink	-0.03160284	0.63229056	GO:0006355,GO:0003700	ACS47560.1	ABR1	Integrase-type DNA-binding superfamily protein
Sapur.004G417140.1	42.26270204	0.34861683	0.13053625	2.671433	0.00760722	0.11166188	pink	0.16302016	0.04062885	GO:0043565,GO:0006355,GO:0003700	ACS54450.1	ATWRKY70,WRKY70	WRKY DNA-binding protein 70
Sapur.008G067300.2	39.7991553	0.23365116	0.08751506	2.669117	0.00765105	0.11166258	pink	0.19183597	0.01634549		ACS02280.1		Phototropic-responsive NPH3 family protein
Sapur.002G078400.1	7.61661389	0.27224466	0.10207584	2.666319	0.00767084	0.11207446	pink	0.12423604	0.07132064		ACS29360.1		HSP20-like chaperones superfamily protein
Sapur.017G038500.1	160.3972695	-0.26680605	0.09841483	-2.6489	0.00807576	0.11826293	pink	-0.19152538	0.01264885				hypothetical protein
Sapur.015G102300.1	0.46466413	0.00073035	0.19740687	2.00468	0.0451648	0.21990733	pink	0.07854831	0.32814867	GO:0016846	ACS24630.2	TAR2	tryptophan aminotransferase related 2
Sapur.006G116900.1	331.7928827	-0.50650977	0.19319738	-2.62214	0.0873379	0.01275632	pink	0.02279322	0.77690475	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ACS07980.1	CYP75B1,D501,T77	Cytochrome P450 superfamily protein
Sapur.006G213300.1	39.96744964	0.30067121	0.10182736	2.559489	0.01048261	0.01598223	pink	0.17061295	0.03261968				hypothetical protein
Sapur.011G086400.1	76.47020227	0.52011876	0.19195441	-2.55551	0.01063288	0.01630777	pink	0.21712419	0.06305098	GO:0007017,GO:0005875	ACS27160.1		Dynein light chain type 1 family protein
Sapur.014G079200.1	10.53415889	0.30735852	0.12112648	-2.49979	0.01243648	0.01787807	pink	-0.16851749	0.03488474		ACS22640.1	ATMYB3,MYB3	myb domain protein 3
Sapur.010G087100.1	7.06466521	0.33691912	0.13648851	2.469399	0.01272783	0.01832257	pink	0.16403541	0.03181224	GO:0046872,GO:0030001	ACS22990.1		Heavy metal transport/detoxification superfamily protein
Sapur.015G137700.1	0.36318098	-1.27685631	0.51181718	-2.48507	0.01292972	0.01859484	pink	0.23167516	0.76887137		ACS05620.3	AS2	Lateral organ boundaries (LOB) domain family protein
Sapur.015G217000.1	2.18215157	0.38240876	0.15475179	2.46898	0.01357248	0.01948425	pink	0.07854831	0.32814867		ACS22640.1		Protein kinase superfamily protein
Sapur.009G094100.1	1.12765521	0.71443725	0.29029397	2.460777	0.01383649	0.01985329	pink	0.13054243	0.10108776	GO:0046872,GO:0030001	ACS08600.2		Heavy metal transport/detoxification superfamily protein
Sapur.006G225300.1	0.79051660	0.26788481	0.11346049	-2.41302	0.01635506	0.02331825	pink	0.04543852	0.57028148		ACS29550.1	ATMYB123,ATTT2,MYB123	Duplicated homeodomain-like superfamily protein
Sapur.012G091900.1	0.96809614	0.30796782	0.41756364	2.413925	0.01578126	0.02463626	pink	0.13139399	0.09645668		ACS21440.1	ATMYB,ATMYB102,MYB102	MYB-like 102
Sapur.005G088000.1	0.44832966	0.33835533	0.15628542	-2.40585	0.01624948	0.02536786	pink	-0.30430416	0.00108521		ACS04770.1	RGF9	transmembrane protein, putative
Sapur.004G068105.1	0.33042744	1.59150687	0.66345847	2.40402	0.01629126	0.02538129	pink	0.08784691	0.27608042	GO:0016747	ACS39550.1		HXXXD-type acyl-transferase family protein
Sapur.002G054840.1	0.36405598	0.91745582	0.38195425	2.402006	0.01635457	0.02535267	pink	0.19324625	0.0142067		ACS27020.1		DNA/ RNA heat shock N-terminal domain-containing protein
Sapur.T075700.1	11.27446213	0.03719772	0.01623436	2.290195	0.02198477	0.03245184	pink	0.17327605	0.03035566		ACS27160.1		Ankyrin repeat family protein
Sapur.015G011200.1	434.9279671	0.21689622	0.09100716	2.381017	0.01726492	0.02466422	pink	0.16863707	0.03478664	GO:0055114,GO:0016491	ACS05010.1	ACO6,EAT1,EFE	ethylene-forming enzyme
Sapur.015G111500.1	1.76225746	0.6828492	0.27859635	2.37004	0.01779743	0.02597851	pink	0.11914166	0.13724982				NA
Sapur.002G209600.1	26.89061407	0.52406089	0.22020998	2.331335	0.01963557	0.02786677	pink	0.09947042	0.21527103		ACS29150.1		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.002G087200.1	12.03588663	0.45157063	0.22274936	2.32815	0.01990414	0.02854952	pink	0.13023214	0.10451617		ACS46150.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Sapur.009G092400.1	0.32716357	-1.40932619	0.61430255	-2.29383	0.02180268	0.03061749	pink	0.02481638	0.75769674		ACS18340.1		alpha/beta-Hydrolases superfamily protein
Sapur.003G104900.1	0.35798593	-1.06334065	0.47000324	-2.26184	0.02372613	0.03303309	pink	0.04543852	0.65007524	GO:0005515	ACS29550.1	ABIL1,RLP1	receptor like protein 1
Sapur.005G021300.1	0.46854778	-0.19286604	0.05088521	-2.28255	0.02245673	0.03482947	pink	0.13953548	0.08134825	GO:0016747	ACS48930.1	HCT	hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyl transferase
Sapur.15WG101100.1	0.35869755	1.54534636	0.67941654	2.274225	0.02292248	0.03550133	pink	0.27928846	0.00039704		ACS62390.1		O-fucosyltransferase family protein
Sapur.004G160001.1	7.08169907	0.32597689	0.14410648	2.261276	0.02368222	0.03669704	pink	0.12182182	0.19198886		ACS29560.1	LAP5	Chalcone and stilbene synthase family protein
Sapur.013G168800.1	62.01082717	0.23683076	0.10583833	-2.23724	0.02507641	0.03523707	pink	-0.14842967	0.07030648	GO:0006355,GO:0003700	ACS08860.1		Integrase-type DNA-binding superfamily protein
Sapur.015G244600.1	1.32740534	0.74656297	0.33670315	2.22437	0.02615266	0.03641921	pink	-0.03325791	0.67925125	GO:0055114,GO:0005506,GO:0046872,GO:0004672	ACS21380.1	ARK1,RK3	receptor kinase 3
Sapur.006G130000.1	7.36235329	-0.32161255	0.14784646	-2.18085	0.02916602	0.04045766	pink	0.0011784	0.98838819	GO:0006355,GO:0003700	ACS64750.1	ABI1	Integrase-type DNA-binding superfamily protein
Sapur.006G184300.1	943.3317224	0.10241169	0.08875077	2.167875	0.03019232	0.04194188	pink	0.1551526	0.02425513		ACS27920.1		hypothetical protein
Sapur.014G003300.1	627.3307546	0.12547039	0.05803816	2.161202	0.03052563	0.04242874	pink	0.14804859	0.06421762	GO:0006623,GO:0003824	ACS42320.1	AWI10,VEP1	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.015G222300.1	0.31602189	0.96008318	0.45142879	2.10861	0.03237032	0.04632746	pink	0.16809321	0.01840214				hypothetical protein
Sapur.009G212300.1	133.6157788	-0.29028751	0.13633947	-2.12942	0.03319267	0.04580183	pink	-0.15143931	0.05845643	GO:0048527,GO:0042545,GO:0030599,GO:0005618	ACS15830.1	ATPME2,PME2	pectin methylesterase 2
Sapur.015G136300.1	132.3312121	-0.45065509	0.21142351	2.100057	0.03573816	0.04909130	pink	0.13058717	0.10362411		ACS16830.1		zinc ion-binding protein, putative
Sapur.006G041100.1	10.57077958	-0.25429653	0.12232538	-2.07985	0.03735928	0.05140171	pink	0.03020146	0.90976731	GO:0006355,GO:0003700	ACS30500.2	NF-YA7	nuclear factor Y, subunit A7
Sapur.005G138200.1	49.38855751	-0.18489755	0.08931936	-2.06788	0.03885135	0.05290086	pink	0.14452017	0.07094184		ACS16810.2		NA
Sapur.004G017000.1	41.33237111	-0.18222123	0.08660162	-2.03415	0.04193667	0.05738075	pink	-0.14158612	0.07692223	GO:0004544,GO:0006468,GO:0004672	ACS21380.1	B120	S-locus lectin protein kinase family protein
Sapur.018G201000.1	68.41223856	-0.25432715	0.12546073	-2.02687	0.04351107	0.05924685	pink	-0.11552476	0.18276318	GO:0016757	ACS56600.1	AtGolS2,GolS2	galactinol synthase
Sapur.014G113300.1	21.38596838	-0.20424219	0.10173542	-2.00752	0.04694271	0.06075721	pink	-0.1649459	0.03898978	GO:0008270,GO:0005515	ACS18720.2		RING/U-box superfamily protein
Sapur.013G122000.1	428.6226611	-0.23519196	0.11722898	-2.0064	0.04813015	0.06261067	pink	-0.14707755	0.06632663		ACS29290.1		NA
Sapur.018G092900.1	1203.188779	0.16442294	0.08209104	1.974068	0.04870424	0.06349815	pink	0.12516262	0.11831092	GO:0051082,GO:0006950,GO:0006457,GO:0005524	ACS60000.1	Athsp90.4,Hsp90.4	HEAT SHOCK PROTEIN 81.4
Sapur.015G011100.1	4.62667336	0.61684535	0.31688307	1.946614	0.05183835	0.06737832	pink	0.02192046	0.7832283	GO:0006508,GO:0004190	ACS07730.1		Eukaryotic aspartyl protease family protein
Sapur.005G145900.1	1.96895089	0.40091904	0.23517208	1.910066	0.05623696	0.07546409	pink	0.12613352	0.10691277		ACS77020.1		DNA/ heat shock N-terminal domain-containing protein
Sapur.002G039200.1	113.6908468	0.34726587	0.18100075	1.896583	0.05782953	0.07760486	pink	0.14216489	0.07571345	GO:0055114,GO:0016491	ACS06620.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.015G267500.1	0.34619664	0.98788356	0.51506401	1.891656	0.05868745	0.07940274	pink	0.10189747	0.22765944		ACS27160.1	ATAUL1,FLA11	FASCICLIN-like arabinogalactan-protein 11
Sapur.006G087700.1	367.1738087	0.36103104	0.18778811	1.880941	0.05997885	0.08030328	pink	0.12927801	0.3560732		ACS11650.1	ATOSM34,OSM34	osmotin 34
Sapur.015G087200.1	0.46079207	0.90000424	0.48004124	1.87022	0.06142762	0.08233746	pink	0.12735476	0.06848938		ACS76570.1		NA
Sapur.015G042400.1	9.90352866	-0.27688465	0.14707167	-1.86974	0.06155298	0.08230693	pink	-0.18165167	0.02791651	GO:0055114,GO:0016491	ACS22240.1	ATEFR1,EFR1	ethylene response factor 1
Sapur.015G047200.1	0.2364793	1.86264794	0.68997848	1.860969	0.06173187	0.08365264	pink	0.10189747	0.22765944		ACS27340.1	CYP81D2	cytochrome P450 family 81, subfamily D, polypeptide 3
Sapur.017G102000.1	6.58145601	-0.43201538	0.23029585	-1.82835	0.06750676	0.08987528	pink	0.13017857	0.10419853	GO:0008168	ACS15125.1		5-adenosyl-L-methionine-dependent methyltransferase superfamily protein
Sapur.015G176100.1	20.53326404	-0.19227592	0.10255224	-1.8241	0.07124944	0.09186132	pink	0.12132109	0.11963185		ACS36460.1		hypothetical protein
Sapur.001G165000.1	261.7859425	-0.24398429	0.13425749	-1.81734	0.06916539	0.09374149	pink	0.12351295	0.09667301		ACS05910.1		Protein of unknown function (DUF567)
Sapur.002G098900.1	1.28857169	0.70466438	0.39156721	1.798987	0.07180876	0.09700341	pink	0.11541724	0.14993573		ACS28575.1	EPF1	epidermal patterning factor 1, putative
Sapur.006G138900.1	13.05617	0.23762605	0.13276636	-1.787	0.07383054	0.09793793	pink	-0.1587153	0.04975369		ACS57526.1	ATZFP2,ZFP2	zinc finger protein
Sapur.001G145300.1	49.31707587	0.29002072	0.16242887	1.785522	0.07417633	0.09829098	pink	0.11414586	0.15459672	GO:0055114,GO:0016630	ACS06120.1	GAPC,GAPC-1,GAPC1	glyceraldehyde-3-phosphate dehydrogenase C subunit 1
Sapur.005G203100.1	26.68216148	0.14375615	0.18217805	-1.77516	0.07587242	0.10050271	pink	-0.1187804	0.18441552		ACS22621.1		Putative membrane lipoprotein
Sapur.019G107400.1	0.49125128	0.7291322	0.4114955	1.771908	0.07649789	0.10108402	pink	0.15907766	0.04559191		ACS03170.1	ATFLA11,FLA11	FASCICLIN-like arabinogalactan-protein 11
Sapur.005G138700.1	51.95388325	0.14009169	0.08205419	1.707485	0.08023115	0.10568181	pink	0.13887315	0.08973668	GO:0006355,GO:0008468,GO:0055114,GO:0004672	ACS17610.1		protein kinase family protein
Sapur.001G192200.1	16.65587561	0.30938631	0.18065971	1.712178	0.08683936	0.11387336	pink	0.06481254	0.41998369	GO:0008324,GO:0006470,GO:0004722	ACS27630.1		Protein phosphatase 2C family protein
Sapur.015G184000.1	17.44846417	0.19881046	0.11642052	-1.7024	0.08865128	0.11966046	pink	-0.14054158	0.07016647		ACS27320.1		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Sapur.012G260300.1	22.78832613	0.33347241	0.19673567	1.693402	0.09039704	0.11830904	pink	0.12617032	0.12918487	GO:0045735	ACS07750.1		RmlC-like cupins superfamily protein
Sapur.015G000500.1	0.31004543	0.94387982	0.56000158	1.685387	0.09172852	0.11988734	pink	0.09182279	0.51346007		ACS29150.1	ATWI-12,SAG20,WI12	senescence-associated gene 20 protein
Sapur.018G182100.1	84.45412383	-0.10982152	0.06605198	-1.66359	0.09619608	0.12546969	pink	-0.13930724	0.08184628	GO:0055114,GO:0050660,GO:0016491,GO:0019139,GO:0009690	ACS21482.1	ATCKX5,CKX7	cytokinin oxidase/dehydrogenase
Sapur.002G088900.1	0.23282934	0.85736737	0.51627192	1.63943	0.09729146	0.12647618	pink	0.19726437	0.01327461	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ACS24910.1	CYP714A1	cytochrome P450 family 714, subfamily A, polypeptide 1
Sapur.016G056600.1	585.4875445	-0.12409869	0.07524264	-1.63858	0.10129892	0.13177521	pink	-0.12469769	0.19397725	GO:0006950,GO:0051082,GO:0005371	ACS12050.1		Ahsp domain-containing protein
Sapur.015G037900.1	14.92753592	0.16431895	0.10058162	1.63162	0.10275963	0.13327388	pink	0.12319724	0.12428829	GO:0006355,GO:0003677	ACS28550.1	OBP4	DNA/ binding protein 4
Sapur.009G208500.1	44.24849329	0.22622195	0.13182164	1.62268	0.10470956	0.13591096	pink	0.10719932	0.31180227		ACS49570.1		Family of unknown function (DUF716)
Sapur.003G134000.1	0.19100686	1.40968889	0.87152658	1.617472	0.10576459	0.13788782	pink	0.28350602	0.00102707	GO:0000160	ACS42880.2	ARR22,RR22	response regulator 22
Sapur.016G166200.1	6.58443856	0.22207192	0.14432575	1

Sapur.15WG1315800.1	0.18350511	0.18458545	0.84068543	-0.21952	0.82624413	0.87702202	pink	-0.13789196	0.08521578	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT4G35510.1	CYP76C4	cytochrome P450 family 76, subfamily C, polypeptide 4	cytochrome P450 family 76
Sapur.01G0213400.1	0.07682792	0.40319282	1.88559584	2.314054	0.83056625	0.88041639	pink	-0.04670386	0.56136596		AT5G03170.1	ATFLA11;FLA11	FASCICLIN-like arabinogalactan-protein 11	fasciclin-like AGP protein
Sapur.01G0284800.1	173.0319369	0.02071527	0.09922642	-0.30873	0.83469364	0.88380086	pink	-0.01617379	0.84101282	GO:0016597;GO:0008152	AC4H	AC4H	AC4 domain repeat 4	four ACT domain protein
Sapur.01G0125600.1	0.56495145	0.41588471	2.03547625	0.204319	0.83810448	0.88642732	pink	0.13743804	0.08607729	GO:0005975;GO:0004553	BGLU13	BGLU13	beta glucosidase 13	beta-glucosidase
Sapur.01G0261100.1	0.99565763	0.23668632	1.37107548	0.165343	0.86867698	0.91079114	pink	-0.00293802	0.97092004		AT5G57670.1	NTT;WIP2	C2H2-type zinc finger family protein	transparent TESTA 1 protein, putative
Sapur.01G0138500.1	28.17180711	0.01972284	0.124390325	0.158608	0.87307783	0.91436882	pink	0.00810924	0.93752262					NA
Sapur.01G0285400.1	344.9220594	0.00686688	0.04388322	-0.15722	0.87027238	0.91595417	pink	-0.01520495	0.85091611		AT4G04440.2		Protein of unknown function (DUF2741)	NA
Sapur.01G0270200.1	0.05162529	0.10245736	1.32376767	0.14536	0.88445667	0.92188673	pink	0.08017415	0.13820384		AT3G11180.1	ATMYB14;MYB14;MYB14A7	myb domain protein 14	NA
Sapur.01G0125200.1	0.08727609	0.14010103	1.069316638	-0.13104	0.89579596	0.92970013	pink	0.04666025	0.614881619	GO:0004857;GO:0042545;GO:0030599;GO:0005618	AT5G50010.1	PME61	pectin methylesterase 61	pectinesterase/pectinesterase inhibitor, putative
Sapur.15WG0511000.1	0.59461379	0.02917617	0.34246455	-0.12882	0.97970605	0.99117506	pink	0.07720231	0.91317506	GO:0016844;GO:0008508	AT5G07000.1	SI3	Peptidase family M1	NA
Sapur.15WG0528800.1	0.05788159	0.16842764	1.57536344	0.106936	0.91483953	0.9445121	pink	-0.00623548	0.90469045	GO:0055115;GO:0006468;GO:0005524;GO:0004672	AT3G47570.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.01G0137800.1	2.191194965	0.08012264	0.27517563	0.018139	0.91893437	0.94688194	pink	0.00033108	0.96605608		AT1G01520.1	ATCCD1;ATNCED3;CCD1;NC	carotenoid cleavage dioxygenase 1	retinal pigment epithelial membrane protein
Sapur.01G0138200.1	215.4143975	-0.19190803	0.15113724	0.090241	0.92665803	0.95182285	pink	-0.00464174	0.95078354	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT4G15500.1	ATB4;CYP83B1;B1D1;RNT1;	cytochrome P450, family 83, subfamily B, polypeptide 1	cytochrome P450 family protein
Sapur.01G0288900.1	0.36931675	0.02373169	0.37588674	0.073352	0.94233106	0.96234173	pink	0.05802604	0.53136653		AT5G36160.1		Transmembrane protein (DUF1421)	NA
Sapur.01G0105500.1	12.84263237	-0.00083713	0.12865671	-0.06521	0.94850202	0.96631655	pink	0.07468203	0.15295861		AT3G23250.1	ATMYB15;ATY19;MYB15	myb domain protein 15	MYB transcription factor
Sapur.01G0281100.1	4.17095028	0.08185265	0.22268165	0.053413736	0.95343178	0.96947139	pink	0.06494219	0.92726485		AT5G18670.1		Ankyrin-repeat family protein	NA
Sapur.01G0266600.1	5.09937167	-0.00988372	0.20977522	-0.04719	0.96236148	0.97493584	pink	0.04651853	0.54290664		AT4G21440.1	ATMM;ATMYB102;MYB102	MYB-like 102	MYB transcription factor, putative
Sapur.01G0144100.1	0.18761075	-0.03680123	0.83006234	-0.04634	0.96462705	0.97646236	pink	-0.05574881	0.48802711		AT5G30130.1	ATLS;LBD12;PCL1	Lateral organ boundaries (LOB) domain family protein	LOB domain protein
Sapur.01G0149100.1	98.47765429	-0.00203471	0.12114663	-0.00409	0.97133877	0.98197441	pink	0.06735495	0.31207461	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP707A2	CYP707A2;CYP707A2	Cytochrome P450 family 707 subfamily A polypeptide 2	cytochrome P450 family 92 protein
Sapur.T01350.1	0.19655974	0.22353993	0.03790565	0.01798	0.96070232	0.9798804	pink	0.07397834	0.37032739	GO:0004544;GO:0006468;GO:0005524;GO:0004672	AT5G60600.1	RLK1	receptor-like protein kinase 1	LRR receptor-like kinase
Sapur.01G0118900.1	0.60318864	0.07209733	0.36700452	0.015333	0.97970604	0.98689125	pink	0.07720231	0.91317506	GO:0016844;GO:0030598;GO:0005618	AT5G07820.1		Plant invertase/pectinesterase inhibitor superfamily	pectinesterase/pectinesterase inhibitor, putative
Sapur.01G0284200.1	1.61439088	0.00351484	0.26291528	0.013369	0.98933624	0.99311704	pink	-0.03521598	0.65869509	GO:0004688;GO:0005524;GO:0004672;GO:0030246	AT5G08870.1		Concanavalin A-like lectin protein kinase family protein	lectin domain receptor kinase
Sapur.01G0132400.1	21.79493427	0.00984932	0.11647068	-0.00729	0.99413785	0.99688598	pink	0.00507771	0.99475553	GO:0055115	AT5G60010.1		Plant regulator RWP-RK family protein	NA
Sapur.01G0182300.1	0.02550673	0.35175576	2.904832694	0.122456	0.90258209	NA	pink	0.11874452	0.13864876					hypothetical protein
Sapur.01G0285600.1	0.02257713	0.34679442	2.904832694	0.122456	0.90498165	NA	pink	0.08809645	0.22378631	GO:0016787	AT4G27440.1	atnudt8;NUDT8	nudix hydrolase homolog 8	nudix hydrolase superfamily protein
Sapur.02G0284800.2	0.02903851	0.34601939	2.904809454	0.118431	0.90572618*	NA	pink	0.05709941	0.47752721	GO:0006355;GO:0006348;GO:0007030;GO:0046983;GO:0003677	AT3G22540.1	AGL22;SVP	K-box region and MADS-box transcription factor family protein	MADS box transcription factor
Sapur.05G0135300.3	0.94261395	0.19845819	1.862860142	0.106538	0.91515853	NA	pink	-0.00784586	0.92234291		AT5G66680.3		Protein of unknown function, DUF547	electron transporter, putative
Sapur.01G0214300.1	0.04166196	0.28010474	2.767105575	0.101806	0.91588192	NA	pink	0.15588423	0.05123985					NA
Sapur.01G0170600.1	0.03712212	0.25943387	2.63947863	0.09829	0.92170231	NA	pink	0.10053607	0.23209631					NA
Sapur.01G0263800.1	0.01307441	0.26859465	2.904819115	0.118437	0.92632678	NA	pink	0.07854531	0.32814687		AT3G61730.1	ANMYB113;MYB113	myb domain protein 113	R2R3 Myb transcription factor, putative
Sapur.15WG0526800.1	0.31267283	0.22609628	2.904820351	0.077805	0.93780144	NA	pink	0.11034081	0.16887359	GO:0055115;GO:0006468;GO:0005524;GO:0004672	AT4G07090.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.05G0103300.2	0.03251202	0.26180193	2.124576242	0.075412	0.93988691	NA	pink	0.06562461	0.41416625		AT5G66020.3		Protein of unknown function, DUF547	electron transporter, putative
Sapur.01G0137800.1	0.06570737	0.16448504	2.351880804	0.066937	0.94424346	NA	pink	0.025403811	0.75215479	GO:0055114;GO:0016491;GO:0005507	AT5G09360.1	LAC14	laccase 14	laccase
Sapur.01G0285100.1	0.07737946	0.07186687	2.9048195	0.0592	0.95270556	NA	pink	0.10966454	0.17038618	GO:0016021;GO:0016020;GO:0022857	AT5G25250.1		nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein SAG4
Sapur.01G0282900.1	0.09028593	0.16533762	2.904823145	0.056987	0.95455317	NA	pink	0.07854531	0.32814687					hypothetical protein
Sapur.01G0285300.1	0.02028563	0.16533762	2.904823145	0.056987	0.95455317	NA	pink	0.07854531	0.32814687	GO:0004531	AT5G17680.1		disease resistance protein (TIR-NBS-LRR class), putative	NA
Sapur.01G0285500.3	0.09968051	0.16428147	2.904821183	0.056555	0.95489948	NA	pink	0.07854531	0.32814687	GO:0055115;GO:0006468;GO:0005524;GO:0004672	AT2G25790.1		Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.01G0257200.4	0.04848364	0.15781443	2.904823279	0.054329	0.95667389	NA	pink	0.13974742	0.17134264	GO:0005085;GO:0016021	AT4G22990.2		Major facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein	SPX domain membrane plant protein
Sapur.05G0125000.1	0.01808451	0.15183426	2.904823101	0.053423	0.95785112	NA	pink	0.00387703	0.96155045		AT5G03170.1	ATFLA11;FLA11	FASCICLIN-like arabinogalactan-protein 11	fasciclin-like AGP protein
Sapur.15WG0546600.1	0.04022874	0.15155893	2.904825569	0.052189	0.95837832	NA	pink	0.07854531	0.32814687	GO:0055115;GO:0006468;GO:0005524;GO:0004672	AT4G37530.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.05G0263200.1	0.00809368	0.14338681	2.904822821	0.049361	0.96063189	NA	pink	0.07854531	0.32814687					NA
Sapur.01G0132300.1	0.00692843	0.14338681	2.904822821	0.049361	0.96063189	NA	pink	0.07854531	0.32814687		AT3G24250.1		RNA-directed DNA polymerase (reverse transcriptase)-related family protein	NA
Sapur.01G0281100.1	0.01176793	0.14178151	2.904821752	0.048798	0.96180644	NA	pink	0.02053148	0.97488143		AT5G41412.1			hypothetical protein
Sapur.01G0105400.1	0.00301756	0.13739195	2.904823005	0.047298	0.96227525	NA	pink	0.07854531	0.32814687		AT3G61730.1	ANMYB9;MYB9	myb domain protein 9	Myb transcription factor
Sapur.01G0260600.1	0.00347994	0.12868173	2.904823276	0.046362	0.96467326	NA	pink	0.06567326	0.28602816		AT3G61730.1	ANMYB113;MYB113	myb domain protein 113	NA
Sapur.01G0239500.2	0.00201437	0.12905626	2.904823455	0.042311	0.96625872	NA	pink	0.07854531	0.32814687	GO:0003711;GO:0000124	AT1G72190.1			Spt20 family protein
Sapur.01G0152300.1	0.00201437	0.12905626	2.904823455	0.042311	0.96625872	NA	pink	0.07854531	0.32814687		AT1G72190.1			NA
Sapur.01G0259900.1	0.00201437	0.12905626	2.904823455	0.042311	0.96625872	NA	pink	0.07854531	0.32814687		AT1G72450.1			NA
Sapur.01G0134800.1	0.00201437	0.12905626	2.904823455	0.042311	0.96625872	NA	pink	0.07854531	0.32814687					Copia-like polyprotein/retrotransposon
Sapur.01T0280900.1	0.00201437	0.12905626	2.904823455	0.042311	0.96625872	NA	pink	0.07854531	0.32814687					hypothetical protein
Sapur.01G0113800.1	0.00201437	0.12905626	2.904823455	0.042311	0.96625872	NA	pink	0.07854531	0.32814687					NA
Sapur.01G0227700.2	0.00201437	0.12905626	2.904823455	0.042311	0.96625872	NA	pink	0.07854531	0.32814687		AT5G08630.1	THA1	threonine aldolase 1	L-allo-threonine aldolase
Sapur.01T0241000.1	0.06238707	0.08765727	2.07207020	0.04216	0.96637437	NA	pink	0.08055727	0.31618725		AT5G66370.1	ANMYB113;MYB113	myb domain protein 113	Myb-related transcription factor
Sapur.01G0261400.1	0.00350724	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT3G20230.1		ER-binding Dnaj-like protein Tu family protein	dnajector factor Tu protein
Sapur.01G0163600.4	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT2G39750.1	ATCOX19-2;COX19-2	cytochrome c oxidase 19-2	cytochrome C oxidase assembly protein COX19
Sapur.01G0157600.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0015291	AT5G41410.1		Phox (PX) domain protein	phox (PX) domain protein
Sapur.01G0179300.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0016787;GO:0005524;GO:0003677	AT1G12810.1	chr13;PKL;SRCAP	SNF2 domain-containing protein / helicase domain-containing protein	NA
Sapur.01G0293500.3	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006468;GO:0004672	AT4G38470.1		ACT-like protein tyrosine kinase family protein	tyrosine kinase domain protein
Sapur.01G0265400.5	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0004531	AT2G07040.1	RPM1;RPS3	NB-ARC domain-containing disease resistance protein	NA
Sapur.01G0132800.2	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006351;GO:0003899;GO:0003677	AT4G00030.1	ATNRPD1B;DMS3;DRD1;NR	nuclear RNA polymerase D1B	DNA-directed RNA polymerase
Sapur.04G0261100.2	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0007264;GO:0005525	AT5G27680.1	ARL;ARL4;ATARL4;A	ADP-ribosylation factor-like A1A	ADP-ribosylation factor like protein
Sapur.05G0105800.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006355;GO:0003700	AT3G56450.1	HRD	Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor, putative
Sapur.01G0260100.4	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0016887;GO:0055085;GO:0042626;GO:0016021;GO:0008810	AT2G28145.1		ABC transporter family protein	multidrug/pheromone exporter, MDR family, ABC transporter family protein, putative
Sapur.01G0135500.4	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006468;GO:0004672	AT5G16670.1		Protein kinase superfamily protein	tyrosine kinase family protein
Sapur.01G0138500.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0055115;GO:0003676	AT4G34810.1	AGO10;PNH;ZLL	Stabilizer of iron transporter SufD / Polynucleotidyl transferase	eukaryotic translation initiation factor 2c, putative
Sapur.01G0160400.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006355;GO:0003700	AT1G61730.1	ATEBP;EBP;ERF73;RAP2.3	ethylene-responsive element binding protein	ethylene-responsive factor 2
Sapur.01G0264100.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT3G47630.1			homeodomain transcription factor superfamily protein, putative
Sapur.09G0270200.2	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT5G59210.2		mycosin heavy chain-related	T-crare
Sapur.09G0258800.2	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006529;GO:0004066	AT4G37440.2	ASN;LAT-ASN;LDN6	glutamine-dependent asparagine synthetase 1	asparagine synthetase [glutamine-hydrolyzing] protein
Sapur.01G0135000.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0009733	AT4G27670.1		SAUR-like auxin-responsive protein family	NA
Sapur.01G0251800.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT5G30165.1			NA
Sapur.01G0136000.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687					NA
Sapur.01G0240000.2	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006355;GO:0003677	AT5G28420.1	HB-1	homeobox-1	homeobox protein, putative
Sapur.01G0261500.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687					hypothetical protein
Sapur.01G0291100.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006468;GO:0004672	AT3G22230.1		Protein kinase superfamily protein	Pto kinase interactor 1
Sapur.01G0122700.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0004629	AT5G23160.1		alpha/beta-Hydrolases superfamily protein	phosphoglycerol A(1)
Sapur.01G0133400.4	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0005515	AT2G04740.1		ankyrin repeat family protein	ankyrin repeat and BTB/POZ domain protein
Sapur.01G0135200.3	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0005085;GO:0016020;GO:0051297;GO:0015138;GO:0006855	AT5G05160.1	CCCH-type zinc fingerfamily protein with RNA-binding domain	zinc finger CCCH domain protein	
Sapur.01G0247900.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0005515	AT5G11440.2	MATE efflux family protein	MATE efflux family protein	pectinesterase/pectinesterase inhibitor
Sapur.01G0133600.5	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		GO:5940002			PGRS-like protein, putative
Sapur.01G0266100.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT4G27610.1		Dynein light chain type 1 family protein	NA
Sapur.01G0111500.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT5G06645.1		Plant self-incompatibility protein S1 family	NA
Sapur.15WG0516600.2	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0005515	AT5G49660.1		Transducin/WD40 repeat-like superfamily protein	WD domain, G-beta repeat protein
Sapur.15WG1550500.2	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687	GO:0006351;GO:0003899;GO:0003677	AT5G49000.1		RNA polymerase III subunit RPC82 family protein	RNA polymerase III subunit RPC82
Sapur.15G0291100.2	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT5G48270.1		Protein of unknown function, DUF1380	DNA-binding protein, putative
Sapur.T0726001.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687					NA
Sapur.T0937001.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT3G42880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.T175800.1	0.00350729	0.08184284	2.904821918	0.037223	0.97070726	NA	pink	0.07854531	0.32814687		AT3G42880.1		Helicase/SANT-associated, DNA binding protein	NA
Sapur.01G0221500.4	0.01784885	0.09702754	2.865268184	0.033863	0.97286051	NA	pink	-0.22579449	0.00446344	GO:0008270;GO:0004089	AT4G15180.2	ATCA1;ATSAH3;CA1;SABP	carbonic anhydrase	carbonic anhydrase
Sapur.05G0135200.2	0.02546144	-0.00481839	2.904824395	-0.01047	0.97409759	NA	pink	-0.24988526	0.05199334	GO:0003677	AT4G04160.1	homeobox protein-40	homeobox protein 40	electron transfer flavoprotein beta
Sapur.01G0105000.1	0.01203257	0.09118602	2.904823276	0.031392	0.97695654	NA	pink	0.07854531	0.32814687		AT5G44990.1		Leucine-rich repeat protein kinase family protein	transmembrane protein, putative
Sapur.15WG0517900.1	0.03317769	0.07606484	2.904823569	0.030389	0.97847254	NA	pink	-0.05326495	0.49229108	GO:0055115;GO:0006468;GO:0005524;GO:0004672	AT5G47570.1		Leucine-rich repeat protein kinase family protein	NA
Sapur.01G0126400.1	0.03929007	0.05727749	2.332302247	0.024558	0.98040721	NA	pink	-0.07538833	0.34803876		AT3G14470.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.01G0131100.1	0.03754117	-0.24969154	2.330251602	0.021654	0.98273639	NA	pink	0.07788304	0.33237059		AT5G19520.1	ATMYB15;ATY19;MYB15	myb domain protein 15	MYB transcription factor
Sapur.01G0075100.1	0.02468668	0.05180493	2.329208483	0.021649	0.98277843	NA	pink	0.07854531	0.32814687		AT5G51460.1		Pectin lyase-like superfamily protein	pectate lyase
Sapur.01G0288200.1	0.02846023	0.04304693	2.29448959	0.019777	0.98567421	NA	pink	0.02944024	0.24694341	GO:0055085;GO:0016020;GO:0051297;GO:0015138;GO:0006855	AT5G05161.1		MATE efflux family protein	MATE efflux family protein
Sapur.01G0137700.4	0.02795038	0.04541162	2.70861882	0.016766	0.98623453	NA	pink	-0.11032439	0.18897692		AT5G65230.1	AS2	Lateral organ boundaries (LOB) domain family protein	asymmetric leaves protein, putative
Sapur.01G0284400.3	0.03645885	0.04756139	2.904823455	0.016051	0.98826766	NA	pink	0.07854531	0.32814687	GO:0050662;GO:0020324	AT5G19440.1		NADP(H)-binding Rossmann-fold superfamily protein	cinnamyl alcohol dehydrogenase-like protein
Sapur.01G0275900.3	0.01124688	0.03182656	2.904823018	0.011423	0.99085729	NA	pink	0.27465763	0.00511978		AT5G20320.1			plant/ETN2-70 protein, putative
Sapur.01T0210900.1	0.01649671	0.01808013	2.904824391	0.00623	0.99528949	NA	pink	0.07845994	0.33876956		AT4G03730.1	ANMYB113;MYB113	myb domain protein 113	NA
Sapur.05G0176500.9	0.05157579	0.01623937	2.73160899	0.005941	0.99529409	NA	pink	0.07854531	0.32814687		AT5G24520.1		alpha/beta-Hydrolases superfamily protein	NA
Sapur.01G0110700.2	0 NA	NA	NA	NA	NA	NA	pink	0.09882817	0.23157189	GO:0005515	AT5G58190.2	ARIA;PB;RIP	receptor kinase protein 9	NA
Sapur.01G0264600.1	189.1363604	-0.94004246	0.24708263	-40.1061	0.97977	0.99	purple	-0.82074373	1.59E-10	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AT2G31261.1	CYP78A10	cytochrome P450, family 78, subfamily A, polypeptide 10	cytochrome P450 family protein
Sapur.01G0290300.1	312.7884776	-2.592179	0.05281105	-49.084	0	0	purple	-0.97329513	6.88E-101	GO:0005515;GO:0006468;GO:0004672	AT4G22730.1		Leucine-rich repeat protein kinase family protein	receptor-like kinase
Sapur.01G0144500.1	109.3164662	-2.920428311	0.10008804	-39.2539	0	0	purple	-0.9325249	1.86E-70		AT2G27270.1		Phototropic-responsive NPH3 family protein	phototropic-responsive NPH3 family protein
Sapur.01G0145500.1	149.3014615	-1.151101879	0.08705679	-27.645	0	0	purple	-0.95183324	3.07E-81	GO:0008270	AT3G15680.1		Ran BP2/NZF zinc finger family protein	zinc finger protein, putative
Sapur.01G0248600.1	5708.753686	-1.509608232	0.08014457	-41.613	0	0	purple	-0.96516182	6.56E-89		AT1G42840.1	PDF1	protodermal factor 1	protodermal factor 1.1, putative
Sapur.01G0262500.1	3202.92995	-13.20100468	0.20520782	64.32988	0	0	purple	-0.94857247	2.51E-79	GO:0006355;GO:0006351;GO:0008270;GO:0046983;GO:0003677	AT5G20240.1	PI	K-box region and MADS-box transcription factor family protein	MADS box transcription factor
Sapur.01G0175800.1	241.1197521	2.837305757	0.09455326	47.72554	0	0	purple	0.93038266	1.91E-69	GO:0043565;GO:0006355;GO:0003700	AT3G60700.1	WRKY46;WRKY46	WRKY family transcription factor	WRKY transcription factor, putative
Sapur.01G0178800.1	237.5481293	-3.445645127	0.07922797	-43.488	0	0	purple	-0.92891126	9.19E-69		AT4G28910.1			hypothetical protein
Sapur.01G0287700.1	1826.708923	2.835404671	0.05237745	53.23397	0	0	purple	-0.9107953	2.13E-61		AT1G27580.1	ATUGE1;UGE1	UDP-D-glucose/UDP-D-galactose 4-epimerase 1	UDP-glucose 4-epimerase
Sapur.05G0608001.1	44.10318872	-0.567661	0.10304653	-47.885	0	0	purple	-0.95817839	4.00E-66		AT5G10510.1		Domain of unknown function (DUF3617)	NA
Sapur.05G0094400.1	1516.874461	6.863940203	0.06231601	78.05709	0	0	purple	0.93157559	6.07E-72	GO:0006355;GO:0005634;GO:0003700;GO:0046983;GO:0003677	AT5G54340.1	AP3;ATAP3	K-box region and MADS-box transcription factor family protein	MADS box transcription factor
Sapur.01G0284900.1	1169.28984	5.647061439	0.07025404	51.50026	0	0	purple	0.95863168	1.64E-78	GO:0006355;GO:0005634;GO:0003700;GO:0046983;GO:0003677	AT5G54340.1	AP3;ATAP3	K-box region and MADS-box transcription factor family protein	MADS box transcription factor
Sapur.05G0134800.1	1543.915782	-7.723601007	0.06891226	-39.5705	0	0	purple	-0.95647258	2.65E-87	GO:0005634	AT5G27260.1	CYCD1;2	CYCLIN D1;2	cyclin D1
Sapur.05G0138700.1	1617.494667	7.864814237	0.10619856	74.05365	0	0	purple	0.85969047	1.87E-47					hypothetical protein
Sapur.05G0158100.1	856.5735211	-2.128531177	0.10609105	-38.492	0	0	purple	0.09882817	0.23157189	GO:0005515	AT4G28840.1	PDF1	protodermal factor 1	transmembrane protein, putative
Sapur.05G0189300.1	47.10124	4.365800443	0.14104368	28.1817	0	0	purple	-0.92825794	1.83E-68	GO:0055115;GO:0006468;GO:0004672	AT5G56451.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.05G0195900.1	201.6715222	4.248649393	0.07656477	53.39815	0	0	purple	0.93257603	1.19E-64	GO:0008270;GO:0005515	AT5G42200.1		RING/U-box superfamily protein	RING-H2 zinc finger protein
Sapur.05G0207600.1	447.394906	2.758577926	0.05584478	-49.3972	0	0	purple	-0.97658674	1.33E-105		AT3G03570.1		Domain of unknown function (DUF23)	glycosyltransferase family 92 protein
Sapur.05G0177000.1	180.3613087	1.023482186	0.07066618	41.78515	0	0	purple	-0.92891826	9.18E-69	GO:0005975;GO:0004553	AT5G08670.1		O-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase, putative
Sapur.05G0189800.1	138.0597108	-4.127904233	0.10147657	-40.6804	0	0	purple	-0.95260211	4.79E-82		AT5G11510.1		ARM repeat superfamily protein	hypothetical protein
Sapur.05T0021700.1	370.0248941	-4.567476703	0.08410486	-55.428	0	0	purple	-0.93917269	1.32E-64		AT5G13180.2		Phosphatidylinositol family / phosphoinositide 1 family protein	lactoylglutathione lyase
Sapur.07G0214400.1	1499.991852	1.529452426	0.04364548	80.85823	0	0	purple	0.95709807	2.86E-85	GO:0006355;GO:0005634;GO:0003700;GO:0046983;GO:0003677	AT5G54340.1	AP3;ATAP3	K-box region and MADS-box transcription factor family protein	MADS box transcription factor
Sapur.01G0209600.1	42.52996612	1.822185895	0.07316566	25.1046	0	0	purple	-0.97137432	1.15E-68	GO:0005515;GO:0008270;GO:0003700;GO:0003700	AT4G28870.1	ATJA18;JAN;JANP	CAP (cysteine-rich secretory protein, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein	CAP-type cysteine-rich protein
Sapur.07G0308900.1	570.1101992	2.969660949	0.06584356

Sapur.01G0524900.1	107158.44778	3.86220999	0.107645651	-35.7303	1.34e-279	6.69E-278	purple	-0.94140889	5.08E-75	GO:0016788		AT5G29670.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase	
Sapur.002G0274000.1	3429.342782	1.949737981	0.054657186	35.66247	1.51e-278	7.47E-277	purple	0.904934517	2.17E-59	GO:0055085		AT5G77610.1	EamA-like transporter family protein	UAA transporter family protein	
Sapur.006G0211000.1	446.9070363	3.880906428	0.108501979	32.6128	8.86E-278	4.36E-276	purple	-0.9002047	7.27E-58	GO:0055114,GO:0020037,GO:0016705,GO:0005506		AT5G11610.1	cytochrome P450 family 77, subfamily B, polypeptide 1	cytochrome P450 family protein	
Sapur.008G0979300.1	1249.57008	3.862761561	0.086048323	35.59351	1.77E-277	8.65E-276	purple	0.893094631	4.99E-55			AT5G48100.1	Pectin lyase-like superfamily protein	polygalacturonase	
Sapur.007G0212300.1	348.2144602	3.544077763	0.07101183	35.3763	3.96E-274	1.93E-372	purple	-0.914441418	8.98E-63	GO:0005515,GO:0006468,GO:0005524,GO:0004672		AT4G36180.1	Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase	
Sapur.006G0200100.1	134.9904045	3.369828207	0.095360881	-35.3376	1.55E-273	7.43E-272	purple	-0.903358808	6.93E-58	GO:0005515,GO:0003676		AT2G27040.2	AGO04,OCP11	Argonaute family protein	argonaute protein
Sapur.013G0141900.1	573.7975511	3.914344866	0.054361254	-35.2116	1.33E-271	6.31E-270	purple	-0.893907055	2.01E-64	GO:0005515,GO:0006468,GO:0005524,GO:0004672		AT5G58300.1	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase	
Sapur.001G0136200.1	45.23857177	4.146951495	0.117805188	-35.1847	3.43E-271	1.63E-269	purple	-0.89218151	2.25E-55	GO:0005634,GO:0003677		AT5G06570.1	Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein	squamosa promoter-binding protein, putative	
Sapur.016G1334900.1	476.7346712	2.996497377	0.085275285	-35.1399	1.66E-270	7.83E-269	purple	-0.932970662	3.04E-65			AT4G39700.1	ATEXPA7,ATEXPA4,ATHEXP A	expansin A4	expansin
Sapur.008G0279000.1	189.3608077	4.030692469	0.12009429	-35.0804	4.48E-268	2.11E-266	purple	-0.943407700	9.04E-73			AT1G17460.1	O-fucosyltransferase family protein	GDP-fucose protein O-fucosyltransferase	
Sapur.005G0088000.1	195.0250292	2.433362757	0.069332314	-35.0852	1.13E-269	5.32E-268	purple	-0.926287517	2.52E-67			AT5G09250.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH48, putative	
Sapur.006G0805200.1	69.62255323	2.005249949	0.057232084	-34.9969	4.17E-269	2.23E-267	purple	-0.929034118	2.02E-67	GO:0006468,GO:0005524,GO:0004672		AT2G37120.2	Protein kinase family protein with ubiquitin-like domain	tyrosine kinase domain protein	
Sapur.019G0195000.1	57.60076484	5.663192508	0.106730117	-34.9808	4.41E-268	2.05E-266	purple	-0.949786419	4.13E-80	GO:0016747		AT5G48930.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase
Sapur.006G1981100.1	90.69436628	1.898807101	0.11153829	-34.405	8.62E-268	4.00E-266	purple	-0.965276007	1.03E-82	GO:0055015		AT5G02380.1	Transducin/WD40 repeat-like superfamily protein	7-bis and WD40 domain protein, putative	
Sapur.005G1913100.1	156.8564886	2.776282126	0.079632766	34.86357	2.65E-266	1.22E-264	purple	-0.857637878	1.27E-46			AT5G75230.2	Plant protein of unknown function (DUF827)	WEB family plant protein, putative	
Sapur.015W0246600.1	435.4525211	4.000000000	0.11780267	-34.8582	3.20E-266	1.48E-264	purple	-0.9668050	1.48E-93			AT5G18250.1	Pathogenesis-related thaumatin superfamily protein	pathogenesis-related thaumatin-like protein	
Sapur.15W0033100.1	80.1681743	2.062620443	0.059186054	-34.8468	4.29E-266	1.98E-264	purple	-0.921837852	1.08E-65			AT5G04420.1	NAD(P)-linked oxidoreductase superfamily protein	aldo-keto reductase family protein	
Sapur.002G0254000.1	2472.354826	1.582017883	0.045629072	34.67127	2.14E-263	9.60E-262	purple	-0.911837011	1.51E-62			AT-GT2,GT2	Duplicated homeobox-like superfamily protein	myb/SANT-like DNA-binding domain protein	
Sapur.016G2671051.1	146.8635885	5.063180114	0.09632802	-34.6178	1.38E-262	6.09E-261	purple	-0.903112325	7E-59			AT4G27280.1	Calcium-binding EF-hand family protein	calcium-binding EF-hand protein	
Sapur.004G0416000.1	24.52048829	4.422164245	0.127847518	-34.5894	3.65E-262	1.63E-260	purple	-0.907787261	2.29E-60					hypothetical protein	
Sapur.011G0308500.1	55.11279634	3.581184584	0.098154844	-34.5814	4.48E-262	1.99E-260	purple	-0.830397329	4.24E-40	GO:0016883		AT5G73830.1	BEE3	BR enhanced expression 3	transcription factor BEE, putative
Sapur.009G0598000.1	100.3230781	1.816196311	0.052610372	-34.5041	6.96E-261	3.06E-259	purple	-0.945691589	1.53E-77	GO:0005975,GO:0004553		AT5G18480.1	D-Glycosyl hydrolases family 17 protein	glucan endo-1%2C3-beta-glucosidase	
Sapur.016G0183000.1	171.7344023	2.383669885	0.040181878	-34.504	6.98E-261	3.06E-259	purple	-0.924983638	1.88E-67			AT5G66310.1	Protein of unknown function (DUF620)	DUF620 family protein	
Sapur.010G0934000.1	21.87086203	-2.863037317	0.083118398	-34.4494	4.60E-260	2.01E-258	purple	-0.938989818	1.09E-73			AT5G68360.1	C2H2 and C3HC zinc fingers superfamily protein	zinc finger protein	
Sapur.004G0194000.1	24.01605948	2.032207328	0.061138966	-34.45	2.12E-259	9.22E-258	purple	-0.92785012	2.67E-68	GO:0006355,GO:0005739,GO:0003690		AT5G06100.1	Ribosomal transcription termination factor family protein	TRF protein	
Sapur.15W0063000.1	37.50554864	2.312507411	0.067275354	-34.3738	6.22E-259	2.70E-257	purple	-0.93912049	8.30E-74	GO:0006783,GO:0004325		AT4G30190.2	ATFC-II,FC-II,FC2	ferrochelatase 2	
Sapur.004G0930600.1	1454.181376	1.593614423	0.064349886	34.32691	3.11E-258	1.34E-256	purple	0.898825835	2.12E-57	GO:0016020		AT4G22120.1		early-responsive to dehydration-like protein	early-responsive to dehydration-like protein
Sapur.008G1372200.1	494.7888994	2.172421114	0.064974406	-34.2803	1.54E-257	6.64E-256	purple	-0.896618875	1.08E-56	GO:0016779,GO:0009058		AT5G10220.1	ADG2,APL1	ADP glucose pyrophosphorylase family protein subunit 1	glucose-1-phosphate adenylyltransferase
Sapur.008G1331000.1	48.62711401	4.001117936	0.092567199	-34.212	1.60E-256	6.87E-255	purple	-0.88806253	1.89E-37			AT5G22130.1	FLO10,FLOW1,SUP	C2H2 and C3HC zinc fingers superfamily protein	
Sapur.016G1414000.1	302.4213019	2.095239939	0.22747027	-34.207	1.86E-256	7.95E-255	purple	-0.90872999	1.08E-60	GO:0005885,GO:0016021		AT3G18170.1	ATCAR1,CAR1,RCH4	carbon starved 1	vacuolar cation/proton exchanger
Sapur.004G0907600.1	395.3017911	-2.378837759	0.068603137	-34.0792	1.50E-254	6.29E-253	purple	-0.951363934	1.70E-81			AT5G07040.1			DUF4378 domain protein
Sapur.15W0118700.1	709.0172244	4.573417427	0.07534344	-34.0682	2.14E-254	9.82E-253	purple	-0.951856416	8.63E-62			AT5G15510.1	EKL1	EKORDIUM like 1	plant(Pt)76S-10 protein
Sapur.014G0573000.1	129.9080216	2.814601095	0.082773734	34.0073	1.74E-253	7.27E-252	purple	-0.83867092	9.69E-43			AT5G12790.1	peptidoglycan-binding LysM domain-containing protein	carbohydrate-binding module family 50 protein	
Sapur.004G0197000.1	161.6592734	5.960131558	0.052969693	-34.0039	1.95E-253	8.16E-252	purple	-0.92620845	5.14E-66			AT5G18170.1	Disease resistance-response (dirigent-like protein) family protein	dirigent like protein	
Sapur.007G0277900.1	358.6128732	3.867423347	0.054935542	-33.993	2.83E-253	1.18E-251	purple	-0.93672271	1.51E-72	GO:0016758,GO:0008152		AT4G38320.1	ATSAGT1,GT-SAGT1,SGT1-LIJ	UDP-glucosyltransferase 74F2	NA
Sapur.014G0289000.1	45.64013300	2.000000000	0.104187345	-33.9744	3.55E-253	1.48E-251	purple	-0.918180642	1.52E-63			AT5G02575.1	Glycosyl hydrolase family 35	hypothetical protein	
Sapur.013G0555500.1	264.5957588	2.111391832	0.062389707	-33.8528	3.30E-251	1.36E-249	purple	-0.952936643	3.08E-82	GO:0006355,GO:0008270,GO:0003700		AT5G25830.1	GATA12	GATA transcription factor	GATA transcription factor, putative
Sapur.014G0940000.1	167.7734658	5.587396388	0.105115988	-33.8392	5.23E-251	2.15E-249	purple	-0.979802945	8.79E-98	GO:0006355,GO:0003700,GO:0007275		AT4G23750.1	ANT,CXC,CXC1,DRG	Integrase-type DNA-binding superfamily protein	AP2 domain transcription factor
Sapur.015G1813200.1	887.6248843	1.605490263	0.047469332	33.83593	5.85E-251	2.40E-249	purple	-0.919814164	1.45E-62			AT4G04320.2	P-loop containing nucleoside triphosphate hydrolases superfamily protein	P-loop nucleoside triphosphate hydrolase family protein	
Sapur.003G0934000.1	96.72006317	2.351264994	0.096121322	-33.8246	8.58E-251	3.52E-249	purple	-0.923307684	2.66E-66	GO:0008270		AT5G15680.1		Ran BP2/NZF zinc finger-like superfamily protein	2n-finger in Ran-binding protein
Sapur.006G0201300.1	955.1647356	1.295248394	0.038385576	-33.7431	1.35E-249	5.52E-248	purple	-0.94553063	1.90E-77			AT5G40820.1			transcription factor, putative
Sapur.007G0498800.1	46.48960853	-2.692076726	0.109885673	-33.6008	1.63E-247	6.57E-246	purple	-0.93707163	9.94E-73			AT5G27310.1			hypothetical protein
Sapur.013G0256000.1	139.2589466	2.145165275	0.042314849	33.47659	1.06E-245	4.23E-244	purple	-0.919070257	1.42E-64			AT1G07920.1	Transmembrane Fragile-X-F-associated protein	zinc finger CZHC4 type domain protein	
Sapur.003G0973000.1	225.8598822	5.598418219	0.107732959	-33.3951	1.61E-244	6.42E-243	purple	-0.942390942	1.31E-75			AT4G04980.1			hypothetical protein
Sapur.004G0183000.1	131.3478739	4.968401017	0.088918725	-33.3836	2.37E-244	9.40E-243	purple	-0.95439007	8.30E-83			AT5G19860.1			hypothetical protein
Sapur.004G0240000.1	40.01478823	3.707545577	0.11107332	-33.3763	2.74E-244	1.08E-242	purple	-0.92916232	7.06E-69			AT5G11125.1			hypothetical protein
Sapur.016G0183000.1	60.89466123	2.341324101	0.105420395	-33.2868	6.05E-243	2.36E-241	purple	-0.918347713	1.02E-63	GO:0005634		AT4G03270.1	CYCD6;1	Cyclin D6;1	D6-type cyclin
Sapur.018G0988000.1	479.0406305	4.707062109	0.051367367	-33.2331	3.58E-242	1.40E-240	purple	-0.903528052	6.40E-59			AT5G20240.1	Exostosin family protein	xylogalacturonan beta-1%2C2-xylosyltransferase	
Sapur.012G0779000.1	457.0964677	-3.341673785	0.040466211	-33.1554	4.73E-241	1.84E-239	purple	-0.93952406	5.03E-74			AT4G38710.1	DIX domain-containing chromatin associated protein		NA
Sapur.014G0880500.1	116.9938877	5.078197547	0.27508573	-33.0013	7.78E-239	2.98E-237	purple	-0.92104893	2.54E-68	GO:0055114,GO:0020037,GO:0016705,GO:0005506		AT2G46660.1	cytochrome P450, family 78, subfamily A, polypeptide 6	cytochrome P450 family 78 protein	
Sapur.007G0863000.1	45.91740694	3.288809768	0.09675207	-32.9953	9.50E-239	3.65E-237	purple	-0.903765662	1.34E-59			AT5G10310.1		epidermal patterning factor-like protein, putative	
Sapur.006G0119100.1	267.4486601	4.513353302	0.07618615	-32.8875	1.18E-238	4.52E-237	purple	-0.818336654	1.02E-42			AT3G24420.1	alpha/beta-Hydrolases superfamily protein	NA	NA
Sapur.012G0985200.1	73.12705887	4.879032824	0.148005586	-32.9659	2.51E-238	9.61E-237	purple	-0.73053641	1.81E-27	GO:0005515,GO:0006468,GO:0005524,GO:0004672		AT5G15560.1	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase	
Sapur.005G0880200.1	5321.2782	-2.233329277	0.026798427	-32.8502	1.13E-236	4.30E-235	purple	-0.88853471	2.05E-57			AT5G65180.1	Transmembrane protein, DUF538	plant(Pt)72P12-38 protein, putative	
Sapur.15W0071000.1	29.79796965	-5.400864628	0.101503042	-32.8416	1.50E-236	5.70E-235	purple	-0.931155651	7.59E-63	GO:0008270,GO:0005515		AT5G05810.1	AT5G05810	RING/U-box superfamily protein	RING-U zinc finger protein, putative
Sapur.009G0679000.1	139.3473819	3.951817669	0.120393767	-32.8341	1.67E-236	6.35E-235	purple	-0.926452332	1.01E-67	GO:0005634		AT1G70210.1	ATCYC1B,CYCC1;1	CYCLIN B1;1	cyclin D-type protein
Sapur.005G0508000.1	187.1459281	-4.973557969	0.060181161	-32.7936	7.26E-236	2.74E-234	purple	-0.952536902	5.81E-82	GO:0009505,GO:0006468,GO:0005524,GO:0004672		AT1G77280.1	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	adenine nucleotide alpha hydrolase-domain kinase	
Sapur.15S0248200.1	421.3232043	1.066498822	0.019319323	32.79003	8.17E-236	3.08E-234	purple	-0.915768617	6.32E-60	GO:0005515		AT1G18370.1	ATSYT7,NTMC2T7.1,NTMC2T	C2 domain-containing protein	plant synaptotagmin
Sapur.015G2794000.1	125.6775362	3.004663277	0.074688497	-32.7607	1.59E-235	6.08E-234	purple	-0.909021087	4.60E-61			AT5G45620.1	zinc finger protein-related	zinc finger protein-related	transcription factor, putative
Sapur.002G1574000.1	1993.859184	1.38287821	0.036133078	-32.735	4.96E-235	1.86E-233	purple	-0.946410575	5.61E-78			AT4G47560.1	PHR2	photolyase/blue-light receptor 2	photolyase/blue-light receptor 2, putative
Sapur.T001600.1	98.62044362	3.000000000	0.07147793	-32.6763	1.28E-232	4.68E-231	purple	-0.926437978	1.07E-68	GO:0016832,GO:0008270,GO:0005975		AT1G32730.1		aldehyde dehydrase class-II family protein	NA
Sapur.011G0627900.1	179.6093331	-2.406063613	0.073785551	-32.6204	2.11E-232	7.84E-232	purple	-0.898825665	1.97E-57	GO:0016788		AT5G19190.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-lipase, putative	
Sapur.015G1133000.1	215.5653229	-1.473394961	0.10651283	-32.5369	2.59E-232	9.25E-231	purple	-0.819877268	2.26E-38	GO:0055114,GO:0016491	AT3G01140.2,AT3G01141.2,AT3G01	AT2G45420.1		gibberellin 20-oxidase	gibberellin 20-oxidase
Sapur.15W0023800.1	20.54859495	-7.632095585	0.234298132	-32.5666	2.22E-232	4.50E-231	purple	-0.904938673	2.16E-59	GO:0006355,GO:0008270,GO:0006355,GO:0003700		AT5G06740.1	GATA15	GATA transcription factor 15	GATA zinc finger protein
Sapur.015G1881000.1	906.4248811	1.488-201	0.073528481	-32.5369	2.88E-232	1.48E-231	purple	-0.880529784	8.98E-55	GO:0055114,GO:0016491,GO:0016705		AT5G27370.1	GDU47,HTH	Glucose-methanol-choline (GMC) oxidoreductase family protein	glucose-methanol-choline (GMC) oxidoreductase, putative
Sapur.014G1390900.1	159.2042614	-0.074106964	0.063815047	-32.441	7.25E-231	2.64E-229	purple	-0.835609174	8.48E-42	GO:0006508,GO:0004252		AT3G04160.1	AIR3	Subtilisin-like serine endopeptidase family protein	subtilisin-like serine protease
Sapur.005G1423200.1	582.9500567	2.353418147	0.063515476	-32.3293	1.71E-229	5.71E-228	purple	-0.91821257	3.17E-64			AT4G21620.1		Heat shock protein DnaJ with tetratricopeptide repeat	DnaJ heat shock amino-terminal domain protein
Sapur.005G1849400.1	265.7239426	-3.057523995	0.094736729	-32.2773	1.46E-228	5.21E-227	purple	-0.858391308	2.38E-46			AT1G15670.1	ATCUH,ATHCOBL1,CUH,CO	chlorophyllase 1	chlorophyllase
Sapur.002G0780000.1	114.0853136	-2.485065453	0.073121469	-32.1394	1.24E-226	4.39E-225	purple	-0.936101816	2.92E-72	GO:0006468,GO:0005524,GO:0004672		AT4G23740.1	Leucine-rich repeat protein kinase family protein	receptor-like kinase, putative	
Sapur.010G0880600.1	1185.902927	1.000883523	0.040502795	-32.1208	2.24E-226	7.98E-225	purple	-0.946847768	2.78E-78	GO:0055114,GO:0016491,GO:0005507		AT5G25401.1	LPR2	Cupredoxin superfamily protein	spore coat-like protein
Sapur.006G1674000.1	19.9795127	-3.609435882	0.112426787	-32.1053	3.71E-226	1.31E-224	purple	-0.931492238	1.10E-61			AT3G25480.1			transmembrane protein, putative
Sapur.005G1215000.1	400.6265267	-1.693622677	0.046687653	-32.0861	6.88E-226	2.42E-224	purple	-0.94727652	7.91E-77			AT4G12080.1	AHL1,ATAHL1	AT-hook motif nuclear-localized protein 1	DNA-binding family protein
Sapur.004G0127900.1	840.6774804	-2.038315577	0.065469951	-32.0742	1.01E-225	3.56E-224	purple	-0.888752324	2.23E-54	GO:0003677,GO:0008289		AT4G04890.1	PDT2	prodormetal factor 2	homeobox leucine zipper protein
Sapur.009G0219100.1	111.7562114	3.859864605	0.110854395	-32.0388	1.14E-225	3.98E-224	purple	-0.909162302	7.51E-61	GO:0016746,GO:0008152		AT2G47240.1	ATGPAT1,GPAT1	glycerol-3-phosphate acyltransferase 1	glycerol-3-phosphate acyltransferase
Sapur.007G0667900.1	25.79505355	-5.723165528	0.178661601	-32.0336	3.72E-225	1.30E-223	purple	-0.913324238	1.62E-61	GO:0046983		AT4G00120.1	EDA33,CET14D,IND,ND1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.006G0898300.1	128.3468027	-2.475727257	0.077232621	-32.0187	5.98E-225	2.08E-223	purple	-0.945709766	1.26E-77	GO:0005975,GO:0004553		AT4G09810.1	AGH9B10,GHB18	glycosyl hydrolase family 9B protein	cel-1%2C4-beta-glucanase
Sapur.013G1343000.1	48.17558855	-4.231754779	0.132198194	-32.0107	7.74E-225	2.68E-223	purple	-0.853816842	2.24E-45	GO:0030247,GO:0004679,GO:0048546,GO:0004688,GO:0004672		AT4G02330.1	S-locus lectin protein kinase family protein	G-type lectin S-receptor-like Serine/Threonine-kinase plant	
Sapur.018G0390600.1	189.3410652	3.509243161	0.109704457	-31.9751	2.71E-224	9.39E-223	purple	-0.929409683	7.96E-69			AT4G25230.1		transmembrane protein, putative	transmembrane protein, putative
Sapur.003G0214000.1	293.8011291	-2.027742561	0.082383045	-31.9171	1.55E-223	5.32E-222	purple	-0.926097547	6.64E-69	GO:0005975,GO:0004553		AT4G45670.1	AT8G4.K,KYI4	beta-D-xylosidase 4	beta-xylosidase/alpha-L-arabinofuranosidase
Sapur.002G0416000.1	1137.866155	-1.466783441	0.045690647	-31.8914	3.51E-223	1.21E-221	purple	-0.929210574	1.90E-68	GO:0006662,GO:0003824		AT2G14140.1	CSP41A	chloroplast stem-loop binding protein of 41 kDa	stem-loop binding protein of 41 kDa protein A
Sapur.006G2054000.1	35.23776647	5.004663248	0.156936857	-31.8863	3.77E-223	1.29E-221	purple	-0.925420618	2.32E-68			AT2G43820.1		Regulator of Vps4 activity in the MVB pathway protein	regulator of Vps4 activity in the MVB pathway protein
Sapur.019G0617000.1	1626.83796	1.896133939	0.059567793	-31.8315	2.37E-222	8.09E-221	purple	-0.914656769	7.45E-63	GO:0055515,GO:0006468,GO:0004672		AT5G63370.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.001G1970001.1	46.37930727	-4.464554442	0.120016968	-31.7838	1.08E-221	3.64E-220	purple	-0.84345113	1.12E-43	GO:0055114		AT1G01480.1	C2 calcium/lipid phospholipid binding and phosphorbosyltransferase carbosy-terminal domain protein	C2 calcium/lipid-binding and phosphoribosyltransferase carbosy-terminal domain protein	
Sapur.013G1915500.1	136.4801959	2.878192143	0.122071512	-31.7699	1.68E-221	5.73E-220	purple	-0.899173884	1.05E-67	GO:0016788		AT5G03610.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase	GDSL esterase/lipase
Sapur.009G0280300.1	15.17267004	3.702181622	0.148850221	-31.7688	1.68E-221	5.74E-220	purple	-0.789729284	2.16E-44	GO:0016788,GO:0008152		AT5G17250.1	GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase	
Sapur.003G0545000.1	60.08527968	-2.070604679	0.122884054	-31.7476	3.42E-221	1.16E-219	purple	-0.840683663	4.91E-43	GO:0004857		AT5G38630.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	plant invertase/pectin methylesterase inhibitor protein
Sapur.003G0200700.1	34.04613924	2.577227572	0.077322621	-31.6867	7.23E-220	2.81E-219	purple	-0.882658679	4.05E-52	GO:0003674		AT5G26120.1	TEL1	Telomere length regulator protein	NA
Sapur.006G1920500.1	8362.987065	1.470065727	0.046515033	31.69005	2.13E-220	7.18E-219	purple	-0.878353023	1.50E-51	GO:0008233,GO:0006508		AT4G22940.1	GAMMA-VPE,GAMMAVPE	gamma vacuolar processing enzyme	vacuolar processing enzyme
Sapur.009G1232000.1	30.90569519	-5.556058985	0.175361763	-31.6804	2.63E-220	8.86E-219	purple	-0.867735256	7.80E-49			AT4G07080.1	LSH6	Protein of unknown function (DUF640)	light-dependent short hypocotyls protein, putative
Sapur.015W0064900.1	203.1445225	-2.174267232	0.068619991	-31.6778	1.05E-219	3.52E-218	purple	-0.862266005	1.09E-58	GO:0006355,GO:0003677		AT4G24650.1	DOT5-LIKE2	Dof-type zinc finger DNA-binding family protein	NA
Sapur.T008800.1	17.42369765	-7.596609232	0.230939955	-31.673	3.66E-220	1.23E-218	purple	-0.89005697	9.66E-56			AT5G49040.1	SCD1	stearoyl cytokinesis defective / SCD1 protein (SCD1)	NA
Sapur.011G1464000.1	51.99338372	-4.004604184	0.158196857	-31.8863	1.16E-219	3.88E-218	purple	-0.892466585	1.65E-55	GO:0055114,GO:0020037,GO:0016705,GO:0005506		AT5G06660.1	CYP78A5	Cytochrome P450 family protein	cytochrome P450 family protein
Sapur.005G1394900.1	2089.368277	-4.457317967	0.046038271	-31.6338	1.27E-219	4.24E-218	purple	-0.93606875	8.84E-74			AT4G4575.1	NPQ6,PSB1	Chlorophyll A-B binding family protein	photosystem II 22 kDa protein
Sapur.006G0880500.1	102.6351042	-3.232609384	0.070013934	-31.6014	1.51E-219	4.97E-218	purple	-0.946818411	1.16E-78	GO:0004688,GO:0016307		AT4G15480.1	ATPHF1,ATPIP4,1,PIP5K1	phosphatidylinositol-4-phosphate 5-kinase	phosphatidylinositol-4-phosphate 5-kinase
Sapur.004G1127000.1	55.45115167	-2.302705349	0.069741277	-31.584	6.13E-219	2.03E-217	purple	-0.888497862	2.62E-54			AT4G16070.2	PDV2	plastid division2	plastid division protein PDV2, putative
Sapur.015G1881000.1	288.3176644	-5.761801107	0.195816118	-31.5644	1.14E-218	3.76E-217	purple	-0.875188789	1.46E-73			AT5G60670.1		Protein of unknown function (DUF760)	DUF760 family protein
Sapur.008G1155000.1	55.3523507	-4.570359422	0.145067471	-31.5051	7.41E-218	2.43E-216	purple	-0.891846658	2.83E-55			AT2G20080.1	AtIDD4,IDD4	indeterminate(ID)-domain 4	C2H2-type zinc finger protein
Sapur.009G0284800.1	61.23253302	-4.152578661	0.139276516	-31.4779	1.74E-217	5.72E-216	purple	-0.867380203	7.97E-49						transcription factor, putative
Sapur.15W0041000.1	22.09917539	-5.122978661	0.162858525	-31.4571	3.35E-217	1.10E-215	purple	-0.83918934	7.57E-43			AT5G18240.1		Reticulon family protein	reticulon-like protein
Sapur.003G0233400.1	36.03864675	-4.653162746	0.148032132	31.43771	6.18E-217	2.02E-215	purple	-0.79501957	1.79E-35						NA
Sapur.005G1277000.1	388.5849512	-1.305388584	0.041631021	31.37007	5.18E-216	1.68E-214	purple	-0.91697281	1.44E-64			AT5G27300.1			hypothetical protein
Sapur.15W0110900.1	88.17284263	-2.988885799	0.095538292	-31.2847	7.54E-215	2.44E-213	purple	-0.919538274	9.52E-65	GO:0006468,GO:0004672,GO:0005524		AT2G37030.1	PIX12	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	Serine/Threonine kinase domain protein
Sapur.010G1510500.1	82.98813384	-2.236063	0.071585119	-31.2665	1.23E-214	3.96E-213	purple	-0.893479411	1.04E-55	GO:0005089		AT3G09240.1	ATROPGEF5,ROPGEF5	ROP guanine nucleotide exchanger 5	NA
Sapur.011G0571000.1	759.9342006	-5.513332578	0.080404499	-31.2586	1.71E-214	5.50E-213	purple	-0.88261787	1.10E-52			AT3G45530.1		Protein of unknown function, DUF642	glutamate-gated kainate-type ion channel receptor subunit GluR5
Sapur.015G1240000.1	1400.2768	-4.285022918	0.07112839	-31.2491	2.30E-214	7.40E-213	purple	-0.922933376	3.81E-66			AT5G20230.1	BR6OX2,CYP85A2	Brassinosteroid biosynthesis / brassinosteroid/sed storage 25 albumin superfamily protein	NA
Sapur.003G1963000.1	9206.613178	5.596624066	0.115278849	-31.1993	1.09E-213	3.49E-212	purple	-0.8731758461	5.42E-50						transmembrane protein, putative
Sapur.003G1883000.1	131.8917532	-3.123815349	0.08075582	-31.1974	1.12E-213	3.75E-212	purple	-0.905098652	8.61E-60			AT4G34100.1		RotC-like cupins superfamily protein	enzyme of the cupin superfamily protein
Sapur.018G0988100.1	783.417508	1.719125601	0.051134138	31.18078	1.94E-213	6.21E-212	purple	-0.898825253	2.46E-57	GO:0005985,GO:0016021		AT4G02050.1	STF7	sugar transporter protein 7	hexose transporter, putative
Sapur.015G1480000.1	534.4441716	2.669390683	0.094968805	31.17469	2.35E-213	7.50E-212	purple	-0.916308238	1.75E-63	GO:0016787,GO:0008152		AT4G44350.1	ILL6	IAA-leucine resistant (ILR)-like gene 6	IAA-amino acid hydrolase ILR1, putative
Sapur.016G0880300.1	204.7578284	-3.016809322	0.050808284	-31.1383	9.37E-213	2.98E-211	purple	-0.937395565	2.78E-71	GO:0016887,GO:0006355,GO:0006352,GO:0003700,GO:0003677		AT2G36990.1	ATSIG5,SIG5,SIG7,SIGF5	RNA polymerase sigma subunit 5	NA
Sapur.009G1855300.1	688.7705679	-4.657878643	0.149628539	-31.1269	1.04E-212	3.31E-211	purple	-0.908127348	1.75E-60			AT4G38660.1		Pathogenesis-related thaumatin superfamily protein	thaumatin-like protein
Sapur.010G0644400.1	422.7386606	-2.017497293	0.067279745	-31.0478	1.24E-211	3.85E-210	purple	-0.887667871	5.64E-54	GO:0016787		AT2G27461.1	HMT3	Homocysteine S-methyltransferase family protein	homocysteine S-methyltransferase
Sapur.005G0094000.1	120.1688559	-2.315857871	0.071575111	-31.0172	3.16E-211	9.99E-210	purple	-0.912003737	6.63E-62			AT5G69525.1			transmembrane protein, putative
Sapur.009G0277000.1	407.1188449	-5.768091221	0.157136154	-31.0607	1.82E-210	5.76E-209	purple	-0.944811167	2.56E-78	GO:0016987,GO:0006355,

Sapur.01G0227900.1	1993.104323	1.194240348	0.042711988	27.96031	4.94E-172	1.16E-170	popular	0.903831443	2.31E-58	GO:0004869	ATSCG5130.1	Cysteine/cysteine-rich protein
Sapur.01G0214300.1	165.3753586	-2.009875841	0.071951975	-27.9336	1.04E-171	2.45E-170	popular	-0.86961167	3.00E-49	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATCSTI5820.1	ATCLV1,CLV1,FAS3,FLO5
Sapur.01G0277900.1	348.7713413	-2.429224267	0.051229076	-27.3881	2.81E-171	6.56E-170	popular	-0.92097655	5.01E-65	GO:0005515	ATCSI5522.1	Leucine-rich receptor-like protein kinase family
Sapur.01G0230900.1	1096.172351	1.385377704	0.049703836	27.87265	5.73E-171	1.33E-169	popular	0.90374957	2.46E-58	GO:0048500,GO:0008312,GO:0006614	ATSBF4160.1	Cytoplasmic/nucleus-localized protein
Sapur.01G0251900.1	1393.132843	-1.138879418	0.040888363	-27.8535	9.78E-171	2.28E-169	popular	-0.91811353	3.46E-64		ATSC17600.1	signal recognition particle 19 kDa protein, putative / SRP19, putative
Sapur.01G0277900.1	176.1175929	-2.340963205	0.084609126	-27.8457	1.21E-170	2.82E-169	popular	-0.90956173	5.45E-61	GO:0006508,GO:0004190	ATSG01300.1	LIL3:1
Sapur.T1060001.1	81.82259869	1.67999891	0.060332282	27.84552	1.22E-170	2.83E-169	popular	-0.90832326	9.41E-59		ATSB58532.1	Chlorophyll a-b binding protein
Sapur.01G0278000.1	551.9899954	-1.019259869	0.036644782	-27.8222	2.24E-170	5.41E-169	popular	-0.92753749	5.68E-68		ATSC92882.2	Eukaryotic aspartyl protease family
Sapur.01T0019200.1	316.81435	-1.87005589	0.067286915	-27.799	4.46E-170	1.03E-168	popular	-0.93246532	1.99E-70		ATSG59400.1	Vacuolar protein sorting-associated protein 26
Sapur.01G0288200.1	116.8539972	2.562462679	0.092384529	27.6271	5.56E-170	1.28E-168	popular	-0.84943732	1.79E-43	GO:0004468,GO:0005524,GO:0004672	ATSG60600.1	NHL domain-containing protein
Sapur.01G0269000.1	1885.132391	-1.475125011	0.053237088	-27.7086	5.50E-169	1.26E-167	popular	-0.85117321	2.87E-56	GO:0003677	ATSG21560.1	enzyme binding;tetrapyrrole binding
Sapur.01G0261200.1	25.68827714	7.357499355	0.187805185	27.6663	7.75E-169	1.77E-167	popular	-0.94764432	1.25E-78		ATSG61990.1	receptor-like protein kinase
Sapur.01G0261400.1	212.4200903	-1.466023837	0.052976802	-27.69	9.21E-169	2.10E-167	popular	-0.91001954	3.74E-61	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATSG57530.1	transmembrane protein
Sapur.01G0286800.1	371.5957368	-1.425314347	0.052426407	-27.6808	1.19E-168	2.71E-167	popular	-0.92098655	5.01E-69		ATSG7000.1	Leucine-rich receptor-like protein kinase family
Sapur.01G0273000.1	98.0957858	1.653881398	0.132068567	27.66742	1.72E-168	3.91E-167	popular	-0.75827634	1.34E-30		ATSG12640.1	Protein kinase family protein (GUF600 and DUF632)
Sapur.01G0284500.1	115.3518541	-1.207613464	0.079819367	-27.6581	2.26E-168	5.13E-167	popular	-0.88050083	7.71E-55	GO:0005634,GO:0003677	ATSG42300.1	SPL9
Sapur.01G0269000.1	401.962205	-1.14452974	0.04139416	-27.6495	2.83E-168	6.41E-167	popular	-0.90502656	1.97E-59		ATSG58932.1	squamosa promoter binding protein-like 9
Sapur.01G0245300.1	65.9763866	-2.362500948	0.07821868	-27.6468	3.05E-168	6.89E-167	popular	-0.87892629	1.78E-51	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATSG49045.1	Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01W0241801.1	9.395913678	-6.872833226	0.241469614	-27.6459	3.12E-168	7.08E-167	popular	-0.87791204	5.68E-48		ATSG57832.1	Leucine-rich receptor-like protein kinase family protein
Sapur.01T0071200.1	43.11705642	-2.579664003	0.093317157	-27.6278	5.16E-168	1.16E-166	popular	-0.93393189	3.84E-71	GO:0008270	ATSG46045.1	Calmodulin-binding family / SCD1 protein (SCD1)
Sapur.01G0137500.1	419.0648882	-1.166424	0.12133647	-27.6271	5.24E-168	1.19E-166	popular	-0.94851604	2.79E-79	GO:0003124,GO:0005634,GO:0003677,GO:0000786	ATSG24630.1	DHHC-type zinc finger family
Sapur.01W0255400.1	8.152254166	-6.505319207	0.235507456	-27.6226	5.96E-168	1.34E-166	popular	-0.91295807	4.90E-62		ATSG49040.1	stomatal cytokinesis defective 1 protein (SCD1)
Sapur.01G0280100.1	5.548023862	-6.127778002	0.240129607	-27.6217	6.10E-168	1.38E-166	popular	-0.87457556	2.56E-50		ATSG25120.1	Disease resistance-response (Bridge-like protein) family protein
Sapur.01G0295300.1	385.8222351	3.712381165	0.134687416	27.60393	9.98E-168	2.25E-166	popular	-0.87297762	1.81E-50		ATSG68500.1	
Sapur.01T0263100.1	65.45057999	-2.517281239	0.091266811	-27.5969	1.39E-167	3.14E-166	popular	-0.90347203	1.68E-58		ATSG6580.1	hypothetical protein
Sapur.01W0261100.1	11.77617843	-4.403310194	0.232262498	-27.5685	2.66E-167	5.95E-166	popular	-0.92881602	2.87E-65		ATSG29820.1	homeobox leucine zipper protein ATHB-40
Sapur.01W0264100.1	8.319215347	-6.534251255	0.24006252	-27.219	3.87E-163	8.34E-162	popular	-0.87387032	2.56E-50			Acyl-CoA N-acyltransferases (NAT) superfamily protein
Sapur.01T0120200.1	586.2376507	-2.176065281	0.07893716	-27.5668	2.78E-167	6.23E-166	popular	-0.89138925	3.91E-55	GO:0003677,GO:0000786	ATSG45980.1	H2B;HTB9
Sapur.01W0288700.1	21.91501572	-3.329202037	0.184015763	-27.5474	4.76E-167	1.06E-165	popular	-0.90013124	3.08E-58		ATSG66680.2	Histone superfamily protein
Sapur.01G0123300.1	534.2175748	1.369240883	0.049733399	27.53129	7.41E-167	1.65E-165	popular	0.88330771	8.24E-53	GO:0071949	ATSG67530.1	ABA1,ATABA1,ATZEP,BG11
Sapur.01G0232200.1	90.4803234	-4.037337324	0.087502717	-27.5163	1.12E-166	2.48E-165	popular	-0.89732188	2.58E-57		ATSG31751.1	zeaxanthin epoxidase
Sapur.01B0269200.1	524.9766125	-1.933742205	0.070192572	-27.4708	3.92E-166	8.69E-165	popular	-0.90022871	7.61E-58		ATSG59970.1	UFA24, putative
Sapur.01G0195200.1	461.4567956	1.32168734	0.08134969	27.44863	7.21E-166	1.59E-164	popular	-0.91051951	1.22E-64		ATSG0190.1	Histone superfamily protein
Sapur.01T0027700.1	313.1946249	-0.85879561	0.075058839	-27.4316	1.15E-165	2.55E-164	popular	-0.88439801	1.01E-52	GO:0005085,GO:0016020,GO:0005737,GO:0015238,GO:0006885	ATSTU8190.1	ATEFF elongation factor
Sapur.01G0224800.1	180.6450503	-1.137871884	0.116004761	-27.3888	1.63E-165	3.58E-164	popular	-0.91858228	2.25E-64	GO:0008829	PLA IIB;PLP9	PATATIN-like protein 9
Sapur.01G0251200.1	46.6549115	-2.094566607	0.076663711	-27.3212	2.37E-164	5.20E-163	popular	-0.88439159	1.03E-53	GO:0051087	ATBAGS;BAG5	BCL-2-associated athanogene 5
Sapur.01G0260800.1	79.66318008	-2.159257147	0.079128344	-27.3153	2.79E-164	6.09E-163	popular	-0.86054829	5.24E-47	GO:0005515,GO:0004468,GO:0005524,GO:0004672	PSK5	receptor-like protein kinase 1
Sapur.01W0241200.1	11.61634141	-4.849020016	0.177537275	-27.3073	3.48E-164	7.60E-163	popular	-0.91978754	7.45E-65		ATSG29820.2	transmembrane protein
Sapur.01W0259300.1	7.833876512	-6.462268867	0.236229607	-27.2711	9.31E-164	2.04E-162	popular	-0.90713567	3.90E-60		ATSG49040.1	Homeobox-leucine zipper protein
Sapur.01G0211500.1	20.61033922	-3.915988811	0.189045971	-27.2709	9.39E-164	2.05E-162	popular	-0.90347203	5.40E-58		ATSG66580.1	Magnesium transporter CorA-like family protein
Sapur.01W0259500.1	11.70169645	-4.93872917	0.181105168	-27.2705	9.50E-164	2.07E-162	popular	-0.92881602	2.87E-65		ATSG29820.1	Magnesium transporter CorA-like family protein
Sapur.01W0264100.1	8.319215347	-6.534251255	0.24006252	-27.219	3.87E-163	8.34E-162	popular	-0.87387032	2.56E-50			
Sapur.01T0027900.1	40.20718383	-2.697562572	0.099161934	-27.2035	5.90E-163	1.28E-161	popular	-0.90964794	5.11E-61	GO:005507,GO:0055114,GO:0016491	ATSG46570.1	LAC6
Sapur.01G0177400.1	236.0150409	-1.326166	0.07409652	-27.2023	6.14E-163	1.32E-161	popular	-0.91470918	1.66E-64		ATSG36145.1	laccase 6
Sapur.01G0290400.1	16.70437879	-4.602463881	0.169242985	-27.1946	7.52E-163	1.62E-161	popular	-0.85204371	2.01E-45		ATSG60890.2	hypothetical protein
Sapur.01G0250500.1	96.32216211	-1.481122272	0.09124344	-27.1924	7.77E-163	1.68E-161	popular	-0.90464641	1.45E-59		ATSG20898.1	protein binding
Sapur.01G0219600.1	128.5190404	-1.191574142	0.04382528	-27.1661	1.63E-162	3.52E-161	popular	-0.91936987	8.90E-65	GO:0043565,GO:0008270,GO:0006355,GO:0003700	ATSG08310.2	GATA11
Sapur.01G0263600.1	115.3206771	-1.051201745	0.038731496	-27.1478	2.69E-162	5.79E-161	popular	-0.92054326	2.54E-65			
Sapur.01G0126200.1	1115.320677	-0.051201745	0.038731496	-27.1478	2.69E-162	5.79E-161	popular	-0.91403681	1.22E-62	GO:0008270	ATSG68420.2	DHHC-type zinc finger family protein
Sapur.01G0138500.1	499.2047994	-2.219067795	0.081765897	-27.1393	3.19E-162	7.28E-161	popular	-0.90798519	1.95E-60	GO:000896,GO:0000077,GO:0003837,GO:0000275,GO:0003677	ATPCN2;PCN2	proliferating cell nuclear antigen 2
Sapur.01G0230200.1	128.1928314	-1.955408897	0.07211882	-27.1163	4.26E-162	9.50E-161	popular	-0.90192090	2.56E-58	GO:0005515	ATSLR4	SALIM-like auxin-responsive protein family
Sapur.01G0295100.1	395.4821649	-1.401161036	0.051695251	-27.1043	8.77E-162	1.88E-160	popular	-0.92303765	2.52E-65	GO:0006508,GO:0004190		Eukaryotic aspartyl protease family protein
Sapur.01G0261600.1	54.47506962	-2.551587827	0.08712285	-27.0913	1.25E-161	2.66E-160	popular	-0.87437454	8.61E-51	GO:0007186,GO:0007264,GO:0005834,GO:0004871	ATSG6535.1	
Sapur.01G0231300.1	26.30239822	-3.174600405	0.117197564	-27.0895	1.31E-161	2.80E-160	popular	-0.92480071	8.14E-68	GO:0046983	ATSG41130.1	GDL domain protein
Sapur.01T0028800.1	993.1312401	-1.339983	0.05147227	-27.0887	1.49E-161	3.19E-160	popular	-0.90790763	1.94E-60		ATSG66610.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.01G0236600.1	1513.292281	0.873671512	0.032273137	27.0721	2.10E-161	4.48E-160	popular	-0.89786346	4.16E-57	GO:0017025,GO:0008270,GO:0006355,GO:0006252	ATSG0190.1	Histone superfamily protein
Sapur.01T0049500.1	50.01993637	-2.151164221	0.10051237	-27.0706	2.24E-161	4.66E-160	popular	-0.90753602	1.81E-60	GO:0055114,GO:0016491	ATSG10320.1	Cyclin-like family protein
Sapur.01W0201400.1	987.1187669	-1.503822676	0.055557244	-27.068	2.35E-161	4.99E-160	popular	-0.93216938	2.77E-70	GO:0044238	ATSG39910.1	transcription initiation factor IIB
Sapur.01G0260300.1	288.1723105	-2.30803169	0.085439872	-27.0426	4.66E-161	9.90E-160	popular	-0.8605415	2.90E-47	GO:0006508,GO:0004190	ATSG49240.1	prolyl 4-hydroxylase alpha subunit, putative
Sapur.01G0285300.1	687.2517947	-1.003690499	0.041604729	-27.0418	4.80E-161	1.02E-159	popular	-0.85203736	9.88E-46		ATSG49370.1	2OG-Fe(II) oxygenase superfamily protein
Sapur.01G0249500.1	137.9164433	-2.001758398	0.074091996	-27.0172	9.28E-161	1.97E-159	popular	-0.89269542	1.69E-55	GO:0005515,GO:0006468,GO:0004672	ATSG41820.1	Histone superfamily protein
Sapur.01G0220300.1	22.60205631	-3.837209147	0.17904729	-27.0167	9.32E-161	2.16E-159	popular	-0.90008038	1.19E-58		ATSJAR4	Leucine-rich receptor-like protein kinase family protein
Sapur.01G0266300.1	226.8792544	-2.845706364	0.105616037	-26.9439	6.73E-160	1.42E-158	popular	-0.93240406	7.97E-59	GO:0006468,GO:0005524,GO:0004672	ATSG36570.1	transcription factor family protein
Sapur.01T0025000.1	597.7013881	-1.15631643	0.042939843	-26.9415	7.17E-160	1.51E-158	popular	-0.91999816	6.14E-65		ATSG75120.1	Leucine-rich receptor-like protein kinase family protein
Sapur.01G0138400.1	311.7737377	-1.172268053	0.051045195	-26.9076	1.79E-159	3.76E-158	popular	-0.92314658	3.19E-66	GO:2001070,GO:0003723	RNE;RG	Ribonuclease II/R
Sapur.01G0221300.1	61.53481469	-2.557164966	0.095113602	-26.9004	2.17E-159	4.56E-158	popular	-0.92885038	8.61E-69		ATSG39700.1	ribonuclease E/G family protein
Sapur.01G0278000.1	704.6838367	-1.207494415	0.07284644	-26.8969	2.46E-159	5.15E-158	popular	-0.87490145	1.54E-50	GO:0007275	RNAse 4;TXEIP;AK4;TXEIP A	Ribonuclease 4
Sapur.01G0220100.1	438.1429123	-1.314847084	0.05	-26.8956	2.48E-159	5.18E-158	popular	-0.92863864	8.66E-69	GO:0016020	AFO;FIL;YAB1	Plant-specific transcription factor YABBY family protein
Sapur.01W0241400.1	62.52639847	-1.722951722	0.064090589	-26.88307	3.46E-159	7.25E-158	popular	-0.88157754	2.13E-52	GO:0020347,GO:0006468,GO:0005524,GO:0004672		ABC-2 type transmembrane protein
Sapur.01W0239100.1	11.83192908	-4.925052209	0.230404721	-26.8752	4.28E-159	8.94E-158	popular	-0.91500795	5.52E-63		ATSG38280.1	PRSK
Sapur.01G0234800.1	43.10001018	-2.814854819	0.086265517	-26.8378	1.17E-158	2.44E-157	popular	-0.89929181	1.14E-57		ATSG27020.2	PLATZ transcription factor family protein
Sapur.01B0287900.1	167.2231961	-2.425264449	0.060413362	-26.8181	1.99E-158	4.13E-157	popular	-0.93463976	1.71E-71	GO:0006468,GO:0005524,GO:0004672,GO:0005515	ATSG31350.1	Heavy metal transport/detoxification superfamily protein
Sapur.01T0029100.1	23.20018802	-3.556488577	0.108397812	-26.8059	2.76E-158	5.73E-157	popular	-0.89702968	5.12E-57	GO:0007275,GO:0006356,GO:0003700	AtLEPL;T3	AINTEGUMENTA-like 3
Sapur.01W0264800.2	11.81796677	-4.801455988	0.216505229	-26.7959	3.61E-158	7.48E-157	popular	-0.92452344	7.07E-67	GO:0051499,GO:0016788	GEX1	Leucine-rich receptor-like protein kinase family protein
Sapur.01G0307500.1	43.10114224	-2.817905511	0.087705502	-26.7904	4.18E-158	8.67E-157	popular	-0.84439466	4.96E-56		ATSG11880.1	D-aminoacyl-tRNA deacylase
Sapur.01G0219700.1	361.503	-0.804287706	0.030559202	-26.7567	1.01E-157	2.14E-156	popular	-0.89094755	5.12E-55		ATSG45230.1	GRX;ATGRX8;BPC;BPC6
Sapur.01W0265400.1	53.95710188	-2.303821469	0.070106428	-26.7383	1.69E-157	3.49E-156	popular	-0.90583663	1.04E-59		ATSG46845.1	Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01G0138800.1	86.53797752	-1.638048955	0.061348462	-26.7007	4.62E-157	9.51E-156	popular	-0.87863685	1.40E-51		ATHB29;ZFHD1	zinc finger homeodomain 1
Sapur.01G0270100.1	56.07091525	-2.977670311	0.074078837	-26.6968	5.12E-157	1.05E-155	popular	-0.91983966	1.54E-62		ATSG15030.3	NEE33;TCP4
Sapur.01G0285200.1	1519.945542	-1.810894595	0.068565537	-26.6458	2.05E-156	4.18E-155	popular	-0.87574754	4.20E-46		ATOSM34;OSM34	TCP family transcription factor 4
Sapur.01G0402200.1	101.1134954	-2.424065465	0.053541322	-26.5063	7.49E-156	1.54E-154	popular	-0.89153147	3.47E-55			Lactosylceramidase / glycosylsaw I family protein
Sapur.01G0280200.1	59.72405686	1.925282367	0.072429	26.51912	9.07E-156	1.86E-154	popular	-0.84449337	2.31E-48	GO:0055114,GO:0016627,GO:0050660,GO:0008152,GO:0003995	ISR3	acyl-CoA dehydrogenase-related
Sapur.01G0269900.1	44.34510712	-3.366177595	0.126601884	-26.5887	9.18E-156	1.88E-154	popular	-0.83824812	1.14E-42	GO:0005975,GO:0004553	ATSC17180.1	ATCEL1,ATGH9B1,CEL1
Sapur.01G0262900.1	313.9833321	-1.575232881	0.059248891	-26.5862	9.79E-156	2.00E-154	popular	-0.89202976	5.12E-57	GO:0003677,GO:0008289	HB-7;HOX3	cellulase 1
Sapur.01B0297600.1	71.92296277	-2.075411891	0.115788657	-26.5789	1.19E-155	2.43E-154	popular	-0.79348519	2.99E-35		ATSG48480.1	homeobox-7
Sapur.01G0281200.1	431.9682314	-1.209389584	0.078977629	-26.5124	4.97E-155	1.01E-153	popular	-0.81617251	2.01E-46		ATSG38460.1	JAG
Sapur.01G0141800.1	54.29681558	-2.296056646	0.124413881	-26.4927	1.18E-154	2.40E-153	popular	-0.85489939	7.42E-46	GO:0006355,GO:0003700	ATSG27950.1	geranylgeranyl reductase
Sapur.01G0285400.1	1329.110859	-1.000241	0.038239781	-26.4768	1.79E-154	3.65E-153	popular	-0.87468884	5.84E-50		CRF4	cytokinin response factor 4
Sapur.01B0240400.1	478.9953835	-2.353752979	0.088923955	-26.4688	2.22E-154	4.51E-153	popular	-0.83791293	1.31E-42	GO:0016747	ATPAL1;PAL1	PHE ammonia lyase 1
Sapur.01W0239300.1	267.5149954	-2.330260865	0.088179474	-26.4263	8.83E-154	1.38E-152	popular	-0.92282317	4.23E-66	GO:0005975,GO:0004553		HXXXD-type acyl-transferase family protein
Sapur.01B0272200.1	2248.545114	-1.217091029	0.12151556	-26.422	1.16E-153	2.54E-152	popular	-0.78791759	2.50E-34		ATOSM34;OSM34	Glycosyl hydrolase family 10 protein
Sapur.01G0258300.1	238.6790768	-1.319763269	0.050007776	-26.3912	1.73E-153	3.50E-152	popular	-0.91938795	2.51E-63			osmotin 34
Sapur.01T0029400.1	328.4074232	-1.016189137	0.038506426	-26.3853	2.02E-153	4.08E-152	popular	-0.90363265	5.32E-59			Dna-binding storekeeper protein-related transcriptional regulator
Sapur.01G0240000.1	849.3867717	-0.387936872	0.041252799	-26.3739	2.73E-153	5.50E-152	popular	-0.89243674	1.90E-55	GO:0055114,GO:0051287,GO:0046168,GO:0016616,GO:0005975,GO:0004367,GO:0009331	GPDHC1	Domain of unknown function (DUF581)
Sapur.01W0265600.1	7.805195684	-6.905027368	0.241437701	-26.1653	3.43E-151	6.91E-150	popular	-0.84482401	6.61E-44			glycerol-3-phosphate dehydrogenase, NAD
Sapur.01G0261300.1	677.1655571	-1.385688885	0.052598855	-26.3525	4.80E-153	9.65E-152	popular	-0.87146221	9.68E-50	GO:0005662,GO:0003824	N/mk;N-like negative transcriptional regulator family	Zinc knuckle (CCHC-type) family protein
Sapur.01G0274000.1	367.5038894	-1.852882202	0.032267656	-26.3498	5.14E-153	1.04E-151	popular	-0.91367808	1.73E-62	GO:0048481	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	phenylcoumaran benzylic ether reductase
Sapur.01G0273400.1	668.5364638	-1.990585778	0.075607462	-26.3315	8.35E-153	1.67E-151	popular	-0.93898645	9.81E-74		ATSG36420.1	BHLH transcription factor, putative
Sapur.01W0267800.1	67.12239939	-2.618885233	0.099532087	-26.3051	1.57E-152	3.14E-151	popular	-0.84609364	3.62E-43	GO:0005515,GO:0006468,GO:0005524,GO:0004672	FUC95A	L-2,4-alpha-L-fucosidase
Sapur.01G0267000.1	1917.716114	-1.354970853	0.051153892	-26.303	1.77E-152	3.54E-151	popular	-0.91451319	8.45E-63	GO:0003676	ATRBP31,ATRBP33,CP31,RB	LRR-receptor-like kinase
Sapur.01G0262100.1	1189.060904	1.019565521	0.038768679	26.29801	2.02E-152	4.03E-151	popular	-0.87524661	9.24E-51		ATSJR3300.1	31-kDa RNA binding protein
Sapur.01G0282400.1	146.2616487	-1.667970322	0.063508171	-26.2629	5.09E-152	1.01E-150	popular	-0.93261148	7.98E-70		ATSJR1	ribonucleoprotein, putative
Sapur.01T0050800.1	59.63434216	-2.650069693	0.100910601	-26.2616	5.27E-152	1.05E-150	popular	-0.88471013	3.01E-53	GO:0004872	ATSG37900.1	disadjglycerol acyltransferase, putative
Sapur.01G0220200.1	244.4420007	-2.424007875	0.092818881	-26.2229	1.42E-151	2.80E-150	popular	-0.91831473	2.88E-64		SDM	BTB/POZ domain protein
Sapur.01G0202200.1	7.088962608	-6.305384	0.240725266	-26.1939	3.12E-151	6.16E-150	popular	-0.87540627	8.49E-51		ATSAD1;BARD1;RING1	Zinc finger C-x8-C-x5-C-x3-H type family protein
Sapur.01G0282000.1	19.58042274	-4.950032624	0.203751348	26.17678	4.89E-151	9.63E-150	popular	-0.78258429	6.02E-32		ATSG61810.1	BRCA1-associated RING domain protein
Sapur.01W0118100.1	264.3354592	-2.371981189	0.052416669	-26.1745	5.18E-151	1.02E-149	popular	-0.90511448	8.89E-60	GO:0006468,GO:0005524,GO:0004672	ATSG0860.1	NA
Sapur.01G0368300.1	3585.481218	-0.030308322	0.030788809	-26.1733	5.35E-151	1.05E-149	popular	-0.90246116	5.68E-59	GO:0005525	ATRABD;ATRABE1B;RABE1	protein kinase superfamily protein
Sapur.01G0261500.1	116.3437751	-1.790061635	0.068433533	-26.1658	6.52E-151	1.28E-149	popular	-0.88523621	2.16E-53		ATSG50150.1	RAB GTPase homologs E1B
Sapur.01G0197900.1	131.0947323	-0.587301806	0.064487957	-26.1648	6.70E-151	1.32E-149	popular	-0.90364529	6.49E-58		ATSG0560.1	Protein of Unknown Function (DUF239)
Sapur.01G0117800.1	459.6219374	-1.507245479	0.046976281	-26.1584	7.92E-151	1.55E-149	popular	-0.91818036	2.88E-64		ATKOPGE1;KOPGE1	Rab guanyl-nucleotide exchange factor 1
Sapur.01T0091100.1	88.23715306	-1.723437924	0.060900147	-26.1517	9.43E-151	1.85E-149	popular	-0.87911663	9.46E-52	GO:0005085,GO:0006310	ATSD0015.1	NADP(H)-binding family protein
Sapur.01W0264900.1	125.4870094	-2.167196	0.142461848	-26.1347	1.74E-150	3.34E-149	popular	-0.94948384	6.13E-80	GO:0004872	ALDH2;ALDH2A;ALDH2B4	Eukaryotic aspartyl protease family protein
Sapur.01T0016900.1	322.5516635	1.123217216	0.043012431	26.11283	2.61E-150	5.09E-149	popular	0.87710062	2.99E-51		ATSB60800.1	aldehyde dehydrogenase family (NAD) family protein
Sapur.01G0138100.1	376.0054862	-1.163388885	0.044547451	-26.1126	3.26E-150	6.11E-149	popular	-0.87539796	5.16E-50	GO:0006468,GO:0004672	ATPRK1;PERK1	Plant protein of unknown function (DUF936)
Sapur.01G0137400.1	502.6377073	-1.556622048	0.059435513	-26.1031	3.36E-150	6.56E-149	popular	-0.89873692	2.27E-57		ATSG6625.2	protein kinase family protein
Sapur.01W0228800.1	15.54629776	-3.154897119	0.192158275	-26.0769	5.09E-150	1.00E-148	popular	-0.93261148	7.98E-70		ATSG27020.1	Leucine-rich receptor-like protein kinase family protein
Sapur.01G0248400.1	428.4318043	-1.624827313	0.062325711	-26.0669	8.00E-150	1.56E-148	popular	-0.91831508	2.78E-64	GO:0019898,GO:0015979,GO:0006364,GO:0005509	ATSG3540.1	Protein kinase superfamily protein
Sapur.01W0258100.1	8.515917127	-6.250444327	0.239887358	-26.0558	1.24E-149	2.25E-148	popular	-0.87412798	5.96E-50		ATTCP1B;BRC1;TCP18	Rab GTPase homologs A5A
Sapur.01G0843300.1	304.6018893	1.456060632	0.055925854	26.05068	1.32E-149	2.57E-148	popular	-0.88905748	1.83E-54		ATSG29195.1	TCP family transcription factor
Sapur.01W0251900.1	56.26026344	-1.55082204	0.059558623	-26.0354	1.97E-149	3.82E-148	popular	-0.88639092	1.05E-53		ATSB8550.1	NA
Sapur.01T0045900.1	207.7796024	-1.021440206	0.042448018	-25.9971	3.14E-149	6.10E-148	popular	-0.90362487	5.01E-59	GO:0005515,GO:0006468,GO:0004672	ATSG27150.1	Vacuolar protein sorting-associated protein 26
Sapur.01T0071100.1	786.9202493	-2.364363744	0.091088178	-25.9566	1.52E-148	2.95E-147	popular	-0.88661974	8.91E-54		ATSG0560.1	Leucine-rich receptor-like protein kinase family protein
Sapur.01G0211200.1	516.4668212	-1.147168	0.044239	-25.9484	1.81E-148	3.51E-147	popular	-0.89211765	3.30E-55	GO:0005634	ATSG46160.1	Histone superfamily protein
Sapur.01G0134200.1	20.85854838	-2.800092181	0.107934357	-25.9428	2.19E-148	4.23E-147	popular	-0.90736688	2.20E-62		CYC2D;CYCD3;1	CYCLIN D3;1
Sapur.01G0229100.1	915.319644	-1.262926184	0.048676919	-25.941	2.30E-148	4.43E-147	popular	-0.87187918	1.41E-50		AIR12	Uncharacterized protein family (UPF0497)
Sapur.01G0257200.1	56.44978849	-1.802293431	0.072946738	-25.9408	2.31E-148	4.45E-147	popular	-0.87459178	1.36E-50			auxin-responsive protein
Sapur.01G0138400.1	134.8561117	-1.342687223	0.052197116	-25.9185	4.12E-148	7.93E-147	popular	-0.91183438	7.29E-62	GO:0010207	PGR27	Excotosin family protein
Sapur.01G0129300.1	31.93668841	-4.967870361	0.191505074	-25.9042	5.97E-148	1.15E-146	popular	-0.9008129	4.94E-58		LAX2	photosystem II family protein Psb27
Sapur.01B0125900.1	172.4920953	-1.404682547	0.054235813	-25.8859	9.60E-148	1.84E-146	popular	-0.93482527	2.36E-71		CVI1	AUXIN RESISTANT 2
Sapur.01G0283800.1	746.6694944	-1.715847754	0.06425479	-25.863	1.24E-147	2.36E-146	popular	-0.89294665	5.01E-57	GO:0015137,GO:0043231		CYP2 like 1
Sapur.01B0281400.1	1283.496855	1.173580695	0.045398151	25.84904	2.49E-147	4.76E-146	popular	0.88724301	5.96E-54		GAL1;GAL4	2 iron, 2 sulfur cluster binding
Sapur.01W0264100.1	1448.11883	-1.365318407	0.049023026	-25.8356	3.13E-147	6.74E-146	popular	-0.90629426	7.50E-60			Metalorate/galactokinase family protein
Sapur.01G0123200.1	475.3476427	-1.728269188	0.066899445	-25.8355	3.54E-147	6.75E-146	popular	-0.89014264	8.88E-55	GO:0008184,GO:0005975		hypothetical protein
Sapur.01G0230300.1	23.76268819	-3.663145966	0.215969869	-25.8267	4.42E-147	8.41E-146	popular	-0.93181687	3.64E-84		ATSG29120.1	Glycosyl transferase, family 35
Sapur.01G0191200.1	130.8143105	-2

Sapur.002G140900.1	70.2924678	-7.70053677	0.71715575	-24.3167	1.31E-130	2.14E-129	purple	-0.90603524	8.99E-60			AT4G22290.1	Ubiquitin-specific protease family C19-related protein	transmembrane protein, putative	
Sapur.015G098200.1	116.9134651	-0.01269123	0.04167596	-24.2982	2.05E-130	3.36E-129	purple	-0.88601404018	1.31E-53			AT3G30680.1	Domain of unknown function (DUF3995)	plant/F3H11-7 protein, putative	
Sapur.005G088100.1	20.68875281	-2.26288216	0.09322592	-24.2733	3.75E-130	6.14E-129	purple	-0.92088601	1.96E-58	GO:0043565,GO:0008270,GO:0006355,GO:0003700		AT5G20870.1	GATA type zinc finger transcription factor family protein	GATA transcription factor	
Sapur.004G007500.1	425.5139002	-1.03476072B	0.04273971	-24.2253	1.20E-129	1.96E-128	purple	-0.88871597	2.28E-54			AT5G37300.1	Pentatricopeptide repeat (PPR) superfamily protein	maternal effect embryo arrest 40 protein	
Sapur.003G095500.1	6.9167366	-0.96718087B	0.14638058	-24.2233	1.28E-129	2.09E-128	purple	-0.84002746	5.34E-43					hypothetical protein	
Sapur.008G092200.1	108.8552261	-1.91147535	0.07691093	-24.2184	1.42E-129	2.32E-128	purple	-0.90152072	2.91E-58			AT1G68780.1	RNI-like superfamily protein	pirforcmosprz indica-insensitive protein, putative	
Sapur.002G094800.1	65.26222754	-1.96330871	0.08112675	-24.2018	2.13E-129	3.45E-128	purple	-0.87261917	4.18E-50			AT4G12080.1	AVL1/LATAVL1	AT-hook motif nuclear-localized protein 1	DNA-binding family protein, putative
Sapur.018G190600.1	168.3539404	-1.47950188	0.06115251	-24.0058	2.19E-129	3.55E-128	purple	-0.82475063	4.12E-40			AT4G25450.1	OPR48	OSP(oxysterol binding protein)-related protein 4B	oxysterol-binding protein-like protein OBP4 protein
Sapur.016G071800.1	540.113977	-1.11459366	0.04610371	-24.1761	3.97E-129	6.41E-128	purple	-0.90418103	3.88E-59	GO:0006414,GO:0005525,GO:0048530,GO:0008312		AT5G03940.1	SAC9,CPSRP54,FFC,SRP54C3	chloroplast signal recognition particle 54 kDa subunit	NA
Sapur.013G046800.1	263.1520468	-0.9619562	0.06829642	-24.1684	4.67E-129	7.54E-128	purple	-0.89301144	1.96E-56			AT5G35340.1	NEG29	helicase domain protein	NA
Sapur.013G047500.1	10.04316313	-2.03765844	0.21680858	-24.1594	5.94E-129	9.58E-128	purple	-0.84031266	4.02E-43			AT5G39160.1	RmlC-like cupins superfamily protein	germin-like protein	
Sapur.015G098700.1	77.57251144	-1.07184114	0.07201108	-24.1554	6.51E-129	1.06E-127	purple	-0.89698429	7.99E-57			AT3G49840.1		hypothetical protein	
Sapur.004G041000.1	209.6213573	-1.71028159	0.07082545	-24.147	8.04E-129	1.29E-127	purple	-0.92771619	3.19E-68			AT3G11120.2		transmembrane protein, putative	
Sapur.013G120900.1	241.1941066	-1.50377184	0.12296674	-24.0509	8.18E-129	1.53E-127	purple	-0.91438106	9.60E-63			AT3G28100.1		NA	
Sapur.005G029700.1	104.9336222	-1.46039947	0.07452658	-24.1277	1.28E-128	2.06E-127	purple	-0.89182601	2.87E-55	GO:0008152,GO:0003824		AT5G27410.2	D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein	branched-chain-amino-acid aminotransferase-like protein	
Sapur.006G081200.1	139.5947086	-1.52832784	0.06318844	-24.1204	1.53E-128	2.45E-127	purple	-0.89268799	1.05E-55			AT5G10080.1		DUF3820 family protein	
Sapur.010G089400.1	7.01123848	-5.51742563	0.22875825	-24.119	1.58E-128	2.53E-127	purple	-0.92316573	2.05E-65			AT1G13290.1	DOT5,WIP6	C2H2-like zinc finger protein	C2H2-like zinc finger protein
Sapur.016G057200.1	11.02842385	-4.57408808	0.18965846	-24.1179	1.62E-128	2.60E-127	purple	-0.71883652	2.96E-26			AT5G58070.1	GIS	C2H2 and C2HC zinc fingers superfamily protein	nucleic acid-binding protein, putative
Sapur.009G056200.1	10.32328848	-3.20182273	0.10579757	-24.1077	2.08E-128	3.32E-127	purple	-0.84947828	4.12E-40	GO:0008270,GO:0005515		AT5G11110.1	RING/U-box superfamily protein	RING-H2 finger protein ATL29L, putative	
Sapur.004G028200.1	361.6144444	1.64879742	0.06839508	24.10083	2.12E-128	3.39E-127	purple	-0.82319806	1.17E-39	GO:0046872		AT4G03510.1	ATRMA1,RMA1	RING membrane-anchor 1	RING finger E3 ubiquitin ligase
Sapur.002G194900.1	103.7492364	-4.52703763	0.17311803	-24.0988	2.42E-128	3.87E-127	purple	-0.8926402	4.63E-57			AT5G49520.1			hypothetical protein
Sapur.008G070500.1	12.96591026	-0.70585105	0.23691504	-24.079	4.14E-128	6.60E-127	purple	-0.71820186	3.43E-26			AT3G04100.1	AMIR9168,MYR168,NOX	myb domain protein 106	miste-like 2 MYB transcription factor, putative
Sapur.018G087300.1	37.14874869	-1.29464786	0.08871526	-24.0719	4.75E-128	7.56E-127	purple	-0.84688188	1.22E-44	GO:0016779,GO:0009058		AP1.2	ADP1G-C-Phase loge subunit	glucose-1-phosphate adenylyltransferase	
Sapur.004G129500.1	769.7963667	-2.37385405	0.35292053	-24.0598	6.59E-128	1.05E-126	purple	-0.90125189	3.61E-58			AT4G38660.1	Pathogenesis-related thaumatin superfamily protein	thaumatin-like protein	
Sapur.006G041300.1	263.1636618	-1.37393894	0.07126393	-24.0509	8.18E-128	1.30E-126	purple	-0.88966802	2.5E-56	GO:0048544,GO:0006468,GO:0004672		AT5G18100.1	Cysteine-like (transmembrane-binding) lectin family protein / PAN domain-containing protein	receptor like 5-receptor-like Serine/Threonine-kinase, putative	
Sapur.016G172600.1	341.984928	0.89448537	0.07192881	24.04193	1.01E-127	1.61E-126	purple	-0.87705337	2.79E-51			AT4G33780.1		transmembrane protein, putative	
Sapur.004G189800.1	876.5618292	-1.80501738	0.07510399	-24.0314	1.30E-127	2.07E-126	purple	-0.87516346	1.80E-50	GO:0055114,GO:0016491,GO:0008270		AT1G27440.1	Oxidoreductase, zinc-binding dehydrogenase family protein	alcohol dehydrogenase, putative	
Sapur.010G082200.1	187.6241344	-0.47577588	0.08132648	-24.0303	2.83E-127	4.47E-126	purple	-0.85876439	1.12E-47	GO:0005975,GO:0004553		AT5G07520.1	glycosyl hydrolase 9B1	endo-1,3(2),4-beta-glucanase	
Sapur.002G074000.8	4.92753638	-5.77951948	0.24088045	-24.0933	3.42E-127	5.39E-126	purple	-0.85809388	1.01E-46	GO:0006355,GO:0003634,GO:0003700		AT4G09660.1	AGL11,STK	K-box region and MADS-box transcription factor family protein	agamous MADS box factor transcription factor
Sapur.002G060600.1	1893.620904	1.00481647	0.04562613	24.0369	4.30E-127	9.30E-126	purple	-0.90967496	4.97E-61	GO:0016301,GO:0008152,GO:0005524		AT5G20560.1	PRK	phosphoribulokinase	phosphoribulokinase
Sapur.006G197500.1	138.0075687	-1.78385265	0.07673543	-23.9296	1.51E-126	2.36E-125	purple	-0.89288921	1.96E-55			AT5G49040.1	Disease resistance-responsive (dirigent-like protein) family protein	disease resistance response protein, putative	
Sapur.004G104900.1	41.24954871	-2.87767601	0.1335116	23.91821	1.98E-126	3.12E-125	purple	-0.82884025	6.10E-41	GO:0045454,GO:0015035,GO:0009055		GRX480,rosy19	Thioredoxin superfamily protein	glutaredoxin	
Sapur.010G095700.1	396.9407057	0.71409256	0.02991697	23.89759	2.14E-126	5.06E-125	purple	-0.88548197	8.91E-53	GO:0008242		AT3G54130.1		ataxin-3 protein	
Sapur.018G081700.1	17.56633866	-0.53852751	0.23168374	-23.8899	3.90E-126	6.08E-125	purple	-0.81003761	2.26E-38			E12A11.MFT	PEBP (phosphatidylethanolamine-binding protein) family protein	mother of FT and TFL1 protein	
Sapur.006G022000.1	233.7774403	-1.49737025	0.06269783	-23.881	4.82E-126	7.52E-125	purple	-0.89373404	7.80E-56	GO:0008408,GO:0006139,GO:0003676		AT3G14310.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	3'-5' exonuclease	
Sapur.013G120700.1	13.95717655	-2.70238115	0.11433738	-23.8811	4.95E-126	7.70E-125	purple	-0.8828487	5.02E-53	GO:0006355		AT5G58190.1	RING/FYVE/PHD zinc finger superfamily protein	zinc finger protein, putative	
Sapur.019W033400.1	51.50064618	-2.61263022	0.13844763	-23.8783	5.15E-126	8.01E-125	purple	-0.87891479	1.07E-51	GO:0006629		AT2G26230.1	PATATIN -like protein 6	patatin-like phospholipase	
Sapur.010G192800.1	559.8545568	0.58075756	0.02432829	23.87616	5.42E-126	8.43E-125	purple	-0.88732278	6.83E-54	GO:0005506,GO:0016226,GO:0005506		AT4G20970.1	ATNFU2,NFU4	NFU domain protein 4	iron-sulfur cluster assembly protein NFU4
Sapur.010G069000.1	645.5275588	-1.46096357	0.06037048	-23.8685	5.61E-126	8.82E-125	purple	-0.85836106	4.95E-49			AT5G66080.1	Histone superfamily protein	histone H4	
Sapur.002G014000.1	183.8910521	-1.67151727	0.07208674	-23.8576	8.44E-126	1.31E-124	purple	-0.91585877	2.02E-63	GO:0004488,GO:0016307		AT1G19980.1	ATIPK5K1,ATIPK1,PIPK5K1	phosphatidylinositol-4-phosphate 5-kinase 1	phosphatidylinositol-4-phosphate 5-kinase
Sapur.005G100100.1	86.60219851	-2.44718318	0.07743771	-23.8522	9.38E-126	1.46E-124	purple	-0.86764307	3.01E-48			AT4G25560.1		hypothetical protein	
Sapur.003G143400.1	57.78522515	-2.28866181	0.09617082	-23.8104	2.61E-125	4.03E-124	purple	-0.89611529	1.49E-56			AT5G07010.1	ATST2A,ST2A	sulfotransferase 2A	flavonol 4'-sulfotransferase, putative
Sapur.019W026900.1	14.45591911	-3.24164278	0.11863978	-23.7949	3.78E-125	5.81E-124	purple	-0.8849129	1.00E-53	GO:0010223,GO:0005634		AT5G13180.1	LAS,LCS1B	GRAS family transcription factor	GRAS family transcription factor lateral protein
Sapur.016G138900.1	135.1422423	-0.49785689	0.06291285	-23.7942	3.83E-125	5.91E-124	purple	-0.88549197	1.67E-58			AT5G58930.1		Protein of unknown function (DUF740)	DUF740 family protein
Sapur.018W042400.1	7.24394204	-5.71424395	0.24103603	-23.7791	5.49E-125	8.45E-124	purple	-0.87384753	2.52E-50			AT3G27030.1	PLATZ transcription factor family	NA	NA
Sapur.008G097000.1	229.0591933	-1.67350229	0.07045361	-23.7541	9.96E-125	1.53E-123	purple	-0.88570125	1.54E-53	GO:0008270,GO:0005622,GO:0005515		AT5G25480.1	B-box type zinc finger protein with CCT domain	zinc finger constans-like protein	
Sapur.008G026400.1	31.45587696	-1.58341603	0.06667044	-23.7478	1.16E-124	1.78E-123	purple	-0.87693877	7.02E-52			AT5G04250.1	Cysteine proteinases superfamily protein	NA	NA
Sapur.010G060500.1	25.06123151	-2.14181148	0.14186553	-23.7349	1.57E-124	2.41E-123	purple	-0.85557836	2.67E-46			AT4G05570.1	alpha/beta-Hydrolases superfamily protein	Dnaf heat shock amino-terminal domain protein, putative	
Sapur.009G087100.1	23.54869719	-2.82336776	0.11054752	-23.734	1.61E-124	2.46E-123	purple	-0.84455007	7.13E-44			AT5G66580.1		DUF4328 domain protein	
Sapur.004G020900.1	523.4378032	-1.50125021	0.06233710	-23.7125	1.97E-124	3.01E-123	purple	-0.85816016	3.77E-47	GO:0005515,GO:0006468,GO:0005524,GO:0004672	HSL1	AT2G44840.1	HAESA-like 1	LRR receptor-like kinase-like1	
Sapur.010G085600.1	3184.145561	0.82156231	0.03462954	23.7178	2.36E-124	3.61E-123	purple	-0.88451096	3.03E-53			AT5G07650.1	TPX2 (targeting protein for Xklp2) protein family	targeting protein for Xklp2 protein	
Sapur.T001100.1	25.70833333	-2.60086422	0.10076884	-23.6976	2.82E-124	5.82E-123	purple	-0.88028512	2.5E-54			AT5G40460.1		hypothetical protein	
Sapur.015G091600.1	15.38445898	-3.98866544	0.16839881	-23.6857	5.07E-124	7.71E-123	purple	-0.78168023	1.35E-33			AT2G38340.1	ATERF12,ERF12	ERF domain protein 12	NA
Sapur.013G021100.1	44.38243584	-2.70508388	0.18090375	-23.6703	7.31E-124	1.11E-122	purple	-0.80111707	1.21E-36			AT1G18120.1	ATLR-1	Pathogenesis-related thaumatin superfamily protein	NA
Sapur.018G102800.1	26.71323118	-2.37462216	0.10048345	-23.6502	1.17E-123	1.78E-122	purple	-0.84434572	4.77E-44	GO:0006355,GO:0003700		AT4G15360.1	SHN1,WIN1	Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.008G031000.1	134.5032143	-2.44511442	0.10350783	-23.6249	2.26E-123	3.42E-122	purple	-0.75488465	3.46E-30			AT5G07900.1	LBD1	LOB domain-containing protein 1	lateral organ boundaries domain protein
Sapur.15W026660.2	5.05534793	-5.70627786	0.24157746	-23.6213	2.33E-123	3.51E-122	purple	-0.86320045	3.44E-47	GO:0055124,GO:0003676,GO:0004386		AT5G48650.2	DEJ(H)-like RNA helicase family protein		NA
Sapur.006G092100.1	66.60734631	-1.38360988	0.05857779	-23.6201	2.40E-123	3.62E-122	purple	-0.89746284	5.68E-57			AT2G28330.1		hypothetical protein	
Sapur.018G125700.1	434.9566689	-0.82408018	0.09026842	-23.5928	4.56E-123	6.86E-122	purple	-0.86214928	2.77E-44					transmembrane protein, putative	
Sapur.002G185800.1	157.885084	-1.71885721	0.07288505	-23.5846	5.55E-123	8.33E-122	purple	-0.89007864	9.71E-55			AT5G25500.1	AFH1,AHF1,ATFH1,FH1	formin homology 1	formin-like 2 domain protein
Sapur.010G074300.1	103.7930095	-1.45001154	0.13006509	-23.5699	1.21E-122	1.81E-121	purple	-0.76963734	1.66E-34	GO:0046872,GO:0030001		AT5G02610.1		Heavy metal transport/detoxification superfamily protein	targeted copper chaperone protein
Sapur.019W026600.1	11.27431825	-2.70491703	0.11326182	-23.5508	1.23E-122	1.84E-121	purple	-0.87155278	7.72E-50	GO:0016851,GO:0005975		AT3G06880.1	DRT102	DNA-damage-repair/toleration protein (DRT102)	NA
Sapur.003G064100.1	25.06123151	-2.14181148	0.14186553	-23.7349	1.57E-124	2.41E-123	purple	-0.88943681	4.6E-54			AT4G05461.1		DNA heat shock family protein	NA
Sapur.004G087100.1	23.54869719	-2.82336776	0.11054752	-23.734	1.61E-124	2.46E-123	purple	-0.84455007	7.13E-44			AT5G66520.1	ATC/VFZ,C/VFZ	cell wall / vacuolar inhibitor of fructosidase 2	NA
Sapur.004G020900.1	523.4378032	-1.50125021	0.06233710	-23.7125	1.97E-124	3.01E-123	purple	-0.85816016	3.77E-47	GO:0005515,GO:0006468,GO:0005524,GO:0004672	HSL1	AT2G44840.1	HAESA-like 1	LRR receptor-like kinase-like1	
Sapur.010G085600.1	3184.145561	0.82156231	0.03462954	23.7178	2.36E-124	3.61E-123	purple	-0.88451096	3.03E-53			AT5G07650.1	TPX2 (targeting protein for Xklp2) protein family	targeting protein for Xklp2 protein	
Sapur.T001100.1	25.70833333	-2.60086422	0.10076884	-23.6976	2.82E-124	5.82E-123	purple	-0.88028512	2.5E-54			AT5G40460.1		hypothetical protein	
Sapur.015G091600.1	15.38445898	-3.98866544	0.16839881	-23.6857	5.07E-124	7.71E-123	purple	-0.78168023	1.35E-33			AT2G38340.1	ATERF12,ERF12	ERF domain protein 12	NA
Sapur.013G021100.1	44.38243584	-2.70508388	0.18090375	-23.6703	7.31E-124	1.11E-122	purple	-0.80111707	1.21E-36			AT1G18120.1	ATLR-1	Pathogenesis-related thaumatin superfamily protein	NA
Sapur.018G102800.1	26.71323118	-2.37462216	0.10048345	-23.65021	1.17E-123	1.78E-122	purple	-0.84434572	4.77E-44	GO:0006355,GO:0003700		AT4G15360.1	SHN1,WIN1	Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.008G031000.1	134.5032143	-2.44511442	0.10350783	-23.6249	2.26E-123	3.42E-122	purple	-0.75488465	3.46E-30			AT5G07900.1	LBD1	LOB domain-containing protein 1	lateral organ boundaries domain protein
Sapur.15W026660.2	5.05534793	-5.70627786	0.24157746	-23.6213	2.33E-123	3.51E-122	purple	-0.86320045	3.44E-47	GO:0055124,GO:0003676,GO:0004386		AT5G48650.2	DEJ(H)-like RNA helicase family protein		NA
Sapur.006G092100.1	66.60734631	-1.38360988	0.05857779	-23.6201	2.40E-123	3.62E-122	purple	-0.89746284	5.68E-57			AT2G28330.1		hypothetical protein	
Sapur.018G125700.1	434.9566689	-0.82408018	0.09026842	-23.5928	4.56E-123	6.86E-122	purple	-0.86214928	2.77E-44					transmembrane protein, putative	
Sapur.002G185800.1	157.885084	-1.71885721	0.07288505	-23.5846	5.55E-123	8.33E-122	purple	-0.89007864	9.71E-55			AT5G25500.1	AFH1,AHF1,ATFH1,FH1	formin homology 1	formin-like 2 domain protein
Sapur.010G074300.1	103.7930095	-1.45001154	0.13006509	-23.5699	1.21E-122	1.81E-121	purple	-0.76963734	1.66E-34	GO:0046872,GO:0030001		AT5G02610.1		Heavy metal transport/detoxification superfamily protein	targeted copper chaperone protein
Sapur.019W026600.1	11.27431825	-2.70491703	0.11326182	-23.5508	1.23E-122	1.84E-121	purple	-0.87155278	7.72E-50	GO:0016851,GO:0005975		AT3G06880.1	DRT102	DNA-damage-repair/toleration protein (DRT102)	NA
Sapur.003G064100.1	135.3607383	-1.14053932	0.04844867	-23.5421	1.51E-122	2.26E-121	purple	-0.88943681	4.6E-54			AT4G05461.1		DNA heat shock family protein	NA
Sapur.007G097000.1	125.2668784	-1.80582637	0.07672602	-23.5376	1.68E-122	2.52E-121	purple	-0.89654609	1.09E-56	GO:0004857		AT5G66520.1	ATC/VFZ,C/VFZ	cell wall / vacuolar inhibitor of fructosidase 2	NA
Sapur.002G294000.1	71.45769047	-1.56324429	0.07828869	-23.5319	1.85E-122	2.76E-121	purple	-0.82707452	1.20E-40			AT1G70710.1		hypothetical protein	
Sapur.016G265100.1	566.5242257	-1.39733746	0.05234172	-23.4861	5.65E-122	8.44E-121	purple	-0.88695216	2.18E-54	GO:0016788		AT5G03610.1	GDSL-like Lipase/Acylhydrolase superfamily protein	NA	NA
Sapur.006G069700.1	79.96237338	-2.54608807	0.10846089	-23.482	6.24E-122	9.33E-121	purple	-0.82860006	3.9E-43	GO:0019538		AT5G27130.1	Cbp amino terminal domain-containing protein	heat shock-like protein	
Sapur.15W042240.1	4.80284343	-5.74150398	0.24452895	-23.4795	6.61E-122	9.88E-121	purple	-0.83915301	7.69E-43						NA
Sapur.016G068800.1	8.07612602	-5.42635195	0.27880342	-23.4764	7.42E-122	1.11E-120	purple	-0.74868887	1.32E-29			AT4G22340.1	ABA2,ATABA2,ATSDR1,GIN1	NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase
Sapur.006G158400.1	407.10141	-1.24287735	0.11184979	-23.4679	8.68E-122	1.29E-120	purple	-0.91609516	1.46E-63	GO:0016788,GO:0016787		AT5G46940.1	DUT1	DUTP-PYROPHOSPHATASE 1	deoxyuridine 5'-triphosphate nucleotidohydrolase
Sapur.017G113000.1	392.5162048	1.11685895	0.04750655	23.46719	8.83E-122	1.31E-120	purple	-0.84988876	5.65E-45			AT5G16560.1	KAN,KAN1	Homeodomain-like superfamily protein	NA
Sapur.014G011800.1	165.4647934	-1.75058388	0.07463859	-23.4613	9.01E-122	1.51E-120	purple	-0.90373992	5.46E-59	GO:0055114,GO:0020037,GO:0016705,GO:0005506		AT5G16020.1	CYP81E2	cytochrome P450 family protein	cytochrome P450 family protein
Sapur.15W026100.1	359.4915313	-2.30756676	0.05129792	-23.4343	1.91E-121	2.83E-120	purple	-0.89660512	1.20E-57			AT3G74370.1		hypothetical protein	
Sapur.015G087000.1	519.7240552	-1.17014572	0.05001158	-23.4287	2.12E-121	3.12E-120	purple	-0.86670588	1.68E-48			AT3G02180,AT3G02180.1	homeobox protein 10	2F-HD homeobox protein	
Sapur.008G157100.1	262.8617775	-1.55246146	0.06636365	-23.3937	4.95E-121	7.31E-120	purple	-0.85431414	6.65E-46			AT3G06035.1	Glycoprotein membrane precursor GPI-anchored	GPI-anchored protein, putative	
Sapur.015W026400.1	4.41777363	-5.69180648	0.23607184	-23.3784	7.10E-121	1.05E-119	purple	-0.88168183	2.26E-52					NA	
Sapur.010G095200.1	595.8378773	-1.01616866	0.04349732	-23.36069	1.07E-120	1.58E-119	purple	-0.85734705	1.47E-46			AT5G68480.1		hypothetical protein	
Sapur.007G025100.1	7.89820613	-4.65196178B	0.19926589	-23.3454	1.53E-120	2.26E-119	purple	-0.9244364	8.81E-67			AT2G07.G5P7	ovate family protein 7	ovate family transcriptional repressor	
Sapur.018G088000.1	6.81659727	-5.38501701	0.23068165	-23.3439	1.56E-120	2.34E-119	purple	-0.90894204	2.4E-59	GO:0003723,GO:0005634		AT5G55180.1	LAS,SCL18	GRAS family transcription factor	GRAS family transcription factor lateral protein
Sapur.017G047400.1	1097.674978	-1.51287979	0.06657419	-23.3028	4.16E-120	6.09E-119	purple	-0.89918764	1.53E-57	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810		AT3G28860.1	ABCB19,ATABCB19,ATMDR	ATP binding cassette subfamily B19	ABC transporter B family protein
Sapur.004G120000.1	333.6382734	-1.23282369	0.05295622	-23.2769	7.58E-120	1.11E-118	purple	-0.82752761	1.66E-40	GO:0016787		AT4G34530.2	ATPAP10,PAP10	purple acid phosphatase 10	purple acid phosphatase
Sapur.010G097900.1	967.2681027	-1.56398404	0.06785518	-23.2752	7.92E-120	1.16E-118	purple	-0.89331227	1.03E-55	GO:0006412,GO:0005840,GO:0003735		AT5G65580.1		Ribosomal protein PSRP-3/Tc70S	plastid-specific 30S ribosomal protein, putative
Sapur.005G138600.1	104.4297674	-1.87528262	0.08073122	-23.2316	2.58E-119	3.81E-118	purple	-0.82281939	9.60E-40			AT5G58260.1	HCF-like superfamily protein with NYN/Nob type zinc finger	zinc finger protein	
Sapur.005G040000.1	183.7232582	-1.13631792	0.05752626	-23.2287	2.94E-119	3.40E-118	purple	-0.89795628	3.99E-57			AT5G28300.1	Duplicated homeodomain-like superfamily protein	NA	NA
Sapur.15W022240.1	17.68871992	-3.91425445	0.18245359	-23.2162	3.12E-119	4.54E-118	purple	-0.85496781	2.62E-46	GO:0006281,GO:0004518		AT5G18090.1	5'-3' exonuclease family protein	exonuclease	
Sapur.002G081900.1	7.90894528	-5.56631563	0.23994312	-23.1976	4.81E-119	6.98E-118	purple	-0.86892512	9.57E-49	GO:0046983		AT5G72210.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH96	
Sapur.015G098500.1	17.3634547	-1.78166866	0.10249645	-23.1943	5.15E-119	7.47E-118	purple	-0.66572464	4.21E-21					NA	
Sapur.15W034800.1	37.62219525	-2.51930676	0.10875265	-23.1649	1.01E-118	1.48E-117	purple	-0.84761656	1.81E-44	GO:0006508,GO:0004190		AT5G25580.1	Eukaryotic aspartyl protease family protein	NA	NA
Sapur.006G022800.1	13.08117271	-4.99636744	0.21582699	-23.15	1.45E-118	2.09E-117	purple	-0.70707524	4.34E-25			AT5G76670.1	Gibberellin-regulated family protein	gibberellin induced protein, putative	
Sapur.016G288000.1	8.18020152	-5.38501701	0.23068165	-23.3439	1.56E-120	2.34E-119	purple	-0.90894204	2.4E-59	GO:0003723,GO:0005634		AT5G55180.1	LAS,SCL18	GRAS family transcription factor	GRAS family transcription factor lateral protein
Sapur.017G047400.1	1097.674978	-1.51287979	0.06657419	-23.3028	4.16E-120	6.09E-119	purple	-0.89918764	1.53E-57	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810		AT3G28860.1	ABCB19,ATABCB19,ATMDR	ATP binding cassette subfamily B19	ABC transporter B family protein
Sapur.004G120000.1	333.6382734	-1.23282369	0.05295622	-23.2769	7.58E-120	1.11E-118	purple	-0.82752761	1.66E-40	GO:0016787		AT4G34530.2	ATPAP10,PAP10	purple acid phosphatase 10	purple acid phosphatase
Sapur.010G097900.1	967.2681027	-1.56398404	0.06785518	-23.2752	7.92E-120	1.16E-118	purple	-0.89331227	1.03E-55	GO:0006412,GO:0005840,GO:0003735		AT5G65580.1		Ribosomal protein PSRP-3/Tc70S	plastid-specific 30S ribosomal protein, putative
Sapur.005G138600.1	104.4297674	-1.87528262	0.08073122	-23.2316	2.58E-119	3.81E-118	purple	-0.82281939	9.60E-40			AT5G58260.1	HCF-like superfamily protein with NYN/Nob type zinc finger	zinc finger protein	
Sapur.005G040000.1	183.7232582	-1.13631792	0.05752626	-23.2287	2.94E-119	3.40E-118	purple	-0.89795628	3.99E-57			AT5G28300.1	Duplicated homeodomain-like superfamily protein	NA	NA
Sapur.15W022240.1	17.68871992	-3.91425445	0.18245359	-23.2162	3.12E-119	4.54E-118	purple	-0.85496781	2.62E-46	GO:0006281,GO:0004518		AT5G18090.1	5'-3' exonuclease family protein	exonuclease	
Sapur.002G081900.1	7.90894528	-5.56631563	0.23994312	-23.1976	4.81E-119	6.98E-118	purple	-0.86892512	9.57E-49	GO:0046983		AT5G72210.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH96	
Sapur.015G098500.1	17.3634547	-1.78166866	0.10249645	-23.1943	5.15E-119	7.47E-118	purple	-0.66572464	4.21E-21					NA	
Sapur.15W034800.1	37.62219525	-2.51930676	0.10875265	-23.1649	1.01E-118	1.48E-117	purple	-0.84761656	1.81E-44	GO:0006508,GO:0004190		AT5G25580.1	Eukaryotic aspartyl protease family protein	NA	NA
Sapur.006G022800.1	13.08117271	-4.99636744	0.21582699	-23.15	1.45E-118	2.09E-117	purple	-0.70707524	4.34E-25			AT5G76670.1	Gibberellin-regulated family protein	gibberellin induced protein, putative	
Sapur.016G288000.1	8.18020152	-5.38501701	0.23068165	-23.3439	1.56E-120	2.34E-119	purple	-0.90894204	2.4E-59	GO:0003723,GO:0005634		AT5G55180.1	LAS,SCL18	GRAS family transcription factor	GRAS family transcription factor lateral protein
Sapur.017G047400.1	1097.674978	-1.51287979	0.06657419	-23.3028	4.16E-120	6.09E-119	purple	-0.89918764	1.53E-57	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810		AT3G28860.1	ABCB19,ATABCB19,ATMDR	ATP binding cassette subfamily B19	ABC transporter B family protein
Sapur.004G120000.1	333.6382734	-1.23282369	0.05295622	-23.2769	7.58E-120	1.11E-118	purple	-0.82752761	1.66E-40	GO:0016787		AT4G34530.2	ATPAP10,PAP10	purple acid phosphatase 10	purple acid phosphatase
Sapur.010G097900.1	967.2681027	-1.56398404	0.06785518	-23.2752	7.92E-120	1.16E-118	purple	-0.89331227	1.03E-55	GO:0006412,GO:0005840,GO:0003735		AT5G65580.1		Ribosomal protein PSRP-3/Tc70S	plastid-specific 30S ribosomal protein, putative
Sapur.005G138600.1	104.4297674	-1.87528262	0.08073122	-23.2316	2.58E-119	3.81E-118	purple	-

Sapur.003G035400.1	909.873109	6.45453237	0.019678542	21.57443	3.12E-113	3.70E-102	purple	0.872565302	4.35E-50	GO:0005525	ATSG27680.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein			developmentally-regulated GTP-binding protein
Sapur.003G039300.2	75.4567884	-1.85863043	0.100165051	-21.5541	4.85E-103	5.74E-102	purple	-0.909410638	6.16E-61		ATKG26140.1	alpha/beta-Hydrolases superfamily protein			alpha/beta fold hydrolase
Sapur.004G020500.1	3.30262984	-2.72728991	0.268414104	-21.5713	5.15E-103	6.09E-102	purple	-0.84621681	3.16E-44	GO:0006284	ATSG07930.3	DNA glycosylase superfamily protein			NA
Sapur.017G074900.1	278.0494617	0.867444431	0.040204388	-21.5437	6.06E-103	7.17E-102	purple	-0.870532398	1.36E-49		ATSG29310.1	calmodulin-binding protein-related			hypothetical protein
Sapur.016G009600.1	113.9701204	-1.81228191	0.130268281	-21.5342	7.45E-103	8.79E-102	purple	-0.804868199	7.05E-37	GO:0008270;GO:0005515	ATSG04420.1	RING/U-box superfamily protein			RING-H2 finger protein
Sapur.004G056300.1	128.6898825	-1.82966586	0.084698758	-21.5321	7.79E-103	9.19E-102	purple	-0.908727236	1.07E-60		ATSG24030.1	MRC11,ATMINDS,MIND			septum site-determining protein MINDS, purple
Sapur.006G028800.1	64.80714973	-2.06188688	0.095900734	-21.5002	1.55E-102	1.83E-101	purple	-0.839884634	7.93E-43	GO:0003677	ATSG19184.1	AP2/B3-like transcriptional factor family protein			B2 DNA-binding domain protein
Sapur.003G137700.1	237.4342264	1.063561698	0.048536188	-21.4856	2.12E-102	2.49E-101	purple	-0.864763536	3.20E-48		ATG15940.1	Tudor/PWWP/MBT superfamily protein			NA
Sapur.016G296700.1	21.8170883	1.701364545	0.079221439	21.4785	2.47E-102	2.90E-101	purple	-0.843490441	1.10E-43		ATG22460.1	APUMB,PUMB			pumilio 8
Sapur.004G015300.1	221.9912806	-1.58942994	0.073813752	-21.4776	2.72E-102	3.23E-101	purple	-0.882818060	5.61E-53	GO:0005524	ATG17261.1	pkwk1,rlk1			homoserine kinase
Sapur.010G040400.1	66.41921223	-1.70381584	0.083576436	-21.4631	3.44E-102	4.03E-101	purple	-0.876087825	5.73E-51		ATG05370.1	Sec14p-like phosphatidylinositol transfer family protein			CRAL/TRIO domain protein
Sapur.004G025400.1	168.5789888	-1.42319287	0.112967171	-21.4517	4.46E-102	5.15E-101	purple	-0.862604334	9.61E-48	GO:0005507	ATG09200.1	Histone superfamily protein			NA
Sapur.016G182300.1	32.71149816	-1.86548312	0.086696547	-21.4503	4.53E-102	5.30E-101	purple	-0.824938676	3.04E-40		ATSG67230.1	Protein of unknown function (DUF579)			polyxenotide biosynthesis protein
Sapur.004G061200.1	3.30482416	-1.19139144	0.167209179	-21.4318	7.47E-102	8.74E-101	purple	-0.61212823	1.92E-18		ATSG17461.1	O-fucosyltransferase family protein			GDP-fucose protein O-fucosyltransferase
Sapur.003G159400.1	177.2268163	-2.83251632	0.132220621	-21.4227	8.22E-102	9.58E-101	purple	-0.877797918	2.08E-51	GO:0003677;GO:0007786	ATSG10390.1	Histone superfamily protein			histone H3
Sapur.004G136600.1	108.3818691	-2.80680809	0.131005587	-21.4241	8.49E-102	9.90E-101	purple	-0.779308323	3.08E-32		ATSG75250.1	RAD-like 6	ATRL6,RLRSM3		transcription factor, putative
Sapur.008G004700.1	66.03715588	-1.43890763	0.067186449	-21.4166	9.35E-102	1.09E-100	purple	-0.833189198	2.65E-41	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATSG70080.1	ATPEPR1,PEPR1			PEPS receptor 1
Sapur.010G004800.1	28.48132045	-1.645381434	0.076809428	21.40489	1.20E-101	1.40E-100	purple	0.845538621	4.07E-43	GO:0003824;GO:0006470;GO:0004722	ATSG27930.2	Protein phosphatase 2C, putative			protein phosphatase 2C, putative
Sapur.003G117200.1	6.913529949	-1.65881426	0.23917979	-21.4024	1.68E-101	1.96E-100	purple	-0.880607946	2.46E-52		ATSG22620.1	allergen-related			transmembrane protein, putative
Sapur.003G020300.1	9.362549374	-1.85070584	0.180179651	-21.3715	2.46E-101	2.85E-100	purple	-0.820682847	1.77E-39		ATSG42410.1	ATZFP11,ZFP11			zinc finger protein 11
Sapur.004G137300.1	195.4723991	-1.56188382	0.075067617	-21.3617	3.12E-101	3.52E-100	purple	-0.84944632	2.30E-43	GO:0006355;GO:0005739;GO:0003690	ATSG38160.2	pkwk161			Mitochondrial transcription termination factor family protein
Sapur.010G171500.1	350.842752	-0.67195796	0.075583003	-21.3603	3.13E-101	3.62E-100	purple	-0.86496633	2.85E-48	GO:0042254;GO:0005622	ATSG13510.1	Ribosomal protein L10 family protein			SDS-ribosomal protein L10
Sapur.003G035100.1	460.5887772	-1.54595455	0.073726513	-21.3585	3.25E-101	3.76E-100	purple	-0.901689862	2.55E-58	GO:0005515;GO:0006503	ATSG18080.1	BGLU44			glycoside hydrolase family 1 protein
Sapur.008G115900.1	133.1832874	-2.05631688	0.096288816	-21.3559	3.44E-101	3.98E-100	purple	-0.855435125	2.45E-46	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATSG08600.1	NIK3			brassinosteroid insensitive 1-associated receptor kinase, putative
Sapur.005G200300.1	51.9618148	-0.943485614	0.044179799	-21.3518	3.94E-101	4.55E-100	purple	-0.875854205	5.32E-51		ATSG61240.1	Ribosomal protein-related			VIL motif protein
Sapur.003G157500.1	26.67803655	-1.71539467	0.080333584	-21.3534	3.63E-101	4.19E-100	purple	-0.857038424	7.12E-50		ATSG76370.1	NTT,WVF2			transparent TESTA 1 protein, purple
Sapur.006G123800.1	106.2415881	1.050622886	0.049215213	21.34773	4.09E-101	4.72E-100	purple	0.86271833	9.35E-48		ATSG19710.1				regulator of V(pv) activity in the MYB pathway protein
Sapur.005G137000.1	16.95814668	-1.79139166	0.221936023	-21.3411	5.44E-101	6.21E-100	purple	-0.62132823	1.92E-18	GO:0005515	ATSG60080.1	Leucine-rich repeat protein kinase family protein	ARILP17,TMM		Serine/Threonine kinase, plant-type protein/K2C pustulate
Sapur.003G042000.1	1985.465612	1.004572176	0.048536425	21.31617	8.04E-101	9.24E-100	purple	0.845291666	8.45E-44	GO:0043565;GO:0006355;GO:0003700	ATSG75390.1	AtSZP44,SZP44			B2/ZP transcription factor
Sapur.005G137500.1	670.1061681	1.154880424	0.054237919	21.3192	8.41E-101	9.90E-100	purple	-0.85092566	5.46E-45		ATSG17670.1				Protein of unknown function (DUF581)
Sapur.006G027500.1	11.07221837	-1.06007823	0.237664112	-21.2952	1.26E-100	1.46E-99	purple	-0.780921894	1.71E-33						transmembrane protein, putative
Sapur.015G089100.1	75.60008941	-1.59188382	0.052086651	-21.2893	1.43E-100	1.64E-99	purple	-0.873344476	7.26E-50		ATSG76900.1	OTP43			Pentatricopeptide repeat (PPR) superfamily protein
Sapur.015W0059200.1	3.36471258	-2.12145589	0.245725921	-21.2495	3.33E-100	3.81E-99	purple	-0.84692097	2.88E-44						
Sapur.003G013300.1	98.48602881	-1.07362809	0.050729222	-21.2383	4.23E-100	4.82E-99	purple	-0.866319305	1.00E-48		ATSG48210.1				chromosome segregation protein Spc25
Sapur.003G161300.1	104.2466697	-0.86344159	0.040675705	-21.2275	5.33E-100	6.06E-99	purple	-0.853196693	1.15E-45		ATSG21390.1	TBL6			Prm5/CacJp GDSL/SGNH-like acyl-esterase family protein
Sapur.010G088600.1	97.74818617	-1.05208802	0.049128499	-21.2268	5.64E-100	6.41E-99	purple	-0.855093905	2.57E-46	GO:0006508;GO:0004190	ATSG25130.1				eukaryotic aspartyl protease
Sapur.010G046800.1	589.7426421	-0.52761027	0.024886653	21.20056	9.44E-100	1.07E-98	purple	-0.85070102	8.33E-46		ATSG24315.1	AtSec20			vesicle transporter Sec20, putative
Sapur.004G085500.1	1621.785962	-0.92802741	0.043779392	-21.1976	1.03E-99	1.16E-98	purple	-0.872151911	4.47E-50	GO:0046961;GO:0046933;GO:0045241;GO:0015986	ATSG06640.1	ATPC1			ATPase, F1 complex, gamma subunit protein
Sapur.013G048100.1	0.09376097	-2.47436196	0.224247818	21.17127	1.39E-99	1.58E-98	purple	-0.837542294	1.54E-42		ATSG61290.1	VIL motif containing protein			VIL motif protein
Sapur.012R016000.1	43.68792099	-1.51795835	0.074165147	-21.1684	1.83E-99	2.07E-98	purple	-0.858987074	6.45E-47	GO:0003677	ATSG46870.1	NGA1			B3 DNA-binding domain protein
Sapur.005G191000.1	62.23654677	-1.06187152	0.09419214	-21.1587	2.62E-99	2.95E-98	purple	-0.829920158	4.64E-41		ATSG75230.1				C2H2-like zinc finger protein
Sapur.003G160800.1	49.8518897	1.152664918	0.101780818	21.15001	2.76E-99	3.12E-98	purple	0.832008714	1.71E-41		ATSG22640.1	ATMYB92,MYB3			myb domain protein 3
Sapur.011G058600.1	38.3696263	-1.81830392	0.079275511	-21.1476	2.99E-99	3.38E-98	purple	-0.874439405	2.39E-42		ATSG03120.1	tic20-IV			translocon at the inner envelope membrane of chloroplasts 20-IV
Sapur.015G042400.1	97.30602549	1.04867702	0.052249556	21.13761	4.43E-99	5.00E-98	purple	0.84189392	2.37E-44		ATSG78172.1				
Sapur.013G032900.1	258.6212217	-1.64078074	0.101816623	-21.1147	5.93E-99	6.56E-98	purple	-0.86843948	2.52E-49		ATSG75240.1	AHI033,HB33			homeobox protein 33
Sapur.007G029300.1	31.32112561	-2.10140484	0.099539795	-21.1073	6.81E-99	7.66E-98	purple	-0.872443879	4.66E-50	GO:0006355;GO:0003700;GO:0007275	ATSG15530.3	AtLqRLT3			AINTEGU,MENTA-like 6
Sapur.T008385.1	62.15326791	-1.85280485	0.087969274	-21.079	1.24E-98	1.39E-97	purple	-0.893802038	2.92E-55		ATSG18230.1				2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.S026G017000.1	417.4268152	-1.176339486	0.050845019	-21.0661	1.41E-98	1.61E-97	purple	-0.8617256	1.56E-55	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATSG16850.1	Leucine-rich repeat protein kinase family protein			receptor-kinase isolog protein
Sapur.019G073300.1	80.34024616	-0.79965320	0.037985514	-21.0622	1.77E-98	1.98E-97	purple	-0.857897412	1.12E-46		ATSG23320.1	Pentatricopeptide repeat (PPR) superfamily protein			PPR containing protein, purple
Sapur.005G161500.1	41.98114988	-1.15237091	0.054779969	-21.0555	2.04E-98	2.27E-97	purple	-0.804175201	1.32E-42	GO:0016788	ATSG29190.1	GDSL-like Lipase/Acylhydrolase superfamily protein			GDSL esterase/lipase
Sapur.003G110700.1	10.7618828	-2.73647688	0.129539515	-21.0442	2.58E-98	2.88E-97	purple	-0.873708762	7.06E-50		ATSG13320.1	UBD4			LOB domain-containing protein 4
Sapur.012G229500.1	24.13564624	-1.28737838	0.160939479	-21.0274	3.68E-98	4.11E-97	purple	-0.648029518	1.12E-22	GO:0005515;GO:0051087	ATSG27220.1	ATBAG1,BAG1			BCL-2-associated athanogene 1
Sapur.002G047000.1	143.2828089	-2.92088606	0.138949072	-21.0177	4.52E-98	5.03E-97	purple	-0.86641553	1.31E-48	GO:0005515;GO:0004553	ATSG24318.1				O-Glycosyl hydrolases family 17 protein
Sapur.003G148700.1	151.9225344	-1.56185196	0.076227511	-21.0119	4.69E-98	5.22E-97	purple	-0.876439401	4.66E-51		ATSG16080.1	carboxyesterase 15	AtCXE17,CXE17		carboxyesterase 17
Sapur.012G232600.1	1382.666545	-0.79666279	0.037920884	-21.0034	6.10E-98	6.78E-97	purple	-0.86374201	4.58E-54		ATSG55680.1	DEK domain-containing chromatin associated protein			DEK carboxy-terminal domain protein
Sapur.013G070100.1	35.58914726	-2.09601444	0.099443387	-21.0005	6.28E-98	6.97E-97	purple	-0.78564606	2.32E-40		ATSG35181.1				TFD1, putative
Sapur.007G022500.1	11.42311274	4.058567927	0.191246959	21.00398	6.29E-98	6.98E-97	purple	-0.782932063	9.12E-34		ATSG75250.1	ATRL6,RLRSM3	RAD-like 6		MYB transcription factor, putative
Sapur.015G188600.1	1549.359335	0.87804022	0.041809043	21.00121	6.39E-98	7.09E-97	purple	-0.86611285	5.54E-48	GO:0003677;GO:0007786	ATKG60030.2		Histone superfamily protein		histone H3
Sapur.015G026400.1	122.8423869	-0.98509165	0.065780869	-20.9921	7.75E-98	8.59E-97	purple	-0.874564675	1.84E-50	GO:0006355;GO:0003677	ATKG40600.1	Dof type zinc finger DNA binding family protein			Dof domain, zinc finger protein
Sapur.016G249700.1	29.7139717	-1.57863476	0.075232521	-20.9837	9.25E-98	1.02E-96	purple	-0.858831619	1.81E-46		ATSG78730.1	APC6			anaphase promoting complex/cyclosome subunit
Sapur.005G130000.1	17.58353324	-1.92179202	0.093264209	-20.9804	9.78E-98	1.07E-96	purple	-0.822143608	9.23E-40	GO:0006355;GO:0003700	ATSG44940.1				Integrase-type DNA-binding superfamily protein
Sapur.006G221800.1	29.75178647	-2.52343221	0.167893782	-20.9796	1.01E-97	1.11E-96	purple	-0.739203431	1.22E-28	GO:0016020;GO:0006970	ATSG29130.1	ATGLR2,B,GLR2.B			glutamate receptor 2.8
Sapur.005G202200.1	416.5854422	0.930024812	0.044553143	20.9662	1.34E-97	1.51E-96	purple	-0.893283232	5.92E-56		ATSG08880.1	G-UX,GALUXARA,-UX,AGUX4	Histone superfamily protein		histone H2A
Sapur.014G096700.1	299.4321483	-1.66041137	0.079246077	-20.9526	1.78E-97	1.96E-96	purple	-0.86851315	4.18E-49	GO:0006260;GO:0005524;GO:0003677;GO:0042555;GO:0006270;GO:0005634;GO:0003677	ATKG02060.1	MCM7,PM1	Minichromosome maintenance (MCM2/3/5) family protein		DNA replication licensing factor MCM7, putative
Sapur.015G184700.1	516.5809616	-0.87264788	0.042635155	-20.9445	2.15E-97	2.37E-96	purple	-0.882576276	1.41E-54		ATSG45680.1	H2A,HTA9	Histone superfamily protein		histone H2A
Sapur.014G049900.1	138.8712207	1.569445065	0.076945163	20.93657	2.49E-97	2.74E-96	purple	-0.816392977	5.00E-38	GO:0006355;GO:0003700	ATKG47680.1	RAP2.1	related to AP2.1		dehydration-responsive element-binding protein, putative
Sapur.006G030400.1	448.8561773	-0.62488653	0.030445387	-20.9346	2.58E-97	2.83E-96	purple	-0.886441767	3.97E-54	GO:0005515;GO:0006468;GO:0004672	ATSG41820.1		Leucine-rich repeat protein kinase family protein		LRR receptor-like kinase family protein
Sapur.006G055600.1	94.52320358	-0.89341173	0.042713811	-20.9162	3.81E-97	4.19E-96	purple	-0.865239348	2.40E-48		ATSG62340.1	pentatricopeptide (PPR) repeat-containing protein			PPR containing plant protein
Sapur.019G013600.1	62.67558862	-0.85209162	0.23125997	-20.8858	7.21E-97	7.89E-96	purple	-0.879631109	9.04E-52		ATSG72520.2	DI-glucose binding protein with Kinesin motor domain			DI-glucose binding protein with Kinesin motor domain
Sapur.003G138300.1	47.45466892	-1.40513033	0.047535115	-20.8826	7.71E-97	8.46E-96	purple	-0.878892647	1.50E-51	GO:0008725;GO:0006284	ATSG79701.1	DNA glycosylase superfamily protein			methylcytosine glycosylase
Sapur.002G015100.1	730.0675269	-2.21203766	0.105954275	-20.8772	8.63E-97	9.43E-96	purple	-0.879607965	7.04E-52	GO:0003677;GO:0007786	ATSG10400.1	Histone superfamily protein			histone H3
Sapur.007G091600.1	3.90816307	-2.46580122	0.260834104	-20.8707	9.28E-97	1.01E-95	purple	-0.781346556	1.50E-33	GO:0005515	ATSG17600.1	early nodulin-like protein 22	AENODL22,ENODL22		basic blue protein
Sapur.010G091600.1	92.86881977	-1.51605278	0.072881224	-20.8583	1.28E-96	1.40E-95	purple	-0.868707089	1.75E-49		ATSG68220.1	Protein of unknown function (DUF1218)			fiber protein Fb34
Sapur.003G070100.1	7.76655155	-1.36624742	0.161435547	-20.8488	1.56E-96	1.70E-95	purple	-0.809214814	1.24E-37						NA
Sapur.005G071500.1	120.2253118	-1.36217438	0.060550192	-20.8451	1.68E-96	1.84E-95	purple	-0.873154892	1.84E-42		ATSG23180.1	TCP family transcription factor			TCP transcription factor, putative
Sapur.010G065800.1	21.62389315	-2.69268133	0.081260561	-20.8364	2.02E-96	2.20E-95	purple	-0.819357159	7.74E-41						NA
Sapur.15W0091200.1	84.813598	-1.45591754	0.069876567	-20.8359	2.04E-96	2.22E-95	purple	-0.865864271	1.76E-48		ATSG26840.1				phosphoglycerate mutase family protein
Sapur.003G113800.1	10.45260884	-2.71697697	0.130420455	-20.8324	2.23E-96	2.39E-95	purple	-0.846117246	1.30E-44						hypothetical protein
Sapur.003G185400.1	208.7507421	-1.07192128	0.06438977	-20.8207	2.85E-96	3.05E-95	purple	-0.882816167	1.77E-52		ATSG25480.1				rhodanese/cdc-25 domain protein
Sapur.15W0085100.1	1064.522312	-1.04124492	0.050014788	-20.8187	2.93E-96	3.18E-95	purple	-0.872219581	5.29E-50	GO:0015031;GO:0006457	ATSG52120.1	trigger factor type chaperone family protein			trigger factor
Sapur.005G178700.1	4326.58443	-2.65382797	0.126688225	-20.804	3.98E-96	4.31E-95	purple	-0.842317662	1.88E-43						NA
Sapur.008G158800.1	290.1910542	-0.46000985	0.022121335	-20.8035	4.02E-96	4.36E-95	purple	-0.854877923	1.86E-46	GO:0004681;GO:0006672	ATSG15080.1		Protein kinase superfamily protein		Serine/Threonine kinase domain protein
Sapur.015Z006100.1	275.9612334	-0.76872263	0.038417803	-20.7907	5.25E-96	5.68E-95	purple	-0.862680303	1.30E-47	GO:0003700;GO:0005779	ATSG46635.1	PEX12,PEX3-2			peroxisome biogenesis protein
Sapur.010G024000.1	22.36686503	-2.87986063	0.088463758	-20.7767	7.03E-96	7.59E-95	purple	-0.84295949	4.03E-44		ATSG68430.1				hypothetical protein
Sapur.004G027200.1	36.04420989	-2.32320834	0.111840466	-20.7752	7.67E-96	8.28E-95	purple	-0.85034275	2.95E-46		ATSG23150.1				haloacid dehalogenase like hydrolase (HAD) superfamily protein
Sapur.016G275200.1	123.806431	-1.37306876	0.062609122	-20.7384	1.56E-95	1.68E-94	purple	-0.862328829	1.15E-47	GO:0019898;GO:0015979;GO:0009654;GO:0009523;GO:0005509	ATSG01440.1	PQL1,PQL2	PsbQ-like 1		oxygen-evolving enhancer protein 3-1
Sapur.005G096800.1	447.2417836	-1.08933397	0.052600204	-20.7097	2.83E-95	3.04E-94	purple	-0.863074601	2.32E-47		ATSG65320.1		Chaperone DnaJ-domain superfamily protein		NA
Sapur.007G007800.1	27.21196417	-3.15194931	0.152264278	-20.7005	3.43E-95	3.68E-94	purple	-0.6021425	7.12E-17	GO:0005085;GO:0016020;GO:0012597;GO:0012338;GO:0006855	ATMT2G01130.1		MATE efflux family protein		MATE efflux family protein
Sapur.008G070600.1	111.2945031	-1.30348255	0.06300541	-20.6887	4.38E-95	4.69E-94	purple	-0.873795614	6.86E-50		ATSG26761.1		Arabinanase/levansucrase/inverase		NA
Sapur.005G177000.1	82.67579002	-1.46132811	0.080318135	-20.6848	4.75E-95	5.08E-94	purple	-0.797846566	7.76E-36	GO:0016020;GO:0006970	ATGLR3.4,GLR3.4,GLUR3		glutamate receptor 3.4		PPR-containing receptor
Sapur.015G037200.1	213.8990767	-1.30162248	0.062931599	-20.6833	4.90E-95	5.24E-94	purple	-0.846491777	7.98E-44	GO:0009570;GO:0004751	ATSG04790.1	Ribose 5-phosphate isomerase, type A protein			ribose-5-phosphate isomerase
Sapur.008G049500.1	622.8372348	-1.07461293	0.051994131	-20.668	5.75E-95	7.20E-94	purple	-0.85240483	4.61E-46	GO:0016758;GO:0008152	AtUGT81A1,UGT81A1		UDP-glucosyltransferase 81A1		UDP-glucosyltransferase family protein
Sapur.018G108300.1	34.45556251	-2.07181938	0.100275506	-20.6597	7.99E-95	8.56E-94	purple	-0.803933988	8.26E-37	GO:0046983	ATSG27510.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein			transcription factor bHLH protein
Sapur.008G041400.1	8.77017431	-1.57484664	0.170286683	-20.6559	8.24E-95	8.82E-94	purple	-0.837978365	1.92E-57		ATSG09180.1	Uncharacterized conserved protein UPF0497/DUF627			CAP-like protein POPTOSHEART 6/2/3/27 protein
Sapur.019G056400.1	904.9307385	-0.81948935	0.039607314	-20.6414	1.17E-94	1.24E-93	purple	-0.87104112	1.01E-49	GO:0006779;GO:0004853	ATSG40490.1	HEME2	Uroporphyrinogen decarboxylase		uroporphyrinogen decarboxylase
Sapur.008G022800.1	33.10461243	-2.41193181	0.116063132	-20.6279	1.54E-94	1.64E-93	purple	-0.880032842	5.27E-55		ATSG68810.1				hypothetical protein
Sapur.019G051300.1	105.0693598	-1.28950788	0.062517831	-20.6263	1.58E-94	1.70E-93	purple	-0.864228318	4.22E-48		ATSG42040.1				WRC protein
Sapur.015G041800.1	98.75324252	-1.85180104	0.092523118	20.62611	1.60E-94	1.70E-93	purple	-0.840844087	5.42E-43		ATSG78172.1				NA
Sapur.003G184000.1	225.2472971	-0.58355409	0.028353878	-20.5942	3.10E-94	3.28E-93	purple	-0.868307004	4.68E-49		ATSG19370.1				tumor suppressing subchromosomal transferable 4 protein, putative
Sapur.I3G025160.0	98.4922101	1.08564888	0.052726699	20.58895	3.45E-94	3.66E-93	purple	-0.84110242	3.15E-43		ATSG78172.1				NA
Sapur.017G084000.1	1145.448816	-2.34880269	0.114056233	-20.5871	3.58E-94	3.79E-93	purple	-0.742667316	8.72E-29	GO:0004681;GO:0005524;GO:0004672	ATSG18250.1		receptor serine/threonine kinase, putative		Serine/Threonine kinase family protein
Sapur.003G109700.1	303.0923426	0.793026499	0.035475543	-20.586	3.67E-94	3.88E-93	purple	-0.84975401	6.02E-45		ATSG66680.1	BLT	brassinosteroid-regulated protein		brassinosteroid-regulated protein
Sapur.012G071100.1	202.6924444	-1.06195456	0.051626848	-20.5689	3.91E-94	4.40E-93	purple	-0.831272508	2.36E-47	GO:0008017;GO:0006887;GO:0000145	ATSG51580.1	exocyst subunit Exo70 family protein F1			exocyst complex component, putative
Sapur.017G115200.1	146.8491733	0.820137076	0.038692372	-20.5597	6.30E-94	6.65E-93	purple	-0.844164857	8.19E-44		ATSG52220.1	ATEXP13,ATEXPA13,ATHEXP	expansin A13		expansin-A13 protein
Sapur.013G041100.1	136.0251766	0.968732163	0.048437837	-20.5414	8.47E-94	8.94E-93	purple	-0.83411127	8.66E-42	GO:0004461;GO:0004668	ATGBH3.51		phosphoserine type peptidyl-arginine deiminase family protein		NA
Sapur.006G091600.1	10.19099978	-0.47200327	0.168923767	-20.5401	8.87E-94	9.35E-93	purple	-0.793733182	2.75E-35	GO:0005515	ATSG50340.1	DNA-binding bromodomain-containing protein			bromodomain protein
Sapur.005G200500.1	6.82068734	-2.34765065	0.32717588	-20.5258	1.07E-93	2.18E-92	purple	-0.870630006	4.07E-49	GO:0046983	ATSG72210.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein			helix loop helix protein
Sapur.013G038800.1	1024.913474	-1.76762727	0.135035581	-20.4976	2.26E-93	2.37E-92	purple	-0.802548994	1.35E-36						transmembrane protein, putative
Sapur.015G077800.1	65.76789949	-2.53364088	0.123608164	-20.4927	2.53E-93	2.62E-92	purple	-0.893482513	3.78E-55	GO:0006355;GO:0003700	ATSG52760.1	CRF2,TWO3	cytokinin response factor 2		AP2/EBP domain transcription factor family protein
Sapur.008G000100.1	42.77639271	-2.17837896	0.092379956	-20.4242	1.02E-92	1.06E-91	purple	-0.844164179	8.21E-44	GO:0005515;GO:0006468;GO:0004672	ATG14740.2	RING/FYVE/PHD zinc finger superfamily protein			PHD zinc finger protein
Sapur.006G195200.1	191.4617999	-1.76079553	0.086123634	-20.4452	6.63E-93	6.92E-92	purple	-0.886770686	8.08E-54	GO:0005515;GO:0005634	ATG16500.1	IAA26,PAP1	phytochrome-associated protein 1		auxin-responsive protein IAA6
Sapur.003G020800.1	375.6889147	-1.87530208	0.09174832	-20.4402	7.34E-93	7.66E-92	purple	-0.80971153	1.03E-37	GO:0005622;GO:0003776;GO:0030042;GO:0015629	ATG31200.1	ADF6,ATADF6	actin depolymerizing factor 6		actin-depolymerizing factor 5
Sapur.016G180300.1	178.3365053	-2.92384907	0.180240969	-20.4242	1.02E-92	1.06E-91	purple	-0.844167119	8.21E-44	GO:0005515;GO:0006468;GO:0004672	ATKG34230.1		Leucine-rich repeat protein kinase family protein		receptor kinase-like protein
Sapur.016G000400.1	62.77639271	-2.17837896	0.092379956	-20.4242	1.02E-92	1.06E-91	purple	-0.848984324	5.56E-44	GO:0016616;GO:0016616;GO:0008152	ATG45630.2	D-isomer specific 2-hydroxyacid dehydrogenase family protein			2-hydroxyacid dehydrogenase family phosphoglycerate dehydrogenase
Sapur.005G183600.1	176.4771135	-1.39200153	0.068203374	-20.4228	1.05E-92	1.09E-91	purple	-0.870794113	1.18E-49	GO:0005622;GO:0008324	ATSG42800.1	DFR,M318,TT3	dihydroflavonol 4-reductase		dihydroflavonol 4-reductase
Sapur.016G180900.1	188.4340003	-1.57197318	0.077184564	-20.4165	1.32E-92	1.41E-91	purple	-0.848817941	3.46E-45	GO:0005515;GO:0006468;GO:0004672	ATSG26310.1		Protein kinase superfamily protein		NA
Sapur.013K127700.1	600.7081505	-1.05850337	0.052080631	-20.4025	1.58E-92	1.66E-91	purple	-0.849267847	1.73E-43	GO:0016758;GO:0008152	ATSG70500.1	UGT78D2	UDP-glucosyl transferase 78D2		UDP-glucose:flavonoid-3-O-glucosyltransferase
Sapur.006G040000.1	73.13656791	-1.28180255	0.07 405551	-20.4005	1.66E-92	1.75E-91	purple	-0.831217358	1.38E-43	GO:0005515;GO:0004681;GO:0006468;GO:0004672	ATSG60640.1		Leucine-rich receptor-like protein kinase family protein		receptor-like kinase
Sapur.15W0084800.1	572.7691771	-0.65651721	0.032168881	-20.3983	1.73E-92	1.80E-91	purple	-0.862852663	8.71E-48	GO:0005515;GO:0016491;GO:0045454	ATSG56680.1	ATGR2,EMB2360,GR	glutathione reductase		glutathione reductase
Sapur.013K190900.1	9.598031669	-1.97031047	0.138574393	-20.3603	3.79E-92	3.89E-91	purple	-0.853285658	4.52E-45		ATSG13650.1	Disease resistance-responsive (dirigent-like protein) family protein			dirigent-like protein
Sapur.016G126200.1	203.4272661	-0.79329992	0.038790656	-20.3598	3.88E-92	3.99E-91	purple	-0.864572231	1.54E-48	GO:0005515;GO:0046653	ATSG55190.1	beta-hexosaminidase 2	HEXO2,HEXO2		beta-hexosaminidase 2
Sapur.015G013400.1	925.9985118	-0.57220111	0.028108066	-20.

Sapur.01G0258600.1	59.85853329	-2.152492977	0.113963189	-18.8869	1.44E-79	1.27E-78	pyrim	-0.829047164	5.71E-41	ATSG70370.2	PG2	polygalacturonase 2	NA
Sapur.T018200.1	11.66673034	3.241813103	0.171698031	18.8809	1.64E-79	1.42E-78	pyrim	0.730187875	1.99E-27	ATSG23270.1			NA
Sapur.0G0174200.1	341.8245168	8.856261591	0.945381149	18.87493	1.83E-79	1.56E-78	pyrim	-0.80697228	3.80E-37	ATSG19190.1	PRA1.F2,PRA7	PRA1 (Prenylated rab acceptor) family protein	PRA1 family protein
Sapur.0G0238100.1	68.8937525	-5.536093803	0.081504023	-18.8572	2.54E-79	2.21E-78	pyrim	-0.85245139	1.65E-45	ATSG69690.1		TCP family transcription factor	TCP transcription factor, putative
Sapur.T006500.1	11.62836315	3.232313904	0.174152328	18.85241	2.81E-79	2.42E-78	pyrim	0.730389263	1.90E-27	ATSG23735.1			NA
Sapur.0G0212400.1	35.31638807	-1.901782384	0.101390747	-18.8457	3.19E-79	2.74E-78	pyrim	-0.853483327	1.00E-45	ATSG12020.1			hypothetical protein
Sapur.1G0W0319900.1	117.5473526	-3.351883491	0.177888186	-18.8402	3.34E-79	2.87E-78	pyrim	-0.653828145	1.76E-20	ATSG18550.1		alpha/beta-Hydrolases superfamily protein	triacylglycerol lipase
Sapur.0G0123000.1	106.1952671	-1.361651164	0.072273235	-18.83983	3.56E-79	3.06E-78	pyrim	-0.754757759	3.50E-30				transmembrane protein, putative
Sapur.0G0287800.1	12.40327881	-2.537316887	0.134703242	-18.8366	3.78E-79	3.25E-78	pyrim	-0.76452287	2.29E-31	ATSG38370.1		Plant protein of unknown function (DUF827)	weak movement under blue light protein
Sapur.0G0211400.1	128.7480564	-1.292497392	0.069218158	-18.8302	4.17E-79	3.56E-78	pyrim	-0.81411881	1.93E-39	ATSG44830.1	GD0.0066468,GD0.0066472,GD.0005524	Protein kinase superfamily protein	Serine/Threonine kinase domain protein
Sapur.01G0283300.1	1452.683071	-2.09602369	0.111135376	-18.8231	4.88E-79	4.19E-78	pyrim	-0.835158016	4.27E-42	ATSG60020.1	ATLAC7,LAC17	laccase 17	laccase
Sapur.0G0205200.1	598.303809	1.00241915	0.053298362	-18.8076	6.53E-79	5.60E-78	pyrim	-0.81510303	1.02E-38	ATSG75188.1	CPuORF5	conserved peptide upstream open reading frame 5	peptide upstream ORF protein
Sapur.01G0251100.1	84.83681822	-1.587670284	0.084645086	-18.7992	7.66E-79	6.56E-78	pyrim	-0.854373868	6.78E-46	GD.0005085,GD.0005741	ATVDAC1,VDAC1	voltage-dependent anion channel 1	voltage-dependent anion-selective channel protein, putative
Sapur.0G0362200.1	23.69663488	2.811984347	0.07539204	-18.7896	9.18E-79	7.85E-78	pyrim	-0.80697228	3.80E-37	GT5E02,AT5PTS6E2,PSR5		type I inositol-3,5,6C,6D,5C-trisphosphate 5-phosphatase	type I inositol-3,5,6C,6D,5C-trisphosphate 5-phosphatase
Sapur.01G0295300.1	4470.117851	-2.082601524	0.110876165	-18.78585	9.86E-79	8.42E-78	pyrim	-0.675073384	1.66E-22	ATSG60390.1	ATMT-L,ATMT-K,MT2A	metallothionein 2A	metallothionein-like protein 2a
Sapur.0G0134400.1	98.46373238	-1.860330645	0.064115979	-18.7853	9.98E-79	8.52E-78	pyrim	-0.84842782	3.66E-43	ATSG36800.1			hypothetical protein
Sapur.01G0175800.1	210.3435512	-1.117026465	0.059580174	-18.7483	2.00E-78	1.70E-77	pyrim	-0.806097562	1.83E-37	GD0005515	BUB3.1	Transducin/WD40 repeat-like superfamily protein	mitotic checkpoint protein BUB3
Sapur.01G0209000.1	78.65810136	-1.834606627	0.097046749	-18.7344	2.60E-78	2.21E-77	pyrim	-0.838693277	9.40E-43	GD0003677	G-HOAX,GAMMA-HOAX,HOX	gamma histone variant HOAX	histone H2A
Sapur.01G0150400.1	279.7514296	-1.09172519	0.047436151	-18.7324	2.68E-78	2.28E-77	pyrim	-0.845282832	4.87E-44	GD0005524		Sodium ion exchanger family protein	sodium bile acid symporter family protein
Sapur.01G0287700.1	78.31248602	-1.230261406	0.065770132	-18.7055	4.47E-78	3.78E-77	pyrim	-0.83148957	2.07E-41	ATSG46890.1		Protein of unknown function (DUF239)	phosphoglycol methyltransferase
Sapur.T004800.1	794.8655572	-2.29E-09	0.065732683	-18.7029	4.68E-78	3.97E-77	pyrim	-0.821275791	2.31E-39	GD0005515	ATSG37880.1	Calcium dependent lipid-binding(C2 domain) plant phosphoribosyltransferase family protein	methylnitrate phosphoribosyltransferase-like protein
Sapur.0G0166700.1	388.3127524	-0.915128461	0.049000277	-18.676	7.50E-78	6.56E-77	pyrim	-0.844515214	8.16E-44	ATSG18660.1	PCB5	NAD(P)-binding Rossmann-fold superfamily protein	divinyl chlorophyllide a 8-vinyl-reductase
Sapur.01G0240600.1	51.11810135	-2.065695651	0.058503875	-18.6649	9.55E-78	8.04E-77	pyrim	-0.82022201	1.85E-41	ATLL7L4	TCMCO5 OR LEVUORA-4	TCMCO5 OR LEVUORA-4	RING finger protein
Sapur.0G0G034400.1	22.4295519	3.321889931	0.178126446	18.65435	1.12E-77	9.43E-77	pyrim	-0.73237918	1.17E-27				NA
Sapur.0G0G0900.1	683.7735661	2.801798347	0.043014164	18.64001	1.52E-77	1.28E-76	pyrim	-0.814983012	8.30E-41	ATSG68320.1	AtMYB62,BWG28,BWG2C,AV	myb domain protein 62	MYB transcription factor
Sapur.01G0158200.1	2852.761285	9.924657452	0.049669659	18.61212	2.56E-77	2.15E-76	pyrim	-0.80054935	2.71E-36	GD0003924,GD0007017,GD0005874	TUB2	tubulin beta chain 2	tubulin, beta chain
Sapur.01G0213800.1	5014.763994	8.859754464	0.04620325	18.60809	2.76E-77	2.31E-76	pyrim	-0.772476071	1.52E-32	GD0005514,GD0005287,GD.0016816,GD.0008152	FDH	formate dehydrogenase	formate dehydrogenase
Sapur.1G0W0228400.1	43.64696137	-2.980764617	0.229261421	-18.5083	3.22E-77	2.70E-76	pyrim	-0.89851976	2.22E-57				hypothetical protein
Sapur.1G0W0240300.1	33.60915645	-2.37882524	0.127905127	-18.5833	4.39E-77	3.67E-76	pyrim	-0.87665703	4.09E-51				hypothetical protein
Sapur.1G0W0230100.1	50.18859897	-1.120026194	0.060277153	-18.5438	4.41E-77	3.69E-76	pyrim	-0.796344976	1.26E-32	GD0003676,GD0007008,GD.0009398	U2B'\'\	U2 small nuclear ribonucleoprotein B	NA
Sapur.0G0139400.1	684.04829	-0.818375247	0.044068084	-18.5789	4.76E-77	3.98E-76	pyrim	-0.838901297	8.58E-43	GD0005525	ARA.ARA-1,ATRAB11D,ATRA	RAB GTPase homolog ASE	Rab-related GTPase family protein
Sapur.0G0150200.1	8.25729362	-4.205885705	0.176512239	-18.5728	5.17E-77	4.45E-76	pyrim	-0.83495511	1.98E-42				hypothetical protein
Sapur.01G0131400.1	7.37772801	-2.511294207	0.135341128	-18.5675	5.89E-77	4.91E-76	pyrim	-0.817090601	6.57E-39	GD0004668,GD0005524,GD.0004672		S-locus lectin protein kinase family protein	G-type lectin S-receptor-like Serine/Threonine-kinase, putative
Sapur.0G0260800.1	1932.15584	5.521550224	0.028106625	18.55645	7.23E-77	6.02E-76	pyrim	-0.816604792	7.80E-39			Alpha helical repeat protein	NADH dehydrogenase (ubiquinone) iron-sulfur protein
Sapur.1G0W0309900.1	18.8373447	-2.678641314	0.144692349	-18.5371	1.04E-76	8.63E-76	pyrim	-0.829105254	2.05E-40			Magnesium transporter CorA-like family protein	NA
Sapur.0G0149100.1	40.3137384	2.851715452	0.098837783	-18.5271	1.25E-76	1.04E-75	pyrim	-0.779562458	2.02E-31				SR protecting protein, putative
Sapur.0G0161500.1	412.6602618	-0.485438209	0.076032645	-18.5254	1.28E-76	1.07E-75	pyrim	-0.828323232	7.69E-41				hypothetical protein
Sapur.0G0269900.1	78.53423993	-2.46427851	0.13308046	-18.52	1.42E-76	1.18E-75	pyrim	-0.796615472	4.69E-25	GD0005514,GD0020037,GD.0016705,GD.0005506	CYP84A1,FAH1	ferulic acid 5-hydroxylase 1	coniferyl aldehyde 5-hydroxylase
Sapur.0G0524900.1	60.06912254	-1.067936169	0.059060383	-18.5185	1.46E-76	1.22E-75	pyrim	-0.81299125	3.43E-38	GD0005515	SR1,STY1	Leucine rich protein kinase (LRP) protein related	short internodes protein/kinase family protein
Sapur.0G0350600.1	14.50384004	-2.048157738	0.110744468	-18.4945	2.29E-76	1.89E-75	pyrim	-0.816621615	8.79E-39	GD0007020,GD0005515		RING/U-box superfamily protein	RING finger protein
Sapur.0G0185200.1	50.43879525	-1.425188236	0.075830756	-18.4864	2.66E-76	2.20E-75	pyrim	-0.79392408	3.48E-35			peptidase inhibitor-containing protein	carboxypeptidase inhibitor-like protein
Sapur.01G0280600.1	19.37717526	-1.662210304	0.089938848	-18.4816	2.91E-76	2.40E-75	pyrim	-0.839631697	6.71E-43				hypothetical protein
Sapur.0G0237300.1	8.58809815	-2.550475209	0.138425168	-18.4578	4.28E-76	3.52E-75	pyrim	-0.788910734	1.26E-32	GD0004668,GD0004672		Protein kinase superfamily protein	serine kinase
Sapur.01G0290500.1	150.49801	-2.664168566	0.144466621	-18.4553	4.73E-76	3.89E-75	pyrim	-0.80503872	2.93E-36			RNA-ligase kinase-cyclase protein	calien cyclic protein CP12
Sapur.0G0424400.1	266.3542083	-0.909976068	0.054119737	-18.4552	4.74E-76	3.90E-75	pyrim	-0.82057012	7.21E-39		CP12,CP12-2	CP12 domain-containing protein 2	AvrRpt2-P-inducibly elicited protein, putative
Sapur.1G0W0109800.1	249.3853904	-1.638542471	0.08885456	-18.4408	6.18E-76	5.08E-75	pyrim	-0.823382728	1.40E-39	GD0008153,GD0003824			acyl CoA ligase
Sapur.0G0280700.1	27.77512346	-0.685125665	0.095639831	-18.4258	8.15E-76	6.69E-75	pyrim	-0.82384976	1.64E-38			AMP-dependent synthetase and ligase family protein	hypothetical protein
Sapur.01G0131800.1	1385.19564	-0.766482654	0.046730494	-18.4175	9.51E-76	7.78E-75	pyrim	-0.818734774	3.52E-39	GD0005789	PapD-like superfamily protein		NA
Sapur.0G0047000.1	200.2835496	-1.437291915	0.078025512	-18.4135	1.02E-75	8.38E-75	pyrim	-0.843383631	1.16E-43	GD0043565,GD0006355,GD0007000	ATWRKY28,WRKY28	WRKY DNA-binding protein 28	WRKY transcription factor
Sapur.01G0132200.1	52.47472297	-1.302081033	0.108445015	-18.4049	1.25E-75	9.81E-75	pyrim	-0.83218399	5.92E-41			Protein of unknown function (DUF3741)	DUF4378 domain protein
Sapur.1G0W0200400.1	102.9261828	-2.397170484	0.184788888	-18.3943	1.76E-75	1.43E-74	pyrim	-0.622392204	2.28E-18	GD0006829		alpha/beta-Hydrolases superfamily protein	NA
Sapur.0G0349400.1	561.3100202	-2.014187761	0.10112277	-18.3766	2.02E-75	1.65E-74	pyrim	-0.84416507	2.52E-43	GD0010370,GD0008776,GD.0008737,GD.0006508		peptidase M1 family protein	leukotriene A-4 hydrolase, putative
Sapur.1G0W0259800.1	5.89614508	-2.614665752	0.142324182	-18.3697	2.30E-75	1.87E-74	pyrim	-0.82607561	1.93E-40		GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.01G0268300.1	182.7909824	-1.197109155	0.068185718	-18.3659	2.46E-75	2.00E-74	pyrim	-0.760074291	8.06E-31	GD0016020,GD0016586,GD.0008539,GD.0072488	AMT1;1,ATAMT1,ATAMT1.1	ammonium transporter 1 protein	ammonium transporter 1 protein
Sapur.1G0W0260500.4	2.213025317	-5.737073202	0.246063776	-18.3635	2.58E-75	2.09E-74	pyrim	-0.831614041	8.94E-38	GD0007165,GD0003155,GD0003155,GD.0018298,GD.0009584	HY3,DOPL,PHY8	phytochrome B	phytochrome protein
Sapur.T005400.1	69.58643253	-2.110436	0.113038084	-18.3631	2.58E-75	2.11E-74	pyrim	-0.725353682	1.24E-26	GD0005891,GD0042626,GD.0016815,GD.0008810,GD.0005524,GD.0016887	ATMRP1,MRP3	multidrug resistance-associated protein 3	multidrug resistance protein ABC transporter family protein
Sapur.0G0115300.1	14.31425847	-2.265225849	0.123400095	-18.3568	2.93E-75	2.37E-74	pyrim	-0.843372345	4.48E-43		CLE26	CLAVATA/ESR-RELATED 26	CLAVATA 3/ESR (CLE)-related protein, putative
Sapur.01G0214400.1	156.7789139	-2.25429073	0.123857914	-18.3525	3.15E-75	2.56E-74	pyrim	-0.817838588	5.23E-39	GD0005514,GD0016499,GD.0005507	LACS	laccase 5	laccase
Sapur.01G0029100.1	2701.226913	-1.330774224	0.068258847	-18.3379	4.12E-75	3.33E-74	pyrim	-0.82073926	1.41E-36		PG2	polygalacturonase 2	polygalacturonase non-catalytic protein
Sapur.0G0182900.1	3481.164123	0.557513397	0.030459433	18.30618	7.39E-75	5.96E-74	pyrim	-0.831958156	1.70E-41			Nucleic acid-binding, OB-fold-like protein	OB fold Sc0.SSB-DBF-A subfamily protein, putative
Sapur.0G0120700.1	126.0254886	-1.202104	0.059394357	-18.3054	7.46E-75	6.04E-74	pyrim	-0.823869672	5.04E-41	GD0006468,GD0005524,GD.0004672,GD.0030246		Concanavalin A-like lectin/glucanase family protein	NA
Sapur.0G0134900.1	1033.919554	-0.666711942	0.034329063	-18.3016	8.07E-75	6.47E-74	pyrim	-0.85270927	5.52E-46			HR-like lesion-inducing protein family	HR-like lesion-inducing protein
Sapur.0G0227800.1	1865.478931	-1.856792138	0.106083979	-18.2604	8.86E-75	7.10E-74	pyrim	-0.751136497	9.41E-30	GD0005514,GD0020037,GD.0016705,GD.0005506	CYP94B3	cytochrome P450, family 94, subfamily B, polypeptide 3	cytochrome P450 family protein
Sapur.0G0246600.1	74.46824067	-2.171762115	0.119076659	-18.2379	2.58E-74	2.06E-73	pyrim	-0.72242748	1.28E-26	GD0046863	ED4,ED,CT140,IND,IND1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor HEC3, putative
Sapur.0G0279100.1	174.1614349	-2.270133604	0.123375526	-18.2264	2.70E-74	2.17E-73	pyrim	-0.80080447	1.24E-36			Protein of unknown function (DUF231)	stress-induced protein, putative
Sapur.0G0262600.1	180.5617576	-1.133867862	0.062146092	-18.21	4.30E-74	3.43E-73	pyrim	-0.832309969	1.00E-41	GD0006468	ATMYB88,MYB88	myb domain protein 86	RAD3-MYB transcription factor, putative
Sapur.0G0350300.1	6.66944488	2.824143322	0.131722211	18.19969	4.51E-74	3.61E-73	pyrim	-0.64459601	2.84E-20	GD0005514,GD0020037,GD.0016705,GD.0005506	CYP87A2	cytochrome P450, family 87, subfamily A, polypeptide 2	cytochrome P450 family protein
Sapur.01G0251500.1	321.281345	-1.234231924	0.067827018	-18.1968	5.48E-74	4.36E-73	pyrim	-0.87801821	1.83E-51	GD0006468,GD0005524,GD.0004672		Protein kinase superfamily protein	brassinosteroid insensitive 1-associated receptor kinase, putative
Sapur.0G0102300.1	11.66703169	-2.924392449	0.146503512	-18.1515	1.25E-73	9.90E-73	pyrim	-0.782487511	6.01E-34	GD0016788	GLIP6	GDSL-motif lipase/hydrolase family protein	GDSL esterase/lipase
Sapur.0G0239400.1	21.44304444	-2.780217931	0.126809829	-18.106	2.88E-73	2.26E-72	pyrim	-0.658308642	1.27E-19	GD0005514	CYP90D1	cytochrome P450, family 90, subfamily D, polypeptide 1	NA
Sapur.01G0131700.1	36.88316466	-2.3416904	0.129431017	-18.0951	3.48E-73	2.75E-72	pyrim	-0.834555653	5.66E-42				hypothetical protein
Sapur.0G0146500.1	138.7145108	-0.877979151	0.037486779	-18.0945	3.52E-73	2.78E-72	pyrim	-0.828315669	7.94E-41	GD0003026	AI-A/N-Inv,C/N-I	alkaline/neutral invertase	alkaline/neutral invertase
Sapur.0G0421800.1	3004.401097	-1.588341869	0.087798787	-18.0926	3.65E-73	2.88E-72	pyrim	-0.851647135	2.72E-45		THI1,THI4,TZ	thiazole biosynthetic enzyme, chloroplast (AtRA6) (THI1) (THI4)	thiamine thiazole synthase
Sapur.0G0145200.1	12.05481291	-2.246237832	0.124274247	-18.0752	5.06E-73	3.93E-72	pyrim	-0.768896015	6.46E-32				NA
Sapur.01G0250500.1	64.6731356	-1.296187644	0.071798125	-18.0522	7.44E-73	5.84E-72	pyrim	-0.784315134	5.81E-34	GD0016567,GD0008842		plant U-box 8	NA
Sapur.01G0253200.1	92.01566115	-5.246219267	0.176745136	-18.0526	7.52E-73	5.90E-72	pyrim	-0.791884498	5.58E-35				transmembrane protein, putative
Sapur.0G0285600.1	196.0125842	1.150857761	0.063816752	18.03379	1.06E-72	8.28E-72	pyrim	-0.766280983	1.38E-31				hypothetical protein
Sapur.01G0122200.1	1611.932795	-1.037466183	0.057778089	-17.9583	4.13E-72	3.21E-71	pyrim	-0.847164777	2.02E-44		PDC83	plasmodesmata-callose-binding protein 3	carbohydrate-binding module family 43 protein
Sapur.0G0288000.1	577.9628669	-1.047605974	0.058037575	-17.9555	4.34E-72	3.37E-71	pyrim	-0.848895055	5.57E-45			Eukaryotic aspartyl protease family protein	aspartic proteinase nepenthesin-1 protein, putative
Sapur.01G0229600.1	154.1398923	-0.601458085	0.033513384	-17.9476	5.01E-72	3.89E-71	pyrim	-0.829837309	4.14E-41				NA
Sapur.01G0040600.1	403.076754	1.473662648	0.082487284	17.94516	5.24E-72	4.06E-71	pyrim	-0.727287842	4.04E-27			Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Sapur.0G0121700.1	57.58588777	-1.548814335	0.086440084	-17.9178	8.57E-72	6.63E-71	pyrim	-0.807848836	2.31E-37			Protein of unknown function (DUF594)	transmembrane protein, putative
Sapur.01G0124300.1	17.63226561	-1.603783017	0.089928377	-17.9007	1.16E-71	8.96E-71	pyrim	-0.767883871	1.88E-34				alkaline/neutral invertase
Sapur.0G0245800.1	240.7349885	-1.011360729	0.056577607	-17.8758	1.84E-71	1.41E-70	pyrim	-0.74011887	1.68E-28	GD0005515	PLX1	plant UBX domain-containing protein 1	plant UBX domain protein
Sapur.0G0238100.1	0.88857743	-4.462231929	0.248881188	-17.8574	2.53E-71	1.94E-70	pyrim	-0.799602586	1.16E-31				hypothetical protein
Sapur.01G0245200.1	14.16060864	-1.126196178	0.119199796	-17.8372	3.63E-71	2.78E-70	pyrim	-0.796297723	1.12E-35		ATHB22,HB22,ZHD4	homeobox protein 21	ZF-HD protein dimerization region protein
Sapur.0G0264600.1	4.55057804	-2.261235869	0.168076649	-17.8262	4.42E-71	3.39E-70	pyrim	-0.818849902	2.42E-41				hypothetical protein
Sapur.1G0W0301300.1	1.96082424	-4.351460419	0.244129648	-17.8243	4.58E-71	3.50E-70	pyrim	-0.88496614	2.47E-49				microtubule-associated protein TORTIFOLIUA protein
Sapur.0G0203900.1	768.8252022	-1.367960861	0.076779311	-17.8168	5.24E-71	4.00E-70	pyrim	-0.828757887	6.43E-41	GD0003677	HTA7	histone H2A 7	core histone H2A/H2B/H2/H4
Sapur.01G0278300.1	172.6049984	-0.958635375	0.050790204	-17.816	5.34E-71	4.06E-70	pyrim	-0.818846904	9.40E-41		CKL3PK2,TOR1	AMM repeat-containing protein	microtubule-associated protein TORTIFOLIUA protein
Sapur.0G0151500.1	583.8352631	-0.962661172	0.054080539	-17.8061	6.33E-71	4.84E-70	pyrim	-0.804163788	7.65E-37	GD0005515	ATLP5,TLP5	tubby like protein 5	tubby like 5 protein
Sapur.0G0268700.1	425.6752793	-1.171260648	0.065690271	-17.773	1.14E-70	8.71E-70	pyrim	-0.81224118	1.38E-40			TCP family transcription factor	TCP transcription factor, putative
Sapur.01G0264800.1	401.9731932	-0.84025884	0.047206529	-17.768	1.25E-70	9.52E-70	pyrim	-0.826891914	1.38E-40			Protein of Unknown Function (DUF239)	carboxyl-terminal peptidase
Sapur.01G0268400.1	447.4664689	-1.213872272	0.077038276	-17.7516	1.66E-70	1.26E-69	pyrim	-0.816034529	1.80E-38	GD0005515		C2 calcium/lipid binding plant phosphoribosyltransferase family protein	NA
Sapur.0G0134950.1	491.6313401	2.200916461	0.123869639	17.75081	1.70E-70	1.29E-69	pyrim	-0.73318146	1.07E-26		ATSTU6,ST2A	sulfotransferase 2A	flavonol 4'-sulfotransferase, putative
Sapur.0G0227900.1	114.1191444	3.341364431	0.18026701	-17.746	2.46E-70	1.87E-69	pyrim	-0.802027786	2.39E-36		ATAHK9,OPR8	zeatin family cytokinin receptor	zeatin transcriptional repressor
Sapur.0G0281400.1	124.4158325	-2.071662249	0.116741261	-17.7482	1.78E-70	1.35E-69	pyrim	-0.772062409	2.54E-32	GD0008152,GD0003824	AKS1	acyl activating enzyme 1	acyl-CoA synthetase
Sapur.0G0240000.1	114.1491084	-1.382595293	0.106602126	17.74457	1.90E-70	1.44E-69	pyrim	-0.762767543	2.79E-30	GD0006468,GD0006468	GSB3,TS1	pectinesterase/pectinesterase inhibitor family protein	NA
Sapur.0G0126700.1	12.59071299	-3.747120569	0.211338732	-17.7387	2.52E-70	1.90E-69	pyrim	-0.822660138	5.12E-40	GD0005514,GD0015116,GD.0008872,GD.0005085,GD.0016020,GD.0008275	AST12,SULTR2;1	sulfate transporter 2;1	sulfate/bicarbonate/oxalate exchanger and transporter sat-1
Sapur.01G0118800.1	928.5943968	-0.772716997	0.043503269	-17.7256	2.68E-70	2.01E-69	pyrim	-0.814508822	1.75E-38	GD0018807,GD0005524	STI	AAA-type ATPase family protein	DNA polymerase III subunit gamma/tau
Sapur.0G0121900.1	788.4976687	-0.658606986	0.042631326	17.71943	2.97E-70	2.24E-69	pyrim	-0.811387673	4.50E-38	GD0016392,GD.0016021	ATSEC22,SEC22	Synaptosome-associated protein family	26-S-kDa vesicle transporter
Sapur.01G0262400.1	140.7682549	-3.703429967	0.196235877	-17.695	4.59E-70	3.45E-69	pyrim	-0.817922741	4.77E-39	GD0005515,GD0006468,GD0005524,GD.0004672		Leucine-rich repeat receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.0G0028400.1	951.8262861	-0.504338853	0.03986139	-17.6687	7.17E-70	5.38E-69	pyrim	-0.806012239	5.38E-37	GD0005515	RGA,RGA1	GRAS family transcription factor family protein	GRAS family transcription factor family protein
Sapur.0G0761300.1	1058.915207	0.664807761	0.037083302	17.64338	1.14E-69	8.56E-69	pyrim	-0.805892551	4.12E-37	GD0016597,GD0018152		ACT domain-containing small subunit of acetolactate synthase protein	acetolactate synthase, small subunit
Sapur.01G0153000.1	86.84114582	-1.436231102	0.081408423	-17.6421	1.17E-69	8.56E-69	pyrim	-0.771719304	2.80E-32	GD0016758,GD0008152		UDP-Glycosyltransferase family protein	UDP glycosyltransferase
Sapur.0G0159800.1	49.12556434	-2.191073391	0.124564926	-17.6402	1.21E-69	9.05E-69	pyrim	-0.743800787	1.62E-29				transmembrane protein, putative
Sapur.0G0826300.1	5.31863157	-4.367963891	0.247686455	-17.6385	1.23E-69	9.10E-69	pyrim	-0.760210084	7.78E-31	GD0005085,GD0046873,GD.0030001,GD.0016020	ZIP1	zinc transporter 1 precursor	ZIP zinc/iron transport family protein
Sapur.1G0W0240300.1	1959.429159	-0.948808505	0.053841262	-17.6242	1.61E-69	1.20E-68	pyrim	-0.842629765	1.63E-43	GD0004386	RNA helicase family protein	RNA helicase family protein	NA
Sapur.0G0276300.1	86.32528808	-3.354064022	0.176831708	-17.6238	1.62E-69	1.21E-68	pyrim	-0.790052034	9.38E-35		ATMYB93,MYB63	myb domain protein 63	R2r3-Myb transcription factor, putative
Sapur.0G0220900.1	1099.176752	-1.017885974	0.058556389	-17.6043	2.28E-69	1.70E-68	pyrim	-0.789153146	1.24E-34	GD0003677,GD0007786	HTB1	Histone superfamily protein	histone H2B
Sapur.01G0289600.1	16.60287766	-1.806664175	0.102741916	-17.5889	2.99E-69	2.22E-68	pyrim	-0.814881161	1.52E-38			Pectin lyase-like superfamily protein	glycoside hydrolase family 28 protein
Sapur.0G0241900.1	26.90274753	-2.656450982	0.151232827	-17.5803	3.46E-69	2.58E-68	pyrim	-0.819371246	2.73E-39			Rhl-like superfamily protein	NA
Sapur.0G0184800.1	3768.102086	0.556348879	0.031676363	17.56341	4.70E-69	3.48E-68	pyrim	-0.786299213	1.33E-34	GD0003561,GD0006355,GD0007000	AtbZIP44,bZIP44	basic leucine-zipper 44	bZIP transcription factor
Sapur.0G0229300.1	292.8602029	-1.513853391	0.141037669	-17.5181	5.16E-69	3.81E-68	pyrim	-0.77397407	4.12E-32	GD0016758,GD0008152	ACHE,PAE9	alpha/beta-Hydrolases superfamily protein	UDP-glucose:sterol glucosyltransferase, putative
Sapur.01G0289600.2	3.82054186	-5.364105506	0.305657157	-17.5494	6.01E-69	4.44E-68	pyrim	-0.757841335	1.51E-30	GD0006863,GD0003677,GD.0004355,GD.0005634,GD.0003700	AGL11,STK	K-box region and MADS-box transcription factor family protein	agamous MADS box factor transcription factor
Sapur.01G0288600.1	80.96223175	-2.656450982	0.151232827	-17.5288	8.64E-69	6.36E-68	pyrim	-0.78604042	1.27E-33	GD0006829		alpha/beta-Hydrolases superfamily protein	phosphatidylcholine-sterol O-acyltransferase
Sapur.0G0600700.1	835.4739008	0.600255938	0.034259723	17.52075	9.91E-69	7.33E-68	pyrim	-0.80772295	2.46E-37				plant/T27K7-10 protein
Sapur.0G0545500.1	61.81423793	-1.006861378	0.057634145	-17.511	1.13E-68	8.70E-68	pyrim	-0.834237555	1.64E-42	GD0006528,GD0004185	scp50	serine carboxypeptidase family	serine carboxypeptidase
Sapur.0G0280600.1	68.62188006	-1.884964402	0.107688411	-17.5037	1.34E-68	9.87E-68	pyrim	-0.784537878	6.43E-34			Transmembrane amino acid transporter family protein	amino acid transporter, putative
Sapur.0G0261800.1	70.28829427	-2.029727893	0.098584336	-17.497	1.51E-68	1.11E-67	pyrim	-0.797413777	9.56E-36				hypcin protein
Sapur.01G0245100.1	26.67947738	-1.854972524	0.106456833	-17.4845	1.87E-68	1.37E-67	pyrim	-0.798418082	1.14E-34		ATXG1,ATS1,CLO1	seed gene 1	calexin CLO1-1
Sapur.01G0291500.1	471.4537889	-0.453356672	0.025944179	-17.4743	2.25E-68	1.65E-67	pyrim	-0.797946633	6.63E-36			Regulator of chromosome condensation (RCC1) family protein	chromosome condensation regulator RCC1 repeat protein
Sapur.01G0277100.1	229.0843182	-0.647214207	0.035580075	-17.4724	2.26E-68	1.65E-67	pyrim	-0.760482225	1.83E-24	GD0016758,GD0008152	ATUGT85A1,UGT85A1	UDP-Glycosyltransferase family protein	NA
Sapur.0G0127300.1	2.12602918	-5.074605047	0.258939366	-17.4659	2.63E-68	1.91E-67	pyrim	-0.761827872	9.74E-31			Defensin-like (DEFL) family protein	defensin-like protein
Sapur.0G0239200.1	73.28677705	-1.622449103	0.093024716	-17.4426	3.92E-68	2.86E-67	pyrim	-0.794823232	5.20E-35				transmembrane protein, putative

Sapur.00G182700.1	112.3826609	-19.9576183	0.13557522	-16.1959	5.38E-59	3.42E-58	pyrole-28	-0.73512928	5.90E-28	ATMYB111,MYB111,PFG3	myb domain protein 111	AT4G03330.1	tannin-related R2R3 MYB transcription factor, putative
Sapur.01G0289900.1	274.7976663	-0.53977235	0.03331327	16.19349	5.61E-59	3.56E-58	pyrole	-0.76076767	5.01E-32	GO:0016020,GO:0008375	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	AT4G03340.1	core-2/I-branching beta-1h2C6-N-acetylglucosaminyltransferase family protein
Sapur.05G0288700.1	108.7739565	-0.62104581	0.03600235	-16.187	6.23E-59	3.95E-58	pyrole	-0.79818253	6.10E-36	GO:0007049,GO:0006281,GO:0005634	RADIATION SENSITIVE 17	AT4G01301.2,RAD17	cell cycle checkpoint protein RAD17
Sapur.00B0281100.1	20.3564178	-2.21870409	0.13709716	-16.1834	6.60E-59	4.18E-58	pyrole	-0.77391443	1.46E-32	GO:0004857	Plant invertase/pectin methylesterase inhibitor superfamily protein	AT4G17130.1	NA
Sapur.01G0722301.1	564.8439865	-0.63782576	0.03839438	16.1791	7.08E-59	4.48E-58	pyrole	-0.79788001	6.78E-36	NO1	RPM1-interacting protein 4 (RIN4) family protein	AT5G05810.3	RPM1-interacting protein 4 (RIN4) family protein
Sapur.00N0260600.1	10.0558441	-1.58603822	0.22168587	-16.1762	7.43E-59	4.70E-58	pyrole	-0.80187926	1.70E-36	ATRIL,RIL,RSM3	RAD-like 6	AT5G52510.1	MYB transcription factor
Sapur.05W0122800.1	47.4922885	-2.34526136	0.13900345	-16.1516	1.11E-58	7.00E-58	pyrole	-0.66583468	5.02E-21		Rubredoxin-like superfamily protein	AT5G51010.1	NA
Sapur.01G2281100.1	280.4749065	-1.05259814	0.06520349	16.1455	1.23E-58	7.72E-58	pyrole	-0.76136775	5.62E-31			AT5G15115.1	hypothetical protein
Sapur.00G0410000.1	18.0916717	-1.95820888	0.12134307	-16.1377	1.39E-58	8.75E-58	pyrole	-0.76685813	1.17E-31	GO:0005515,GO:0006468,GO:0005524,GO:0004672	Leucine-rich repeat protein kinase family protein	AT5G45780.1	LRR receptor-like kinase
Sapur.00G0193300.1	24.4769266	-1.35228728	0.13521707	-16.1349	1.51E-58	9.27E-58	pyrole	-0.66274299	5.15E-21		Protein of Unknown Function (DUF239)	AT5G59910.1	NA
Sapur.00G1210000.1	2014.080249	-0.54833765	0.03400945	-16.1232	1.75E-58	1.10E-57	pyrole	-0.76567904	1.66E-31	GO:0050662,GO:0008824	NADP(H)-binding Rossmann-fold superfamily protein	AT4G05400.1	BEN1	dihydroforamsyl-4-reductase
Sapur.00G0181900.1	1101.051977	-0.57786311	0.03581022	16.11659	1.95E-58	1.23E-57	pyrole	-0.79765132	7.32E-36		DNA/RNA-like protein	AT4G11370.1	clathrin adaptor complex medium chain
Sapur.01T0321900.1	80.6963045	-2.35105451	0.07763187	16.1103	2.16E-58	1.36E-57	pyrole	-0.76132846	5.78E-31		Gibberellin-regulated family protein	AT2G36730.1	gibberellin regulated protein
Sapur.01T0171800.1	6.6321883	-2.72477211	0.18526618	16.1068	2.38E-58	1.50E-57	pyrole	-0.73509844	6.08E-28			AT2G32370.1	NA
Sapur.01G0222700.1	26.2498751	-3.97112035	0.12489934	-16.0922	2.89E-58	1.82E-57	pyrole	-0.75852393	1.41E-30	GO:0055085,GO:0016021,GO:0016020,GO:0006810,GO:0005215	Major facilitator superfamily protein	AT5G54450.1	peptide transporter
Sapur.00G0681300.1	2719.162824	-0.94356868	0.04233756	16.0868	4.57E-58	2.84E-57	pyrole	-0.76648928	2.31E-30		Cos16-like DUF4 family protein	AT5G05731.1	CHC6 domain protein
Sapur.05G0293500.1	20.1043303	-2.00092166	0.12662129	-16.0508	5.64E-58	3.52E-57	pyrole	-0.71376081	1.49E-25	GO:0016747	HXXXD-type acyl-transferase family protein	AT3G26040.1	acyltaxan acetyltransferase
Sapur.01B2099600.3	1.6703738	-4.20628379	0.26218615	-16.0431	5.98E-58	3.88E-57	pyrole	-0.67325558	5.14E-20	GO:0044981,GO:0003677,GO:0006355,GO:0005634,GO:0003700	K-box region and MADS-box transcription factor family protein	AT4G09960.1	AGAMOUS-MADS box factor transcription factor family protein
Sapur.01B0288700.1	5.92941398	-3.57350272	0.20557874	-16.0415	6.15E-58	4.00E-57	pyrole	-0.71265121	2.96E-27	GO:0016747	HCT	AT5G48930.1	hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyl transferase
Sapur.01G0251600.1	79.1015511	-1.35201508	0.08450239	-16.0096	1.09E-57	6.81E-57	pyrole	-0.77345199	3.08E-32			AT5G01860.1	hypothetical protein
Sapur.00B2089100.1	1170.80646	-0.26422994	0.01602615	16.0026	1.19E-57	7.01E-57	pyrole	-0.64973326	2.90E-20			AT5G42420.1	alpha-dioxygenase
Sapur.00A0269400.1	14.2621125	-2.34363631	0.14017024	16.00117	1.25E-57	7.76E-57	pyrole	-0.68907813	1.62E-23	GO:0005524	ATPase,AAA-type	AT4G00510.1	AAA-ATPase 1
Sapur.00G1341200.1	4.58183915	-5.51923071	0.21060572	15.99622	1.36E-57	8.45E-57	pyrole	-0.80829409	7.78E-37			AT5G01600.1	NA
Sapur.00B1160700.1	80.8848878	-0.80788836	0.05169739	-15.9793	1.78E-57	1.10E-56	pyrole	-0.78547339	4.07E-34			AT3G16730.1	condensin-2 complex subunit H2, putative
Sapur.01B2240600.1	17.0464658	-2.72427211	0.14244216	-15.9668	2.13E-57	1.32E-56	pyrole	-0.73509844	6.08E-28		PNP-A	AT2G18660.1	nre lipoprotein A-like double-psi beta-barrel protein
Sapur.01G0232500.1	4.80828743	-7.92114375	0.17034394	-15.9628	2.32E-57	1.44E-56	pyrole	-0.75556416	2.32E-30		CYP721A1	AT5G67110.1	cytochrome P450, family 721, subfamily A, polypeptide 1
Sapur.01G0212600.1	615.3619428	0.466623	0.03117227	15.95974	2.44E-57	1.51E-56	pyrole	-0.78102515	1.66E-33	GO:0005515	ATBPM2,BPM2	AT5G06190.2	BTB-POZ and MATH domain 2
Sapur.01W0264380.1	384.7129173	-0.95181104	0.03398767	15.94182	2.51E-57	2.01E-56	pyrole	-0.75854516	1.24E-30	GO:0005634,GO:0004719	ATPMT4,PIMT1	AT4G38330.1	protein-L-isoaspartate(D-aspartate) methyltransferase 1
Sapur.00A0107900.1	6.95964494	-2.41684049	0.15178754	-15.9211	4.53E-57	2.79E-56	pyrole	-0.76083015	5.58E-31			AT3G26520.1	transmembrane protein, putative
Sapur.00G0980600.1	6.35837979	-3.81787869	0.20836165	-15.8081	4.54E-57	2.80E-56	pyrole	-0.76827608	1.25E-25		BUR2 domain-containing protein	AT3G22410.1	BUR2 domain protein
Sapur.01G0255400.1	745.8208855	-0.94732827	0.05952849	-15.9104	5.37E-57	3.30E-56	pyrole	-0.81961207	2.45E-39		Plant protein of unknown function (DUF827)	AT5G16730.1	NA
Sapur.01W0297400.1	1.52870384	-4.06322499	0.25497187	-15.9084	5.54E-57	3.41E-56	pyrole	-0.80897789	1.36E-37	GO:0000160	response regulator 5	AT5G62670.1	response regulator 5
Sapur.01W0009900.1	107.6745349	-2.31410663	0.07639392	-15.9002	6.31E-57	3.88E-56	pyrole	-0.72177623	8.17E-24		Homeobrain family protein 55	AT4G01680.1	AtMYB55,MYB55	MYB transcription factor
Sapur.00B0281600.1	212.9586402	-1.26164424	0.08127527	-15.8927	7.12E-57	4.37E-56	pyrole	-0.82003785	2.58E-41	GO:0005634,GO:0016491	Flavin-binding monooxygenase family protein	AT5G07800.1	flavin containing monooxygenase FMO GS-OX-like protein
Sapur.01G1176800.1	11.6250804	-1.91619245	0.12057019	15.89265	7.13E-57	4.37E-56	pyrole	-0.72178717	1.49E-26	GO:0006468,GO:0004672	Protein kinase superfamily protein	AT5G16670.1	NA
Sapur.00G1260600.1	500.6377318	-0.81850504	0.07362766	15.89086	7.33E-57	4.50E-56	pyrole	-0.68617429	7.25E-24		HXXXD-type acyl-transferase family protein	AT5G03980.1	NA
Sapur.01G0703300.1	484.1643354	-0.62878888	0.05995218	-15.8788	8.58E-57	5.46E-56	pyrole	-0.80542142	4.82E-37	GO:0005515	Tetratricopeptide repeat (TPR)-like superfamily protein	AT1G11540.1	SPY	O-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase spindly protein, putative
Sapur.00G1267900.1	551.7775328	1.56786525	0.07557029	15.87413	9.57E-57	5.86E-56	pyrole	-0.68770478	3.22E-24	GO:0016747	HXXXD-type acyl-transferase family protein	AT5G02890.1	transferase family protein
Sapur.00G0290600.1	725.6511131	-0.56138839	0.08709408	-15.8603	1.19E-56	7.30E-56	pyrole	-0.73631564	4.15E-28	GO:0016758,GO:0008152	UDP-glucuronosyltransferase 85A2	AT2G15480.1	UDP-glucosyltransferase family protein
Sapur.00G0584000.1	332.2988518	-0.82532117	0.05224208	-15.8587	1.23E-56	7.49E-56	pyrole	-0.74585886	8.80E-29		Nucleotide/sugar transporter family protein	AT5G07680.1	organic anion transporter, putative
Sapur.00G1120900.1	220.6279881	-1.56081424	0.06125201	-15.8329	1.84E-56	1.13E-55	pyrole	-0.75803176	1.39E-30	GO:0005515	AN11,LL,WD1	AT4G33760.1	Transducin/WD40 repeat-like superfamily protein
Sapur.00N0207300.1	126.3863959	-0.59985278	0.07958801	-15.8028	2.97E-56	1.81E-55	pyrole	-0.7788729	2.36E-33		TTN9	AT3G20570.2	hypothetical protein
Sapur.00B0281700.1	228.8687059	-0.84928288	0.05356062	-15.7918	3.25E-56	1.98E-55	pyrole	-0.77923292	1.36E-33	GO:0016787		AT3G17920.1	purple acid phosphatases superfamily protein
Sapur.00G1487800.1	269.9031258	-0.72726549	0.04606719	-15.7925	3.50E-56	2.13E-55	pyrole	-0.77923569	8.64E-33		ABIL1	AT4G26225.1	ABI-1-like 1
Sapur.00G1421200.1	137.7684587	-1.60182784	0.10142120	-15.7921	3.52E-56	2.14E-55	pyrole	-0.68831081	1.68E-23			AT1G20260.1	UDP-Glycosyltransferase superfamily protein
Sapur.00G0291600.1	285.7188392	-1.80087607	0.11410893	-15.7832	4.06E-56	2.46E-55	pyrole	-0.77074201	3.75E-32	GO:0003824,GO:0005515	PLDBETA,PLDBETA1	AT4G20150.1	phospholipase D beta 1
Sapur.00G1118800.1	396.8653932	-2.40351288	0.09149138	-15.7776	4.44E-56	2.69E-55	pyrole	-0.78155446	1.40E-33	GO:0005114,GO:0020037,GO:0016705,GO:0005506	aldose oxide synthase	AT4G20310.1	AOS,CYP74A,DDE2
Sapur.00G0501500.1	6.65527626	-7.02442194	0.19051689	-15.7766	4.51E-56	2.73E-55	pyrole	-0.75312067	5.49E-30			AT5G37020.1	NA
Sapur.01G0243700.1	1.58941896	-4.13228235	0.26203182	-15.7711	4.92E-56	2.98E-55	pyrole	-0.74926025	3.60E-29				NA
Sapur.01W0264901.1	2.11287316	-4.88464996	0.25051959	-15.7612	5.76E-56	3.48E-55	pyrole	-0.77957637	2.32E-33				NA
Sapur.01W0075300.1	1.49035798	-0.01372636	0.25178044	-15.7607	5.80E-56	3.51E-55	pyrole	-0.80480622	6.08E-37	GO:0000160	response regulator 17	AT4G31380.1	ARR17,RR17
Sapur.00G1414800.1	440.3022232	-1.24265613	0.07885748	-15.7564	6.20E-56	3.75E-55	pyrole	-0.72845314	1.27E-27	GO:0008152,GO:0003824	4-coumarate:CoA ligase 2	AT3G21240.1	4-coumarate:CoA ligase
Sapur.00G0490900.1	7.84005489	4.56664579	0.28858212	15.7541	6.44E-56	3.89E-55	pyrole	-0.64384394	9.44E-20		calmodulin 8	AT4G16460.1	CAM8
Sapur.00B0288800.1	114.9761898	-0.54227275	0.04302132	-15.7332	8.95E-56	5.40E-55	pyrole	-0.79968043	1.46E-36		Excision repair family protein	AT4G38040.1	NA
Sapur.00B1167800.1	8579.586069	0.95407246	0.06070784	15.73207	9.12E-56	5.50E-55	pyrole	-0.76835287	1.94E-32		Aluminum induced protein with YGL and LRDR motifs	AT4G19140.1	AIL7,ALAT4,PL1
Sapur.00G0341600.1	9.08857422	-2.48831344	0.15807381	-15.7151	1.26E-55	7.61E-55	pyrole	-0.78073334	1.83E-33	GO:0005114,GO:0016491	downstream target of AGL15-4	AT5G67010.1	DTA4
Sapur.15W0291600.1	262.034003	-0.46296783	0.03821729	15.69954	1.52E-55	9.16E-55	pyrole	-0.74989214	1.31E-29		Tetratricopeptide repeat (TPR)-like superfamily protein	AT5G62370.1	NA
Sapur.01G0241100.1	558.5377197	-0.8185519	0.05167016	-15.6926	1.78E-55	1.02E-54	pyrole	-0.77993615	2.33E-33	GO:0003677,GO:0009725,GO:0006355,GO:0005634	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related	AT4G17115.1	ARF11,ETT	auxin response factor
Sapur.01B2028400.1	81.0528947	-0.86703269	0.05528715	-15.6917	1.72E-55	1.04E-54	pyrole	-0.75393992	1.46E-30	GO:0005975,GO:0004553	Glycosyl hydrolase superfamily protein	AT5G64660.1	mannan endo-1h2C4-beta-mannosidase
Sapur.01G0300600.2	12.3804889	-1.77606664	0.11334632	-15.675	2.24E-55	1.35E-54	pyrole	-0.75053876	1.11E-29	GO:0005515	Transducin/WD40 repeat-like superfamily protein	AT5G12120.1	katanin p80 WD40 containing subunit B1
Sapur.01W0297100.1	1.50461812	-3.73164551	0.25058182	-15.6852	2.46E-55	1.48E-54	pyrole	-0.80621982	2.35E-37	GO:0000160	response regulator 17	AT4G31380.1	ARR17,RR17
Sapur.01G0609900.1	2.62387855	-8.30851149	0.27500699	-15.6675	2.56E-55	1.52E-54	pyrole	0.718936	2.90E-26	GO:0003677	WOX11	AT3G03660.1	WUSCHEL related homeobox 11
Sapur.00G0642200.1	4.38585657	-5.18589307	0.31031727	-15.6627	2.55E-55	1.51E-54	pyrole	-0.59138323	1.67E-16			AT2G38230.1	Lactoylglutathione lyase / glyoxalase I family protein
Sapur.00G0121200.1	55.7768703	-2.55287213	0.16310592	15.65166	3.24E-55	1.94E-54	pyrole	-0.75438358	3.90E-30	GO:0008270,GO:0005515	RING/U-box superfamily protein	AT5G42200.1	RING-U2 finger protein
Sapur.00G0208300.1	101.1639307	-1.94561328	0.09747983	-15.6515	3.24E-55	1.94E-54	pyrole	-0.68380835	1.88E-23		Transducin/WD40 repeat-like superfamily protein	AT5G24530.1	F-box and WD40 domain protein, putative
Sapur.01G0281000.1	44.33285486	-2.40775298	0.15409419	-15.6247	4.94E-55	2.95E-54	pyrole	-0.75171537	2.71E-30		Protein of unknown function, DUF642	AT5G29980.2	Protein of unknown function, DUF642
Sapur.01W0135600.1	54.06863176	-2.58128607	0.16428347	-15.6238	5.24E-55	3.13E-54	pyrole	-0.77304463	1.88E-32	GO:0043531	LRR and NB-ARC domains-containing disease resistance protein	AT4G14460.1	CC-NBS-LRR resistance protein
Sapur.00B0134500.1	33.7820365	-1.37589105	0.08290284	-15.5803	9.91E-55	5.88E-54	pyrole	-0.74289616	8.22E-29	GO:0008270,GO:0005515	RING/U-box superfamily protein	AT4G04360.1	RING finger protein
Sapur.01B1397000.1	4.47246713	-4.49725982	0.28859419	-15.5691	1.18E-54	7.02E-54	pyrole	-0.85867032	6.85E-21		Family of unknown function (DUF566)	AT2G08511.1	DUF566 family protein
Sapur.00G0517200.1	404.5558714	-0.98809713	0.06204119	-15.5649	1.28E-54	7.47E-54	pyrole	-0.71817047	3.45E-26	GO:0016787	LBD1	AT2G37950.1	LOB domain-containing protein 1
Sapur.01G0227300.1	431.1433646	-0.53389305	0.03428551	-15.5611	1.34E-54	7.92E-54	pyrole	-0.7790773	2.52E-33	GO:0080068	monosaccharide sensor	AT4G26850.1	VTC2
Sapur.00G0204000.1	741.1083854	-1.60008614	0.10283837	-15.5189	1.34E-54	8.16E-54	pyrole	-0.7916006	1.00E-30	GO:0003824	CAMEL	AT3G59551.1	CAMEL
Sapur.01B0099600.1	945.614162	-2.36467639	0.0812566	-15.5156	1.45E-54	8.57E-54	pyrole	-0.77073783	1.76E-32		thiazole biosynthetic enzyme, chloroplast (AKR4) (THI1) (THI4)	AT5G54770.1	THI1,THI4,TZ
Sapur.00G0341600.1	1753.102421	-1.15341247	0.09077553	15.54961	1.60E-54	9.46E-54	pyrole	0.81224842	4.06E-38	GO:0005114,GO:0016491	Zinc-binding alcohol dehydrogenase family protein	AT5G42250.1	class III alcohol dehydrogenase family protein
Sapur.15W0075400.2	1.50794443	-3.87502293	0.24926324	-15.5488	1.62E-54	9.58E-54	pyrole	-0.94376205	2.56E-76		RNA-binding CRS1 / YhbY (CRM) domain protein	AT4G13030.1	NA
Sapur.01G0241300.1	172.3722249	-0.91486223	0.04482764	-15.5355	2.00E-54	1.18E-53	pyrole	-0.80668491	1.37E-37	GO:0005515	Leucine-rich repeat protein kinase family protein (DUF641)	AT5G66081.1	DUF641 family protein
Sapur.01T0276600.1	2.15300862	-4.30461305	0.27735312	-15.518	2.62E-54	1.55E-53	pyrole	-0.70348698	6.26E-23		ATEXP23,ATEXPA23,ATHEXP	AT4G28280.1	expansin A23
Sapur.01G0281100.1	69.3412142	-1.39788761	0.09010338	-15.5115	2.90E-54	1.71E-53	pyrole	-0.78070816	1.83E-33			AT5G08840.1	hypothetical protein
Sapur.01G0189300.1	296.6872101	-1.26080083	0.08128483	-15.4984	3.76E-54	2.21E-53	pyrole	-0.72282568	1.26E-27	GO:0046872,GO:0030001	ATATX1,ATX1	AT4G24640.1	copper transporter atox1 protein
Sapur.00G1284400.1	999.3369198	0.41550133	0.02684174	15.47982	4.75E-54	2.79E-53	pyrole	-0.76015029	8.75E-32	GO:0008138,GO:0004470	Phosphotyrosine protein phosphatases superfamily protein	AT4G35680.1	tyrosine phosphatase
Sapur.00G0508600.1	63.22579371	-1.33197584	0.08059624	-15.4704	5.48E-54	3.22E-53	pyrole	-0.78377552	6.98E-34	GO:0005515,GO:0016021	Ankyrin-repeat family protein	AT2G19110.1	ankyrin effector kinase 1
Sapur.01G0209900.1	28.6605248	-2.07045983	0.13642728	-15.4489	7.67E-54	4.49E-53	pyrole	-0.79175475	1.31E-35	GO:0048544,GO:0006468,GO:0004672	curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein	AT3G41890.1	Serine/Threonine kinase domain protein, putative
Sapur.15W0263700.2	1.41614881	-4.90480158	0.25629168	-15.4383	9.05E-54	5.29E-53	pyrole	-0.80024855	3.93E-37		Vacuolar protein sorting-associated protein 26	AT5G48510.1	NA
Sapur.00G1747300.1	2.02545635	-4.21365492	0.27264866	-15.4377	9.13E-54	5.33E-53	pyrole	-0.68884826	2.03E-23		ankyrin repeat family protein	AT3G04730.2	NA
Sapur.01G0281200.1	86.94789419	-0.76532429	0.04958856	-15.4341	9.61E-54	5.64E-53	pyrole	-0.76072751	7.14E-32		alpha/beta-hydrolases superfamily protein	AT2G18241.1	NA
Sapur.00T0294200.1	64.3276969	-1.27518735	0.08265587	15.47295	1.06E-53	6.20E-53	pyrole	-0.74341208	7.15E-29	GO:0016567,GO:0006842	plant U-box 26	AT4G29780.1	PUB26
Sapur.00G0221300.1	455.1780664	-0.61537222	0.05669457	15.45237	1.12E-53	6.61E-53	pyrole	-0.80668491	3.6E-35			AT4G21580.1	NA
Sapur.01B2561600.1	785.914924	-0.46493424	0.03164672	-15.4119	1.36E-53	7.93E-53	pyrole	-0.79477805	1.94E-35		Alcohol dehydrogenase transcription factor Myb/SANT-like family protein	AT3G24490.1	transcription factor, putative
Sapur.00B0271200.1	756.5589085	-0.12008759	0.07287686	-15.3692	2.63E-53	1.52E-52	pyrole	-0.79325123	1.60E-35	GO:0005114,GO:0020037,GO:0016705,GO:0005506	cytochrome P450, family 77, subfamily A, polypeptide 4	AT5G66681.1	cytochrome P450 family 77 protein
Sapur.00G1190000.1	315.3860095	-0.61859492	0.02727552	15.3628	2.94E-53	1.70E-52	pyrole	-0.74858636	2.36E-29			AT4G17960.1	hypothetical protein
Sapur.00B0260300.1	91.0180459	-1.61114999	0.10490503	-15.3588	3.09E-53	1.79E-52	pyrole	-0.76785269	8.75E-32	GO:0005515,GO:0020037,GO:0008079,GO:0004601	Peroxidase family protein	AT5G14550.1	lignin-forming anionic peroxidase, putative
Sapur.01G0200600.1	199.0876564	-1.31537584	0.08576688	-15.3469	3.72E-53	2.15E-52	pyrole	-0.75304835	1.61E-30	GO:0005515,GO:0020037,GO:0016705,GO:0005506	allene oxide synthase	AT4G24150.1	AOS,CYP74A,DDE2
Sapur.00G1313300.1	58.3944843	-2.02949455	0.06708719	-15.3453	3.81E-53	2.21E-52	pyrole	-0.78225588	1.12E-33			AT3G22030.1	transmembrane protein, putative
Sapur.01G2179800.1	107.6870799	-1.10454164	0.07106557	-15.342	4.05E-53	2.32E-52	pyrole	-0.78373905	7.27E-34			AT3G09180.1	amine oxidase
Sapur.1T0730001.1	3.57208915	-0.03234945	0.19781344	-15.3293	4.87E-53	2.82E-52	pyrole	-0.79331216	3.16E-35		CLE25	AT4G28455.1	CLAVATA/ESR-RELATED 25
Sapur.00B0280200.1	15.1672484	-1.18284809	0.2077187	-15.3224	5.34E-53	3.08E-52	pyrole	-0.64084365	1.08E-19			AT5G25640.1	DUF617 family protein
Sapur.01G0261600.1	10.4029753	-2.18784463	0.14288802	-15.3137	6.20E-53	3.58E-52	pyrole	-0.72517746	6.67E-27	GO:0046872,GO:0000166	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	AT4G33380.1	calcium-transporting ATPase
Sapur.01G0277200.1	331.4810694	-0.95381028	0.06162015	-15.3132	6.24E-53	3.60E-52	pyrole	-0.75289004	2.34E-30		CCR1 intermediate protein 1	AT4G17780.1	cortical microtubule disorganization 1
Sapur.00G0230600.1	151.7203198	-0.96570226	0.06049235	-15.3079	6.77E-53	3.90E-52	pyrole	-0.75082502	1.12E-29		TCP family transcription factor	AT5G66980.1	TCP transcription factor, putative
Sapur.15W0262600.1	29.8639915	-1.94424579	0.12723737	-15.2827	9.97E-53	5.75E-52	pyrole	-0.76273292	3.82E-31	GO:0000160,GO:0007165,GO:0000155	histidine kinase 3	AT4G27320.1	AHK2,HK3
Sapur.01G0600300.1	193.7177577	-1.31339368	0.08618678	-15.2704	1.26E-52	6.92E-52	pyrole	-0.77551568	8.88E-33		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	AT5G55281.1	AC15
Sapur.00B0240900.1	875.012694	0.93688451	0.06135733	15.26624	1.28E-52	7.37E-52	pyrole	-0.74364974	8.76E-29			AT5G56613.1	NA
Sapur.00G0107000.1	759.0701616	-0.60763656	0.03983956	-15.2592	1.43E-52	8.20E-52	pyrole	-0.74431768	5.66E-29		RGA,RGA1	AT4G37390.1	GRAS family transcription factor GAI
Sapur.00G0520200.1	68.0247859	-2.59077647	0.16990784	-15.2481	1.68E-52	9.70E-52	pyrole	-0.77352136	1.64E-32	GO:0005114,GO:0020037,GO:0016705,GO:0005506	CYP87A2	AT5G12740.1	cytochrome P450, family 87, subfamily A, polypeptide 2
Sapur.01B2061200.1	1210.11037	-0.39856405	0.02619026	-15.2194	2.63E-52	1.50E-51	pyrole	-0.79552707	1.51E-35			AT5G58190.1	Plant protein of unknown function (DUF827)
Sapur.00G0875000.1	20.2017533	-1.36393103	0.09869167	-15.2193	2.63E-52	1.50E-51	pyrole	-0.78304954	1.64E-33	GO:0008270,GO:0005515	RING/U-box superfamily protein	AT3G13125.1	zinc finger, C3HC4 type (RING finger) protein
Sapur.00G0980600.1	45.3164424	-2.36567253	0.14906347	-15.1991	3.56E-52	2.06E-51	pyrole	-0.60601439	1.82E-17		ankyrin repeat family protein	AT5G06370.1	NA
Sapur.01G0258600.1	231.4697579	-0.79665274	0.05240629	-15.1974	3.68E-52	2.09E-51	pyrole	-0.79488034	2.44E-35		conserved peptide upstream open reading frame 35	AT3G29551.1	CPuORF35
Sapur.01B0132800.1	24.5443781	-1.8837869	0.07892527	-15.1884	4.22E-52	2.40E-51	pyrole	-0.78728975	2.28E-34		Tetratricopeptide repeat (TPR)-like superfamily protein	AT4G21020.1	NA
Sapur.1T0000400.1	181.9919429	0.58523163	0.03804885	15.17624	5.05E-52	2.88E-51	pyrole	-0.75196298	1.88E-31	GO:0046468	DSPB2,PXS	AT5G47750.1	DG protein kinase like 2
Sapur.00G2293200.1	18.2119369	-1.76379488	0.11658371	-15.1545	7.07E-52	4.00E-51	pyrole	-0.72798042	3.41E-27	GO:0009733	SAUR-like auxin-responsive protein family	AT3G24480.1	auxin-induced protein 6B
Sapur.01B2624400.1	6.42727885	-3.61418197	0.23976188	-15.1478	7.83E-52	4.42E-51	pyrole	-0.76423134	2.46E-31		Tetratricopeptide repeat (TPR)-like superfamily protein	AT1G21930.1	NA
Sapur.01G0227300.1	53.6642197	-1.44176031	0.09125594	-15.1404	8.77E-52	4.95E-51	pyrole	-0.56007054	2.41E-14	GO:0016851,GO:0015995,GO:0019379	ALB-1V,ALB1.CHLD,PDE186	AT4G01480.1	magnesium chelatase subunit CHD
Sapur.01B0136200.1	48.3854896	-1.19884137	0.07916506	-15.1387	9.06E-52	5.07E-51	pyrole	-0.75196298	1.88E-31	GO:0006468,GO:0005515,GO:0000877	ATMAC4,MAC4	AT3G27230.1	NAC transcription factor 050
Sapur.00G1321800.1	98.3917557	-0.70429617	0.11263483	-15.1312	1.01E-51	5.68E-51	pyrole	-0.76495136	2.02E-31		Pectin lyase-like superfamily protein	AT4G13730.1	pectate lyase, putative
Sapur.00G1162600.1	1233.954669	-0.61421121	0.08613678	-15.1264	1.14E-51	6.39E-51	pyrole	-0.74503171	1.25E-28		ATBI-1,ATBI1,BI-1,BI1	AT5G47120.1	Bax inhibitor-1 protein
Sapur.00G0880300.1	62.7255664	-2.19062677	0.08069728	-15.1133	1.32E-51	7.43E-51	pyrole	-0.74741936	2.52E-29	GO:0006355,GO:0005634,GO:0003700	AGL16	AT5G27230.1	AGAMOUS-like 16
Sapur.00G0770300.1	121.4876664	-1.31372596	0.08713739	-15.0967	2.32E-51	1.30E-50	pyrole	-0.73682656	1.27E-27	GO:0005515	C2 calcium/lipid-binding plant phosphoribosylbisphosphate family protein	AT5G22630.1	C2 domain second repeat present in synaptotagmin
Sapur.15W0075700.1	1.61416253	-3.89369711	0.25888607	-15.0394	4.05E-51	2.26E-50	pyrole	-0.73947864	2.37E-27				NA
Sapur.15Z0209700.1	757.3188429	0.65821821	0.04384857	15.0342	4.38E-51	2.45E-50	pyrole	-0.77380494	1.51E-32			AT5G07960.1	asterix protein
Sapur.01G0297600.1	2.20884985	-4.00502877	0.26317879	-15.0261	5.76E-51	3.21E-50	pyrole	-0.64894129	2.8E-20				transmembrane protein, putative
Sapur.01G1021700.1	40.5738139	-0.99847398	0.06635531	-15.0067	6.64E-51	3.70E-50	pyrole	-0.78806658	1.77E-34			AT3G04940.1	hypothetical protein
Sapur.00G0851100.1	12.7461043	-2.52179202	0.15345821	-14.9916	7.58E-51	4

Sapur.0004G0490600.1	451.125887	0.838756679	-0.05953851	14.08777	4.52E-05	2.28E-04	purple	0.74346159	7.10E-09	GO:0043565,GO:0006355,GO:0003700	AT4G04540.1	AHWRKY42,WRKY42	WRKY transcription factor, putative
Sapur.0003G0799800.1	77.62047768	-1.172302739	-0.083218706	-14.0858	4.64E-45	2.34E-44	purple	-0.725947607	5.55E-27	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G22730.1	Leucine-rich repeat protein kinase family protein	receptor-like kinase
Sapur.0001G0194000.4	29.92354684	-1.629761627	-0.118580107	-14.0623	4.63E-45	3.24E-44	purple	-0.686312864	1.40E-20	GO:0004457,GO:0003755,GO:0000413	AT2G26160.1	rotamase CYP 4	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.0008G0918500.2	270.0889418	0.704669943	-0.050145097	14.05854	6.83E-45	3.43E-44	purple	0.732845247	1.04E-27	GO:0016746,GO:0008152	AT5G52200.1	LTA3	Dihydrolipoamide acetyltransferase, long form protein	pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase
Sapur.0006G1941000.1	7283.218917	-0.476268888	-0.034028275	-14.0501	7.17E-45	3.60E-44	purple	-0.74326927	7.48E-28		AT4G22440.1	FRG02A-like protein	hydroxyproline-rich glycoprotein-like protein, putative
Sapur.0161G2340800.2	22.38312402	-1.133295897	-0.080668855	14.04874	7.84E-45	3.93E-44	purple	-0.860603305	3.08E-49		AT4G18160.1	ATKCDL4,ATTPK2,KCDL,TPK2	Ca2+ activated outward rectifying K+ channel 4	outward rectifying potassium channel protein
Sapur.0050G0920800.1	27.22715431	-1.564052234	-0.083000771	-14.0244	1.11E-44	5.58E-44	purple	-0.72872209	2.85E-27	GO:0007165,GO:0005515	AT5G63930.2	Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.0051G874000.1	68.81831043	-1.38327424	-0.09060221	-14.0226	1.13E-44	5.68E-44	purple	-0.715888479	6.12E-26		AT5G55100.1	glycine-rich protein	NA
Sapur.0162G795900.1	72.50068603	-0.05281065	0.075079916	-14.0226	1.13E-44	5.68E-44	purple	-0.76961376	6.03E-32		AT5G30600.1	NDR1	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	Non-race specific disease resistance-like protein, putative
Sapur.0105G0388800.1	1301.508096	-0.486463324	-0.034707495	14.01043	1.29E-44	6.27E-44	purple	0.78323805	6.70E-34	GO:0016020,GO:0006886,GO:0005801	AT5G47430.1	NA	NA	NA
Sapur.0161G390000.1	404.1196127	-1.464327295	-0.10448751	-14.0144	1.27E-44	6.36E-44	purple	-0.790757138	7.36E-35	GO:0005507,GO:0055114,GO:0016491	AT1MC04.8K612.LAC.6.LMC	Laccase/Diphenol oxidase family protein	laccase 1a
Sapur.0004G0132600.1	22.61840904	-1.04278927	-0.086837643	-14.013	1.30E-44	6.48E-44	purple	-0.74852606	1.85E-29		AT3G17260.1	ATP binding cassette family protein	PFR containing plant protein, putative
Sapur.0070G0178000.1	4.610263105	-0.097889464	-0.231150062	-14.0081	1.39E-44	6.95E-44	purple	-0.725292319	6.58E-27	GO:0005524	AT5G05930.1	BCS1	cytochrome BC1 synthesis	BCS1 protein, putative
Sapur.0062B0160.1	2616.224137	0.558770148	-0.030600584	-14.0072	1.44E-44	7.05E-44	purple	-0.758988583	1.10E-30		AT5G60160.1	NA	Ribosomal protein family protein	nucleoplasmin nucleosome assembly protein
Sapur.0159G0632300.1	8.072264678	-1.532293619	-0.190432206	-14.0023	1.51E-44	7.54E-44	purple	-0.719343153	5.79E-26	GO:0006468,GO:0004672	AT1G10940.1	AGK1,SNRK2-4,SNRK2.4,SRK	Protein kinase family protein	Serine/Threonine-kinase
Sapur.0159G0344700.1	135.7700274	-1.164865569	-0.081780207	-13.9969	1.65E-44	8.12E-44	purple	-0.737818239	1.66E-29	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT2G31180.1	CYP66A1	cytochrome P450, family 66, subfamily A, polypeptide 1	NA
Sapur.0158G0899001.1	224.9250569	-1.183864679	-0.08455465	-13.9955	1.68E-44	8.28E-44	purple	-0.838894054	8.62E-43					hypothetical protein
Sapur.0096G0471000.3	12.02602857	-2.918272685	-0.13712547	-13.9892	1.81E-44	9.05E-44	purple	-0.687708202	2.51E-24		AT5G51370.1	ATCSLA5,ATH-B,CESA5,CLCV	Cellulose synthase family protein	cellulose synthase A, catalytic subunit
Sapur.0050G0410200.1	191.4910752	-0.604095166	-0.054585453	-13.9868	1.88E-44	9.36E-44	purple	-0.764371839	1.36E-31		AT5G09195.2	NA	NA	Pyo-Gpdh phosphatase
Sapur.0172G0610000.1	2.383910201	-0.908203859	-0.208015694	-13.9807	2.04E-44	1.02E-43	purple	-0.873337747	2.80E-50		AT5G38455.1	CLE25	CLAVATA/ESR-RELATED 25	NA
Sapur.0101G1167000.1	1567.891396	-0.387904136	-0.049150425	-13.9783	2.12E-44	1.05E-43	purple	-0.82494653	8.61E-40		AT5G17220.1	ATHCL,HS1	heat stable protein	cross responsive A/B barrel domain protein
Sapur.0102G0813000.2	7.512977976	-2.559848889	-0.183135796	13.97787	2.13E-44	1.06E-43	purple	-0.67823505	1.40E-22		AT5G70670.1	Calexcoin-related family protein	calcium ion binding protein, putative	calcium ion binding protein
Sapur.0159G0327400.1	2.890134386	-2.511629403	-0.176609345	-13.9773	2.14E-44	1.07E-43	purple	-0.81295572	2.08E-38					hypothetical protein
Sapur.0132G0112200.1	51.9945024	-0.011127877	0.072357704	-13.974	2.25E-44	1.12E-43	purple	-0.742226477	9.77E-29	GO:0003824,GO:0006470,GO:0004722	AT5G27930.2	Protein phosphatase 2C family protein	protein phosphatase 2C, putative	protein phosphatase 2C, putative
Sapur.0162G0960600.1	256.8763873	-0.558770148	-0.042470284	-13.972	2.30E-44	1.15E-43	purple	NA	NA		AT5G07760.1	Homeobox-leucine zipper protein family protein	NA	myb-DNA-binding domain protein, putative
Sapur.0003G0661000.1	417.6765507	-0.804486649	-0.057609041	-13.9667	2.49E-44	1.24E-43	purple	-0.715934153	5.79E-26	GO:0005515	AT1G02080.1	membrane protein, putative	NA	plastidial glycolate/glycerate translocator 1
Sapur.0106G1023000.2	8.608012258	-1.777032651	-0.127337677	-13.9553	2.92E-44	1.45E-43	purple	-0.73709638	4.54E-32		AT5G25640.1	Protein of unknown function, DUF617	Protein of unknown function, DUF617	DUF617 family protein
Sapur.0135G0223000.1	1952.20953	-0.886456515	-0.060587897	-13.9302	3.81E-44	1.89E-43	purple	-0.740748664	1.36E-29	GO:0009378,GO:0006310,GO:0006281	AT5G22882.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	P-loop nucleoside triphosphate hydrolase-like protein	DNA-dependent helicase family protein
Sapur.0030G0190900.1	1397.712825	-0.50202753	0.03606254	-13.921	4.17E-44	2.34E-43	purple	-0.743202269	7.59E-29	GO:0003676	AT5G64200.1	ATSC35,SC35	orthologs of human splicing factor SC35	serine/arginine-rich splicing factor SRSF10 RNA recognition motif protein
Sapur.0010G0740700.1	260.5442156	-1.606014221	-0.115438303	-13.9104	4.98E-44	2.47E-43	purple	-0.62667017	4.31E-18	GO:0004861	AT2G45461.1	AtWIP,CJA1,JMJ14,WIP1,CJ	Basic helix-loop-helix (bHLH) DNA-binding family protein	LWFC3
Sapur.0051G7600000.1	1.446515889	-2.912370886	-0.281268248	-13.9097	5.13E-44	2.73E-43	purple	-0.692741597	9.12E-24		AT2G42410.1	AT2PP11,2PP11	zinc finger protein 11	C2H2-type zinc-finger protein
Sapur.0113G0930600.1	111.1163726	-0.882661521	-0.064368832	-13.9065	5.24E-44	2.79E-43	purple	0.726348872	1.20E-27		AT2G16220.1	Leucine-rich repeat (RPR) superfamily protein	NA	NA
Sapur.0131G4130600.1	2403.923089	-0.858941365	-0.060378871	-13.8944	6.85E-44	3.38E-43	purple	-0.747353953	2.57E-29	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G11640.1	ATC4H,C4H,CYP73A5,REF3	cinnamate-4-hydroxylase	cytochrome P450 family 73 cinnamate-4-hydroxylase
Sapur.0012G1881000.1	641.8542309	-0.461604754	-0.033235573	-13.8926	7.02E-44	3.47E-43	purple	-0.726039104	2.07E-28	GO:0006468,GO:0004672	AT2G20200.1	Protein kinase superfamily protein	Protein kinase superfamily protein	receptor-like Serine/Threonine-kinase
Sapur.0180G0247000.1	151.6404436	-0.810998853	-0.058380086	-13.8917	7.11E-44	3.51E-43	purple	-0.718993379	2.86E-26		AT2G32400.1	ATBT1,EMB3104,EMB342,SHS	Mitochondrial substrate carrier family protein	substrate carrier family protein
Sapur.0105G0528000.2	2.020769266	-2.302852803	-0.170928738	-13.8824	8.10E-44	3.98E-43	purple	-0.866281215	3.57E-48		AT5G58210.1	NA	NA	hypothetical protein
Sapur.0092G0957000.1	519.7040015	-1.29285968	-0.093225207	-13.8789	8.51E-44	4.19E-43	purple	-0.762364529	4.27E-31	ATCSLA09,ATCSLA9,CSLA09	AT5G03760.1	Nucleotide-diphospho-sugar transferases family protein	Vacuolar protein sorting-associated protein 26	cellulose synthase-like protein A2
Sapur.0156G0969000.2	36.93946915	0.969215152	-0.069868559	13.87247	9.30E-44	4.58E-43	purple	-0.72475669	7.38E-27		AT5G48550.1	Vacuolar protein sorting-associated protein 26	NA	NA
Sapur.0156G0830300.1	33.60791224	-0.552628361	-0.070050162	13.87126	9.46E-44	4.65E-43	purple	-0.764652028	2.11E-31		AT5G07320.1	RNA-like superfamily protein	NA	NA
Sapur.0156G0833700.1	18.80725633	-0.038184504	-0.076082722	13.85941	1.12E-43	5.48E-43	purple	-0.76601175	1.30E-31		AT5G01720.1	RNA-like superfamily protein	NA	NA
Sapur.0199G1111000.1	893.9632368	-0.587363973	-0.042390851	-13.8564	1.19E-43	5.81E-43	purple	-0.719945996	2.29E-26		AT5G45100.1	SBP (S-ribonuclease binding protein) family protein	NA	NA
Sapur.0161G750000.1	232.6067237	-0.410631516	-0.026053135	13.84783	1.31E-43	6.43E-43	purple	-0.720716419	1.92E-26		AT4G25230.1	DNA-binding storekeeper protein-related transcriptional regulator	DNA-binding storekeeper protein-related transcriptional regulator	transcription regulator, putative
Sapur.0180G0247000.1	120.9885168	-0.496450495	-0.032860146	-13.8332	1.69E-43	8.26E-43	purple	-0.726326951	3.18E-28		AT5G10010.1	Transmembrane protein with chloroplast membranes superfamily protein	Transmembrane protein with chloroplast membranes superfamily protein	NA
Sapur.0071G0380600.1	447.1144006	-0.480319971	-0.034730589	-13.8288	1.68E-43	8.24E-43	purple	-0.737978609	2.86E-28		AT5G52730.1	Trafficking protein	Trafficking protein	Trafficking protein
Sapur.0092G2920600.1	5.140508151	-1.982272896	-0.14320656	-13.8137	2.11E-43	1.03E-42	purple	-0.725228204	5.76E-28	GO:0043565,GO:0006355,GO:0005634,GO:0003700	AT4G26241.1	heat stress transcription factor B-4	heat stress transcription factor B-4	heat stress transcription factor
Sapur.0122G0645000.1	104.7923866	-0.988916573	-0.071774433	-13.7812	3.45E-43	1.68E-42	purple	-0.706989862	4.32E-25	GO:0003677,GO:0006355,GO:0005634	AT5G31180.1	KNAT6,ATH6,ATK1,KNAT6	KN/TOTEX1-like homeobox gene 6	homeobox knotted-like protein
Sapur.0156G0930300.1	1050.512251	-0.804486304	-0.055629410	-13.7681	3.97E-43	1.93E-42	purple	-0.744946456	2.08E-29	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT4G08480.1	RKL1	receptor-like kinase 1	receptor-like kinase RKL0001, putative
Sapur.0030G0231300.1	29.75811884	-2.738469424	-0.092575811	-13.7605	4.43E-43	2.14E-42	purple	-0.708725519	2.94E-25	GO:0006468,GO:0004672	AT5G58890.1	Protein kinase superfamily protein	Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.0161G395000.1	36.2035947	-1.344888837	-0.097729498	-13.7569	4.63E-43	2.25E-42	purple	-0.74372622	6.63E-29		AT5G26490.1	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.0030G0454000.1	230.7796253	0.681101922	0.049594754	13.7331	6.40E-43	3.10E-42	purple	-0.744849042	5.52E-29		AT5G66660.1	NA	NA	NA
Sapur.0010G0872000.1	214.7095766	-1.323271189	0.096356191	-13.7331	6.43E-43	3.12E-42	purple	-0.685892296	1.65E-23		AT5G66680.1	NA	NA	D27 family protein, putative
Sapur.0175G2760.1	-2.275097917	-4.488556022	0.242165557	-13.7256	7.14E-43	3.46E-42	purple	-0.690853642	3.21E-23		AT5G04570.1	NA	NA	NA
Sapur.0050G0010900.1	186.6418899	-3.368243311	0.099748878	-13.7177	7.96E-43	3.85E-42	purple	-0.761151589	5.97E-31	GO:0046983	AT5G05530.1	PAP1,PAP2,POC1	phytochrome interacting factor 3	phytochrome-interacting factor 3-1, putative
Sapur.0194G0940800.1	1.088882009	-2.918122557	0.291812257	13.71248	8.54E-43	4.14E-42	purple	-0.64852271	3.85E-20	GO:0005515	AT4G38370.1	F-box and kelch-repeat protein domain-containing protein	NA	NA
Sapur.0162G0271000.1	244.8040032	-0.603216141	-0.16597272	-13.7053	9.44E-43	4.56E-42	purple	-0.61627222	5.68E-18		AT5G56880.1	VQ motif-containing protein	VQ motif-containing protein	VQ motif protein
Sapur.0042G0280300.1	464.2949568	-0.824233103	-0.025042679	-13.6847	1.34E-42	6.46E-42	purple	-0.756246663	4.20E-30		AT5G47960.1	NA	NA	trafficking protein particle complex subunit 13, putative
Sapur.0096G0351300.1	8.088091621	-1.083591539	-0.125531868	-13.6725	1.48E-42	7.14E-42	purple	-0.724230586	8.36E-27	GO:0006468,GO:0005524,GO:0004672	AT5G59560.1	ATCBR1,CCR1	CRINKLY4 related 3	Serine/Threonine kinase-like protein
Sapur.0080G0700800.1	124.051185	0.832603287	0.133591131	13.64764	2.09E-42	1.00E-41	purple	0.782798697	9.51E-34	GO:0016021	AT3G19690.1	EXS (ERD1/PHO1/SPX1) family protein	EXS (ERD1/PHO1/SPX1) family protein	phosphate transporter PHO1-like protein
Sapur.0001G0616100.1	12.98602775	-2.728464409	-0.20051893	-13.6072	3.63E-42	1.74E-41	purple	0.547331147	1.22E-13	GO:0015743	AT5G11680.1	Aluminum activated malate transporter family protein	Aluminum activated malate transporter family protein	aluminum activated malate transporter
Sapur.0105G0283000.1	546.4898713	1.263504118	0.092090946	13.59931	4.04E-42	1.93E-41	purple	-0.798149393	6.09E-36	GO:0015937,GO:0005524,GO:0004594	AT2G21180.3	ATPANK2,PANK2	pantothenate kinase 2	pantothenate kinase
Sapur.0064G1462000.1	16.77866007	-1.164148222	-0.085423104	-13.5662	4.22E-42	2.02E-41	purple	-0.668889214	2.10E-23	GO:0003247,GO:0006468,GO:0005524,GO:0004672	AT5G67340.1	WAK2	wall-associated kinase 2	tyrosine kinase family protein
Sapur.0152G0396000.1	1.370558234	3.866695524	-0.281930746	13.58447	4.95E-42	2.37E-41	purple	-0.686115184	2.55E-23		AT5G68910.1	NADP(+)-linked oxidoreductase superfamily protein	NA	NA
Sapur.0105G1790000.1	151.6082313	0.532378197	0.059207553	13.5467	5.17E-42	2.47E-41	purple	-0.731967373	3.50E-29	GO:0031966	AT5G41451.1	NA	NA	cytochrome C oxidase assembly protein COX16
Sapur.0196G0321000.1	46.50523174	-1.112943631	0.081971079	13.57727	5.46E-42	2.61E-41	purple	-0.751765507	7.07E-30		AT4G12690.1	Plant protein of unknown function (DUF868)	Cation/calcium exchanger family protein	protein phosphatase 2c, putative
Sapur.0066G0352200.1	167.9929569	-0.481194264	0.075522584	-13.5567	5.51E-42	2.64E-41	purple	-0.664373008	1.66E-21		AT5G42260.1	Calcium-binding EF-hand family protein	receptor-like kinase RKS003, putative	receptor-like protein kinase
Sapur.0950G0818000.1	10.78762794	-1.462367512	0.106302206	-13.5656	5.61E-42	2.93E-41	purple	-0.708725119	2.96E-25	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT3G27320.1	cytochrome P450, family 81, subfamily D, polypeptide 8	cytochrome P450, family 81, subfamily D, polypeptide 8	tyrosine kinase domain protein
Sapur.0062B0600.2	71.07899914	-0.638141466	0.050608135	-13.5636	5.92E-42	3.13E-41	purple	-0.705021487	1.94E-25	GO:0005515,GO:0006840	AT1G12570.1	UPL5	ubiquitin protein ligase UPL5	E3 ubiquitin protein ligase UPL5, putative
Sapur.0096G0753000.1	12.32926768	1.73685952	0.128057599	13.56307	6.63E-42	3.46E-41	purple	-0.659813599	5.57E-21		AT3G07820.1	ATMYB73,MYB73	myb domain protein 73	MYB transcription factor
Sapur.0120G0990600.1	21.88094988	-1.887116201	0.130008873	-13.5562	7.28E-42	3.47E-41	purple	-0.701930228	1.49E-24		AT5G51670.1	Protein of unknown function (DUF688)	Protein of unknown function (DUF688)	hypothetical protein
Sapur.0051G961000.1	10.54749497	-0.964167622	0.200763583	-13.5556	7.34E-42	3.49E-41	purple	-0.623639704	2.04E-18		AT5G66985.1	NA	NA	hypothetical protein
Sapur.0046G0123600.1	66.86320664	-2.064966007	0.152368028	13.55231	7.68E-42	3.65E-41	purple	-0.649372217	3.61E-20	GO:0009407,GO:0006952	AT5G70840.1	MLP31	MLP-like protein 31	NA
Sapur.0151G0280900.1	488.3465113	-0.667348428	0.047796279	-13.5442	8.54E-42	4.06E-41	purple	-0.772849456	2.01E-32	GO:0006270,GO:0006277	AT5G60210.1	HIS2-1,HIS1,VAL2	histone 2A family protein	transcription factor, putative
Sapur.0105G1118800.3	3.360418578	2.421039426	0.253178145	13.51238	1.32E-41	6.28E-41	purple	-0.663310373	9.52E-20	GO:0003677,GO:0003899,GO:0003677	AT5G16980.1	NIRMNA,NIRPOMA,NIRPRA	RNA polymerases M/15 kD subunit	DNA-directed RNA polymerase subunit
Sapur.0195G0102600.1	501.0570227	-0.436141497	0.056261812	-13.5117	1.34E-41	6.46E-41	purple	-0.749371315	1.50E-29		AT5G01510.1	ATCDS15,SGR5	C2H2-like zinc finger protein	C2H2L domain class transcription factor
Sapur.0195G0260900.1	153.0318838	0.393665529	0.029145093	13.50624	1.44E-41	6.82E-41	purple	-0.712172565	1.36E-25		AT5G62370.1	Tetratricopeptide repeat (TPR)-like superfamily protein	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.0199G0893300.1	148.7239661	-0.672428262	0.049715643	-13.5017	1.51E-41	7.25E-41	purple	-0.715938477	7.76E-26	GO:0006355,GO:0005667,GO:0003700	AT5G48160.2	DP-EF2F-like 1	DP-EF2F-like 1	antagonist of E2F-dp complex repressor
Sapur.0195G0831000.1	9.602322227	-1.536306936	0.113807419	-13.49918	1.58E-41	7.50E-41	purple	-0.714839662	5.65E-26	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G37370.1	CYP81D8	cytochrome P450, family 81, subfamily D, polypeptide 8	NA
Sapur.0010G0233000.1	15.91842694	-1.547904984	0.11475935	-13.4808	2.03E-41	9.60E-41	purple	-0.72308164	1.84E-26	GO:0006468,GO:0004672,GO:0005524	AT4G08870.1	Protein kinase superfamily protein	Protein kinase superfamily protein	receptor-like kinase
Sapur.0006G1857000.1	8.970787792	-1.612778184	0.104836649	-13.4756	2.18E-41	1.03E-40	purple	-0.744817659	4.86E-29					hypothetical protein
Sapur.0021G1991000.1	4879.214164	-0.547261901	0.040621218	-13.4715	2.32E-41	1.09E-40	purple	-0.738308863	2.12E-28	GO:0008152,GO:0016818	AT2G36460.1	Transketolase	Transketolase	transketolase
Sapur.0174G1720000.1	34.77436211	-1.310641308	0.097275262	-13.4719	2.31E-41	1.09E-40	purple	-0.819391958	7.78E-24	GO:0008810	AT5G49060.1	GLIP1	GDSL lipase 1	NA
Sapur.0096G0647000.1	1442.121105	0.360822124	0.026813642	13.45666	2.81E-41	1.33E-40	purple	-0.726352087	5.04E-27		AT5G49730.1	NA	NA	transmembrane protein, putative
Sapur.0092G7920.1	11.56543978	-1.565802308	0.112751384	-13.4466	3.31E-41	1.56E-40	purple	-0.705201998	1.26E-25	GO:0008270,GO:0005515	AT1G71520.1	TOXICOS EN LEVADURA 2	TOXICOS EN LEVADURA 2	zinc-RING finger protein
Sapur.0071G0100600.1	149.3466665	-0.805845079	0.060087387	-13.4112	5.20E-41	2.46E-40	purple	-0.743481086	7.07E-29		AT5G50011.1	CPuORF37	conserved peptide upstream open reading frame 37	transcription factor, putative
Sapur.0195G0102600.1	865.5872504	-0.496585286	0.036507518	-13.4007	5.61E-41	2.65E-40	purple	-0.726820215	4.75E-27		AT2G39570.1	ACT domain-containing protein	ACT domain protein	ACT domain protein
Sapur.0191G0100100.1	2312.978165	0.654817486	0.048879274	13.39663	6.33E-41	2.97E-40	purple	0.69341928	7.80E-24		AT3G20820.1			transmembrane protein, putative
Sapur.0191G0249000.1	238.9980905	-0.854881844	0.070899948	-13.395	6.47E-41	3.04E-40	purple	-0.705844164	6.52E-25		AT4G28100.1			DUF unchanged protein, putative
Sapur.0060B6200.1	55.47571243	-1.020654019	0.076265939	-13.3828	7.62E-41	3.57E-40	purple	-0.681069237	9.75E-23	GO:0043565,GO:0006355,GO:0003700	AT4WRKY31,WRKY31	WRKY DNA-binding protein 31	WRKY transcription factor	WRKY transcription factor
Sapur.0051G199700.1	8.035242067	-2.173581284	0.162555607	-13.3713	8.90E-41	4.17E-40	purple	-0.766572752	1.27E-31		AT4G35240.1	Protein of unknown function (DUF680 and DUF632)	Protein of unknown function (DUF680 and DUF632)	DUF632 family protein
Sapur.0062G2010500.1	13.59278328	1.951590576	0.144846026	-13.3649	9.08E-41	4.26E-40	purple	-0.629242167	1.06E-18		AT2G35720.1	NA	NA	hypothetical protein
Sapur.0091G1330000.1	42.00028846	-1.724331912	0.120639441	-13.3629	9.98E-41	4.66E-40	purple	-0.705738877	5.69E-25	GO:0055114,GO:0050662,GO:0019338,GO:0006420	AT1G76490.1	HMG1,HMG1	hydroxy methylglutaryl coenzyme A reductase	3-hydroxy-3-methylglutaryl coenzyme A reductase, hydroxymethylglutaryl-CoA reductase
Sapur.0100G0990800.1	566.1138601	-0.551264224	0.051417726	-13.3164	1.16E-40	5.42E-40	purple	0.699462895	2.21E-24		AT5G25175.1	NA	NA	NA
Sapur.0021G1763000.1	130.6218266	-0.858681898	0.064338271	-13.3505	1.18E-40	5.50E-40	purple	-0.720805055	1.87E-26	GO:0055114,GO:0016491,GO:0005507	AT5G76160.1	sks5	SKU5 similar 5	multicopper oxidase
Sapur.0075G0381200.1	206.9280604	-0.668249949	0.051454888	-13.3447	1.27E-40	5.94E-40	purple	-0.705026998	2.61E-25		AT5G01750.1	VQ motif-containing protein	VQ motif-containing protein	VQ motif protein
Sapur.0191G00.1	3.724966665	-2.417530867	0.181393075	13.33486	1.45E-40	6.77E-40	purple	0.741039356	1.30E-28		AT5G23270.1			hypothetical protein
Sapur.0100G0375000.1	147.3605115	-0.114601204	0.083548115	-13.334	1.47E-40	6.86E-40	purple	-0.660232303	1.53E-22	GO:0045454,GO:0015035,GO:0006662	AT4H4Q	Thioredoxin superfamily protein	Thioredoxin superfamily protein	thioredoxin M-type protein
Sapur.0131G0570000.1	32.0017382	1.422990862	0.107006817	13.29813	2.37E-40	1.10E-39	purple	-0.674673891	3.41E-22					hypothetical protein
Sapur.0006G8870000.1	53.78214666	-1.302436124	0.1	13.14336	3.51E-40	1.17E-39	purple	-0.648529535	1.10E-21	GO:0043565,GO:0006355,GO:0003700	AT2G37430.1	AT2G37430.1,BZIP53	basic region/leucine zipper motif 53	BZIP transcription factor, putative
Sapur.0074G00.1	2.33827996	-3.420609279	0.257551177	-13.2813	2.97E-40	1.38E-39	purple	-0.723955663	8.93E-27		AT4G16447.1			hypothetical protein
Sapur.0060G2940600.1	57.33887022	-0.788249499	0.059350331	-13.2812	2.98E-40	1.38E-39	purple	-0.723400009	9.06E-28		AT5G14440.1	HSP20-like chaperones superfamily protein	HSP20-like chaperones superfamily protein	HSP20-like crystallin family protein
Sapur.0120G0201200.1	2.988035946	-2.207617974	0.316849021	-13.2796	3.04E-40	1.41E-39	purple	-0.712854653	1.57E-25	GO:0055114,GO:0020037,GO:0008379,GO:0004601	AT5G05260.1	Peroxidase superfamily protein	Peroxidase superfamily protein	peroxidase
Sapur.0162G0130600.1	379.2975917	0.383057959	0.036821115	13.26115	3.89E-40	1.80E-39	purple	-0.731881815	8.18E-28		AT5G65760.1	SBP1	S-ribonuclease binding protein 1	S-ribonuclease-binding protein SBP1, putative
Sapur.0195G0102600.1	159.7115593	-1.062307026	0.080188451	-13.2548	4.23E-40	1.96E-39	purple	-0.648818317	5.50E-22	GO:0055114	AT5G20120.1	CKX25	cytokinin oxidase/dehydrogenase 25	cytokinin oxidase 2
Sapur.0026B1500.1	224.9607251	0.95311595	0.068151816	13.25153	4.42E-40	2.04E-39	purple	-0.673977601	3.90E-22		AT1G14095.1			transmembrane protein, putative
Sapur.0062G2100.1	297.5182006	-0.620885322	0.031173693	-13.2455	4.79E-40	2.21E-39	purple	-0.738884604	2.32E-28		AT5G48270.1	GCR1	G-protein-coupled receptor 1	G-protein coupled receptor, putative
Sapur.0010G0583000.1	157.5099406	-0.884813204	0.066906313	-13.2152	7.17E-40	3.30E-39	purple	-0.738376099	2.61E-28	GO:0005515,GO:0006468,GO:0055114,GO:0004672	AT3G20270.1	BAM3	Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.0051G170000.1	133.0885283	-1.127594884	0.085485182	-13.2069	8.01E-40	3.68E-39	purple	-0.737481224	2.57E-28	GO:0016021	AT4G06720.1	TET1,TRN2	Tetraspanin family protein	tetraspanin family protein
Sapur.0072G100.1	3.456679228	2.433377948	0.184259071	13.20628	8.07E-40	7.71E-39	purple	-0.751303801	5.47E-30		AT2G32730.1			NA
Sapur.0084G200.1	3.516291333	2.405705288	0.182345623	13.20049	8.72E-40	4.01E-39	purple	-0.752495589	6.51E-30		AT3G32730.1			NA
Sapur.0110G0540001.1	3.109570949	-4.689892624	0.341136345	13.1813	1.12E-39	5.16E-39	purple	0.57580973	2.01E-15	GO:0046983	AT2G27670.1	basic helix-loop-helix (bHLH) DNA-binding family protein	bHLH DNA-binding domain protein, putative	bHLH DNA-binding domain protein, putative
Sapur.0180G0199900.1	10.32906897	-1.797146868	0.136387008	-13.1768	1.19E-39	5.47E-39	purple	-0.693899667	7.16E-24	GO:0046983,GO:0003677	AT5G60460.1	AGL62	AGAMOUS-like 62	SRF-type transcription factor (DNA-binding and dimerization domain) protein
Sapur.0050G0130600.1	98.13843955	-1.025821104	0.077197123	-13.1657	1.38E-39	6.32E-39	purple	-0.72790674	3.47E-27		AT5G29500.1			NA
Sapur.0180G0000300.1	26.08775358	-1.264491402	0.094218565	-13.1652	1.39E-39	6.37E-39	purple	-0.72257674	1.24E-26		AT4G33440.2	Homeodomain-like superfamily protein	Homeodomain-like superfamily protein	hypothetical protein
Sapur.0180G0199900.1	512.7185237	0.613251651	0.046756566	13.16029	1.48E-39	6.76E-39	purple	0.669524736	4.18E-22					NA
Sapur.0020G0972000.2	4.74837628	-2.043835183	0.155248559	-13.1585	1.52E-39	6.96E-39	purple	0.683063149	6.56E-23	GO:0000062	AT2G34230.1	ACBP3	acyl-CoA-binding domain 3	acyl-CoA binding protein
Sapur.0

Sapur.007G076300.1	7.29955642	-2.46993471	0.19913242	-12.303	8.72E-35	3.42E-34	purple	-0.7201148	1.28E-26	GO:0055114;GO:0020037;GO:0016705;GO:0005506	ATSG09970.1	CYP78A7	cytochrome P450 family 78, subfamily A, polypeptide 7
Sapur.010G281900.1	20.79591364	-1.08553637	0.09596429	-12.3018	8.86E-35	3.68E-34	purple	-0.66887723	1.51E-21	GO:0006468;GO:0004672;GO:0005524	ATSG14370.1	WAG2	Protein kinase superfamily protein
Sapur.010G285400.4	3.75451482	-2.42388604	0.10704958	-12.3009	8.93E-35	3.72E-34	purple	-0.68313664	9.16E-22	GO:0003824	ATSG27220.1		RNA-binding (RNA98)(RNP motifs) family protein
Sapur.005G045000.1	181.4185122	-0.58375444	0.04748068	-12.2979	9.30E-35	3.86E-34	purple	-0.70139408	1.49E-24		ATSG13690.1		PRL1-interacting factor, putative
Sapur.010G251400.1	585.4583698	1.64683163	0.13407582	12.2976	9.32E-35	3.87E-34	purple	-0.58617553	7.34E-16	GO:0016020;GO:0010333;GO:0008121;GO:0000287	ATSG25810.1		Terpenoid cyclases/Protein prenyltransferases superfamily protein
Sapur.011G020800.1	4.79614996	-1.72807323	0.14058207	-12.2604	9.83E-35	4.08E-34	purple	-0.59064612	3.89E-16	GO:0016020;GO:0008378;GO:0006486	ATSG05170.1		Galactosyltransferase family protein
Sapur.001G139700.1	137.7837621	0.73795169	0.06003926	12.29097	1.01E-34	4.20E-34	purple	-0.68229586	7.50E-23		ATSG45580.1		Homeodomain-like superfamily protein
Sapur.007G187400.1	48.03197923	-1.17769495	0.09589379	-12.2851	1.14E-34	4.76E-34	purple	-0.56805542	6.64E-16		ATSG16020.1	AtMYB43,MYB43	myb domain protein 43
Sapur.15W0037200.1	3.49705616	-1.79845628	0.14610351	-12.2759	1.22E-34	5.06E-34	purple	-0.75267649	5.27E-30				
Sapur.001G268000.1	11.26048839	-3.18368183	0.26079768	-12.2626	1.31E-34	7.39E-34	purple	-0.56891228	2.07E-20	GO:0006622;GO:0003824	ATSG15950.1	ATCCRL1,CCR1,IRX4	cinnamoyl coa reductase 1
Sapur.003G169100.1	3851.369506	-0.51384898	0.04189449	-12.2425	1.84E-34	7.61E-34	purple	-0.68146993	9.02E-22		ECT2		evolutionarily conserved C-terminal region 2
Sapur.010G161100.1	7.59819071	-0.66302574	0.13136408	-12.2389	1.90E-34	7.86E-34	purple	-0.70033313	1.84E-24		ATDP17,DEF17		ovate family protein 17
Sapur.017G031900.1	152.7564132	-0.75304044	0.06147618	-12.2324	2.09E-34	8.62E-34	purple	-0.70554309	5.93E-25	GO:0042578;GO:0042132;GO:0005975	ATSG64380.1		Inositol monophosphatase family protein
Sapur.014G287800.1	3.90269642	-2.70882107	0.25930926	-12.2311	2.12E-34	8.75E-34	purple	-0.65051504	1.17E-20		ATSG64680.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.006G228400.1	1.75184024	-2.21662308	0.26237801	-12.2264	2.17E-34	8.96E-34	purple	-0.68922886	2.88E-24	GO:0005515	ATSG19260.1		RING/FYVE/PHD zinc finger superfamily protein
Sapur.010G280800.1	1313.844669	-0.31364888	0.03135168	-12.2153	2.38E-34	9.83E-34	purple	-0.71266483	1.09E-26	GO:0005543	ATSG52820.1		ENTH/ANTH/VHS superfamily protein
Sapur.019G076600.1	456.2479093	0.50312768	0.04117535	12.21915	2.46E-34	1.01E-33	purple	-0.69226458	2.33E-24		ATSG47010.1		
Sapur.012G069500.1	88.62269659	1.86901202	0.15235788	12.20127	3.06E-34	1.26E-33	purple	-0.61627581	8.58E-18	GO:0016787	HXXXD-type acyl-transferase family protein		
Sapur.013G202000.1	10.01745548	-1.31305242	0.11258386	-12.1862	3.68E-34	1.51E-33	purple	-0.66273979	3.95E-24	GO:0005515	zinc finger (B-box type) family protein		
Sapur.009G203000.1	202.8705636	0.37231695	0.03050782	12.18182	3.89E-34	1.59E-33	purple	-0.67372625	6.01E-22	GO:0005634;GO:0003677	AtMBD5,MBD05,MBD5		methyl-CpG-binding domain protein 5
Sapur.15W0251400.1	17.14161466	-0.75966182	0.06227524	-12.1623	4.38E-34	1.80E-33	purple	-0.61518235	2.45E-20	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ASP5575.31		Leucine-rich receptor-like protein kinase family protein
Sapur.15W0111900.1	254.9788206	-0.34950723	0.02879378	-12.1383	6.62E-34	2.71E-33	purple	-0.69317806	8.32E-24	GO:0005515	ATSG14370.1	CHC1	SWIB/MDM2 domain superfamily protein
Sapur.003G205300.1	14.96015456	-1.40197702	0.11527819	-12.1354	6.86E-34	2.80E-33	purple	-0.70174701	1.56E-24		ATSG45140.1		Protein of unknown function (DUF241)
Sapur.018G105800.1	55.90501068	-1.84933424	0.15239424	-12.1352	6.88E-34	2.81E-33	purple	-0.69149702	1.18E-23	GO:0043531	ATSG50180.1		NB-ARC domain-containing disease resistance protein
Sapur.010G189800.1	240.3676266	-0.70882107	0.05841928	-12.13	7.33E-34	2.99E-33	purple	-0.65551195	1.12E-20		ATSG27230.1		Fragile-like protein
Sapur.012G089600.1	1.13244329	-2.94895842	0.28461897	-12.1269	7.60E-34	3.11E-33	purple	-0.66291129	8.66E-24		ATSG17200.1		polygalacturonase
Sapur.002G031200.1	908.4649661	-0.35240381	0.08659214	-12.1167	8.62E-34	3.52E-33	purple	-0.72343896	1.28E-26	GO:0055114;GO:0016491	ATSG06320.1		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Sapur.008G075600.1	1027.918879	-0.40145622	0.03325659	-12.1184	8.91E-34	3.64E-33	purple	-0.6695216	1.79E-21	GO:0005515;GO:0005634;GO:0003700;GO:0040881;GO:0003677	AGL4,SEP2		K-box region and MADS-box transcription factor family protein
Sapur.010G033300.1	195.5293366	-0.43136214	0.03630605	-12.1065	9.78E-34	3.98E-33	purple	-0.72496401	7.02E-27		ATSG10150.1		DNA/ RNA chaperone family protein
Sapur.7G087800.1	1.18938354	-2.47191144	0.30539391	-12.0943	1.13E-33	4.61E-33	purple	-0.67335048	5.78E-22				
Sapur.007G128200.1	650.1042518	-0.86765779	0.07175757	-12.0912	1.17E-33	4.78E-33	purple	-0.68953841	1.77E-23	GO:0055114;GO:0016491;GO:0008270	ATSG16370.1	AER,AT-AER	alkenal reductase
Sapur.010G179600.1	17.14161466	-0.75966182	0.06209381	-12.0903	1.18E-33	4.84E-33	purple	-0.61132731	2.63E-20		ASG4290.1		F-box protein-related
Sapur.013G125700.1	10.90859135	-2.35177348	0.10381461	-12.0578	1.76E-33	7.16E-33	purple	-0.73545889	6.45E-26		ATSG03630.1		Acyl-CoA N-acetyltransferase (NAT) superfamily protein
Sapur.010G261200.1	13.23139833	-1.32400946	0.10934128	-12.0521	1.89E-33	7.66E-33	purple	-0.67604276	1.45E-22	GO:0016020	ATMYB111,MYB111,PFG1		myb domain protein 111
Sapur.012G034200.1	1.68566391	-3.11943517	0.25898201	-12.0454	2.05E-33	8.31E-33	purple	-0.69962074	2.14E-24	GO:0008168			S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.013G083800.1	27.81918884	-1.03164213	0.09282853	-12.0306	2.45E-33	9.93E-33	purple	-0.68847523	2.47E-24		ATSG05150.1		Plant protein of unknown function (DUF247)
Sapur.15W0080300.1	11.05725651	-1.67602401	0.13964795	-12.0255	2.63E-33	1.06E-32	purple	-0.68595671	3.66E-23		ASP4753.1		
Sapur.002G134600.1	280.3022348	1.08233109	0.09005048	12.01805	2.86E-33	1.15E-32	purple	-0.63175438	7.21E-19		ATSG46670.1		Protein of unknown function (DUF581)
Sapur.010G139800.1	208.8231153	-0.52316197	0.04359928	-12.0048	3.13E-33	1.35E-32	purple	-0.68251035	7.12E-23	GO:0016747	ATSG45450.1		HXXXD-type acyl-transferase family protein
Sapur.002G010500.1	216.1963016	-1.40865891	0.11737821	-12.0015	3.49E-33	1.41E-32	purple	-0.62789882	1.36E-18				Chaperone DnaJ-domain superfamily protein
Sapur.006G070200.1	10.39720356	-1.26779243	0.10820569	-11.984	3.82E-33	1.54E-32	purple	-0.72384826	3.90E-27		APK1,APK1A		Protein kinase family protein
Sapur.15G2049600.1	123.724136	1.00728869	0.09177342	11.99399	3.82E-33	1.54E-32	purple	0.70121035	1.25E-24		ATSG35340.1	MEE29	helicase domain-containing protein
Sapur.009G262200.1	873.3610986	-0.35240381	0.03000117	-11.9869	4.16E-33	1.68E-32	purple	0.61691186	5.41E-21	GO:0005085	ATSG44410.1	ATOPT4,OPT4	oligopeptide transporter OPT family protein
Sapur.004G061400.1	22372.62681	0.63886522	0.05346587	11.94868	6.60E-33	2.65E-32	purple	0.52149726	2.06E-20		ATSG38540.1	ATLTP1,LP,LTP5	lipid transfer protein 1
Sapur.003G088100.1	2.36209437	1.96238144	0.24798015	11.94575	6.83E-33	2.74E-32	purple	0.61973417	8.81E-18	GO:0003723	AFUM412,FUM12		pumilio 12
Sapur.014G241200.1	374.6770883	-0.74548832	0.06251298	-11.9253	8.73E-33	3.50E-32	purple	-0.73921694	7.96E-28	GO:0055114;GO:0006468;GO:0005524;GO:0004672	ATSG43020.1		Leucine-rich repeat protein kinase family protein
Sapur.010G151800.1	485.8005605	0.50736708	0.04256541	11.92452	8.82E-33	3.53E-32	purple	0.67219194	5.92E-22	GO:0016021;GO:0008233;GO:0006465;GO:0005787	ATSG39960.1		microsomal signal peptidase 25 kDa subunit (SPC25)
Sapur.009G054545.1	1307.437756	-0.54913144	0.05025658	-11.9239	9.01E-33	3.57E-32	purple	-0.69325565	1.28E-24	GO:0005524	ATSG07200.2		Double Clp-N motif P-loop nucleoside triphosphate hydrolases superfamily protein
Sapur.001G052000.1	86.81317785	-0.92375359	0.07758766	-11.9059	1.13E-32	4.41E-32	purple	-0.68903645	2.49E-24	GO:0005515	ATSG21060.1		Leucine-rich repeat (LRR) family protein
Sapur.013G051200.1	1168.028092	-0.56592407	0.04751127	-11.9048	1.13E-32	4.42E-32	purple	-0.67580742	7.16E-22	GO:0016020	ATHIR1,HIR1		SPFH/Band 7/PHB domain-containing membrane-associated protein family
Sapur.003G146000.1	237.9896215	-0.32072783	0.02695286	-11.8995	1.19E-32	4.75E-32	purple	-0.68273451	7.00E-23		ATSG02550.1		
Sapur.002G070200.1	4.52069337	-1.75802144	0.14777024	-11.8968	1.23E-32	4.91E-32	purple	-0.69269445	1.48E-23	GO:0018884;GO:0015976;GO:0006564;GO:0009523;GO:0005509	ATSG27190.1	MsgL1Pab1DUF1795-like photosystem II reaction center PsbP family protein	
Sapur.004G087200.1	594.3616878	0.29988246	0.02521707	11.89504	1.26E-32	5.01E-32	purple	-0.67836588	1.66E-22		ATSG28970.1	AAR3	Domain of unknown function (DUF298)
Sapur.010G278300.1	131.1686573	0.75139549	0.06319487	11.8929	1.29E-32	5.14E-32	purple	-0.62633899	2.98E-18	GO:0016788	ATSG7161.2		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.010G176400.1	578.0752021	0.32186552	0.02707545	11.88889	1.32E-32	5.36E-32	purple	-0.68587931	3.72E-23	GO:0016021;GO:0004252	ATSG07950.1		rhomboid protein-related
Sapur.001G138800.1	184.7336051	-0.65426452	0.08014583	-11.8869	1.38E-32	5.52E-32	purple	-0.64682726	1.78E-20	GO:0043531	ATSG07040.1	RPM1,RPS3	NB-ARC domain-containing disease resistance protein
Sapur.010G105300.5	5.16454941	-2.01861484	0.17001659	-11.873	1.63E-32	6.51E-32	purple	-0.72437216	8.15E-27	GO:0005524	ATSG26230.1		TCP-1/cpn60 chaperonin family protein
Sapur.006G128100.1	18.15027544	-2.00086649	0.20928813	-11.8573	1.97E-32	7.80E-32	purple	-0.58233848	1.25E-15	GO:0016021;GO:0016020;GO:0022857	ATSG43650.1		nodulin MtN21 /EamA-like transporter family protein
Sapur.001G026700.1	20.24076588	-0.92600222	0.14336122	-11.8546	2.04E-32	8.07E-32	purple	-0.61972449	5.80E-18				
Sapur.010G181800.1	136.8077719	0.79495111	0.06706234	11.85348	2.06E-32	8.20E-32	purple	-0.67505456	3.17E-22		ATSG03680.1	PTL	Duplicated homeodomain-like superfamily protein
Sapur.010G136400.1	135.4555607	-0.29611	0.0840135	-11.845	2.08E-32	8.24E-32	purple	-0.68541097	4.08E-23	GO:0055114;GO:0016655;GO:0016020	ATSG02280.1		oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor
Sapur.010G075500.1	1.95036291	-2.75079209	0.24056541	-11.837	2.51E-32	9.95E-32	purple	-0.69269316	6.27E-24		ATSG29730.1		
Sapur.009G054545.1	455.5232877	0.58537909	0.04946915	11.83209	2.66E-32	1.06E-31	purple	-0.64426257	2.52E-20	GO:0006754;GO:0005524	ATSG27030.1	UGT71D5	UDP-glucosyltransferase 71D1
Sapur.017G115500.1	216.1815757	0.32658763	0.02764184	11.82685	2.84E-32	1.12E-31	purple	-0.68371673	5.75E-23	GO:0006914;GO:0005737	ATSG17290.1	APG5,ATATG5,ATG5	autophagy protein Atg5 family
Sapur.003G071500.1	93.41326274	-1.01820710	0.08402115	-11.8112	3.43E-32	1.35E-31	purple	-0.62804145	1.37E-19	GO:0016021;GO:0016020	ATMRP11,AWRY11	WRKY DNA-binding protein 11	
Sapur.014G066600.1	42.18668806	-0.71705195	0.06079569	-11.8052	3.67E-32	1.45E-31	purple	-0.70628319	4.94E-25				
Sapur.005G186400.1	1328.145461	-0.88089552	0.07523662	11.80435	3.71E-32	1.46E-31	purple	-0.61782171	1.46E-18	GO:0008234;GO:0006508	ATSG16190.1		Papain family cysteine protease
Sapur.003G064200.1	2.00643085	-1.47752275	0.26665568	-11.8022	3.80E-32	1.50E-31	purple	-0.67382182	2.14E-22	GO:0004866			
Sapur.001G136200.2	62.64928955	-0.57692804	0.04802344	-11.7687	5.65E-32	2.22E-31	purple	0.69816198	2.92E-24	GO:0005789	ATSG45140.1	PVA12	vesicle-associated membrane protein, putative
Sapur.017G053800.1	100.0232511	-0.01294659	0.08608463	-11.767	5.77E-32	2.27E-31	purple	-0.69228385	2.25E-23	GO:0055114;GO:0009186	ATT3D2,T3D2	Ferritin/ribonucleotide reductase-like family protein	ribonucleoside-diphosphate reductase small chain
Sapur.008G172900.1	287.9517213	0.61543289	0.05230234	11.76698	5.78E-32	2.27E-31	purple	-0.66669857	1.57E-21		ATSG18850.1		transmembrane protein, putative
Sapur.015G205100.1	67.09579848	-0.56680593	0.07184144	-11.7624	6.06E-32	2.38E-31	purple	-0.64733241	1.71E-20				hypothetical protein
Sapur.013G104800.1	257.6433487	-0.49464361	0.04205288	11.76085	6.21E-32	2.44E-31	purple	-0.67044056	7.08E-22		ATSG15600.1		transmembrane fusion protein Use1
Sapur.008G225100.1	4000.725124	-0.35848426	0.03060315	-11.7419	7.46E-32	2.92E-31	purple	-0.66948653	4.92E-21	GO:0019904	ATSG26130.1	14-3-3GFPA,GF14 KAPPA,G	general regulatory factor 11
Sapur.010G132100.1	14.35267959	-1.54684928	0.13165867	-11.7336	8.57E-32	3.36E-31	purple	0.57215751	4.97E-15	GO:0005515	ATSG19850.1		Phototropic-responsive NPH3 family protein
Sapur.007G025700.1	963.2696994	-0.35240381	0.04654172	-11.722	9.83E-32	3.85E-31	purple	-0.64034772	2.71E-19		ATSG67281.1		C2H2-like zinc finger protein, putative
Sapur.005G078400.1	93.31432172	-1.38054876	0.11788478	-11.7105	1.13E-31	4.40E-31	purple	-0.66841895	1.13E-21	GO:0008270;GO:0005515	ATG17452.1	RHA3A	RING-H2 finger 3A
Sapur.006G239800.1	717.0847293	0.32692925	0.02792281	11.70827	1.16E-31	4.51E-31	purple	0.72362603	9.65E-27	GO:0008270	ATSG10790.1	UBP26	ubiquitin-specific protease 22
Sapur.005G009065.1	12.68712939	-1.81751521	0.15487245	-11.6987	1.32E-31	5.07E-31	purple	-0.57298506	4.45E-15	GO:0005515	ATSG19190.1	ARSFR,FLR,FLS	receptor like protein 12
Sapur.001G010500.1	57.0765931	-0.78568574	0.07197224	-11.6922	1.40E-31	5.44E-31	purple	-0.69457638	6.93E-24		ATSG22410.1	SLO1	SLOW GROWTH 1
Sapur.7G008800.1	339.8792391	-0.35760202	0.03011851	-11.6647	1.93E-31	7.50E-31	purple	-0.84227423	1.34E-32	GO:0055124;GO:0003676;GO:0004386	ATSG48650.1		DEAD/H box RNA helicase family protein
Sapur.005G069600.1	7.00824681	-2.06386316	0.17526237	11.66467	1.93E-31	7.50E-31	purple	-0.66460349	2.28E-21		ATSG23370.1		GRAM domain-containing protein / ABA-responsive protein-related
Sapur.010G269100.1	7.85157703	-1.53819103	0.13204518	-11.649	2.12E-31	8.21E-31	purple	-0.70621568	5.12E-25		ATSG02020.1		
Sapur.009G051000.1	2.06059822	-2.08544978	0.26133587	-11.6292	2.93E-31	1.13E-30	purple	-0.64793874	4.65E-20		ATSG02220.1		hypothetical protein
Sapur.010G154500.1	5.43861798	-2.02545468	0.24311573	-11.6261	3.03E-31	1.17E-30	purple	-0.57974791	1.78E-15	GO:0006468;GO:0005524;GO:0004672	ATSG17190.1		Leucine-rich repeat transmembrane protein kinase family protein
Sapur.003G125900.1	13.97422742	-1.79647941	0.15454875	-11.624	3.11E-31	1.20E-30	purple	-0.65918378	6.25E-21	GO:0045454;GO:0015035;GO:0009055	ATSG47880.1		Glutaredoxin family protein
Sapur.006G089100.1	1023.129834	-0.35240381	0.03016484	-11.6208	3.11E-31	1.20E-30	purple	-0.67863018	2.37E-22	GO:0008299;GO:0006507;GO:0004553	ATSG47370.1	BGAL8	beta galactosidase 8
Sapur.005G087200.1	653.9423883	0.31963869	0.02750549	11.62184	3.18E-31	1.23E-30	purple	-0.65788233	7.91E-21		ATSG35890.1		winged-helix DNA-binding transcription factor family protein
Sapur.016G108200.1	674.6514849	0.36180248	0.03142252	-11.6183	3.19E-31	1.23E-30	purple	-0.68472018	5.04E-23		ATSG29880.1	TIR1	F-box/RNI-like superfamily protein
Sapur.003G044100.1	54.17668227	-0.06824612	0.00456207	-11.614	3.30E-31	1.26E-30	purple	-0.66882002	8.61E-22		ATSG19190.1		Receptor like protein 12
Sapur.004G101000.1	238.7142493	0.46510359	0.03834701	11.61389	3.50E-31	1.35E-30	purple	0.69151624	1.17E-23	GO:0005515	ATSG16405.1		Transducin/WD40 repeat-like superfamily protein
Sapur.009G129400.1	277.6628868	0.97078919	0.08363799	11.6023	4.16E-31	1.55E-30	purple	-0.67893316	1.77E-22		ATSG47140.1		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.010G105500.1	104.3329763	-0.02308215	0.08235846	-11.5902	4.62E-31	1.78E-30	purple	-0.71771264	1.84E-26	GO:0046983	ATSG68810.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.004G064800.1	1988.290008	-0.66310203	0.03682512	-11.5819	4.97E-31	1.91E-30	purple	-0.66861017	1.38E-21	GO:0016787;GO:0000786	ATSG19280.1	H2B,HTB9	Histone superfamily protein
Sapur.012G058200.1	18459.20781	1.31728368	0.11409349	11.54556	7.77E-31	2.98E-30	purple	-0.66348824	3.98E-21		ATSG15153.1	ATMT3,MT3	metallothionein 3
Sapur.008G047000.1	130.9518174	0.61303003	0.05314571	-11.5347	8.82E-31	3.38E-30	purple	-0.66006003	2.13E-21		ATSG14460.1		LRR and NB-ARC domains-containing disease resistance protein
Sapur.003G102600.1	746.015879	-0.66260337	0.05748894	-11.532	9.10E-31	3.48E-30	purple	-0.71473058	7.62E-26	GO:0043531;GO:0003700	ATSG64380.1		Integrase-type DNA-binding superfamily protein
Sapur.003G144000.1	6.11287377	-2.77538261	0.36275245	-11.5266	9.66E-31	3.69E-30	purple	-0.63972619	3.93E-19		ATSG29420.1	ATST2A,ST2A	sulfotransferase 2A
Sapur.009G065700.1	537.60293	0.62242871	0.05495303	11.50809	1.20E-30	4.56E-30	purple	-0.64729041	6.82E-20		ATSG10020.1		Protein of unknown function (DUF3005)
Sapur.010G280900.1	9.94957194	-1.46708221	0.12578136	-11.5042	1.26E-30	4.79E-30	purple	-0.72435378	8.10E-27		ATSG20160.1		Plant protein of unknown function (DUF247)
Sapur.011G160800.1	17.0563851	-1.12137903	0.09755474	11.50356	1.28E-30	4.88E-30	purple	0.64663081	1.85E-20	GO:0043565;GO:0006355;GO:0003700	AR431,ATWRKY14,WRKY14	WRKY DNA-binding protein 14	
Sapur.012G080600.1	26.95541697	-1.33295427	0.11505102	-11.4983	1.34E-30	5.13E-30	purple	-0.60289438	6.55E-17		ATSG47140.1		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.007G028800.1	24.83519729	-0.67205588	0.08473762	-11.4978	1.35E-30	5.15E-30	purple	-0.64221789	1.64E-19		ATSG60600.1		DNA/ribonucleotide/nucleoside/phosphate family protein
Sapur.008G168800.1	16.17298839	-1.41009982	0.12263	-11.4957	1.39E-30	5.28E-30	purple	-0.62075377	4.25E-18	GO:0008033	ATSG19040.1	ATIPT5,IPT5	isopentenyltransferase 5
Sapur.007G047500.1	544.2443165	-0.46480894	0.03888425	-11.4607	1.97E-30	7.56E-30	purple	0.66057649	1.52E-21	GO:0004554;GO:0015035;GO:0009055	ATSG77330.1		Glutaredoxin family protein
Sapur.012G078300.1	459.310604	0.40442716	0.03216494	11.48522	1.56E-30	5.95E-30	purple	0.63697816	3.03E-19	GO:0005515	ATSG4290.1	ATGP4	Ubiquitin family protein
Sapur.006G007500.1	139.8647633	0.73988434	0.06444543	11.48385	1.61E-30	6.12E-30	purple	0.66703037	4.97E-21		ATSG75330.1		Protein of unknown function (DUF3537)
Sapur.010G029700.1	7.96756035	-1.66588849	0.14525421	-11.4689	1.89E-30	7.18E-30	purple	-0.65950387	5.86E-21	GO:0005515	ATSG60440.2		Leucine-rich receptor-like protein kinase family protein
Sapur.010G186100.1	6.93283923	-2.05989891	0.17753111	-11.4684	1.90E-30	7.22E-30	purple	-0.59079548	3.85E-16		ATSG21280.1		
Sapur.006G230900.1	531.7828976	-0.61845627	0.07147864	-11.4604	2.12E-30	8.09E-30	purple	-0.65651649	2.58E-21	GO:0005085;GO:0016021;GO:0022857	ATSN4,IN74	inositol transporter 4	inositol transporter, putative
Sapur.013G135800.1	46.04023358	-1.21939143	0.10647628	-11.4522	2.29E-30	8.68E-30	purple	-0.65450823	1.46E-20		ATSG09280.1		transmembrane protein, putative
Sapur.006G280400.1	10.27042897	-0.92307254	0.11646155	-11.4401	2.64E-30	9.98E-30	purple	-0.64942234	3.58E-20	GO:0007076	ATSG70502.1		binding
Sapur.002G105600.1	1.09967838	-2.35266205	0.19244124	-11.4347	2.81E-30	1.06E-29	purple	-0.66519008	8.85E-16		ATSG47720.1	OSB1	Primozone PHB/single-strand DNA-binding
Sapur.010G139900.1	4864.917632	0.77733183	0.06800302	11.4299	2.97E-30	1.12E-29	purple	-0.63577568	2.68E-19				
Sapur.010G089100.1	41.60413345	-1.71885222	0.15010074	-11.4178	3.41E-30	1.29E-29	purple	-0.60598261	4.13E-17	GO:0046863;GO:0008171	ATSG15160.1		O-methyltransferase family protein
Sapur.013G082700.1	3.11368393	-2.12317903	0.19755474	-11.4027	3.98E-30	1.51E-29	purple	-0.72757428	1.11E-22	GO:0016868;GO:0005777	ATSG68010.1		peroxisome or glyoxysomal hydrolase with C2H2-type zinc finger domain
Sapur.010G233800.1	61.95300758	0.15032769	0.18879876	11.39044	4.67E-30	1.76E-29	purple	0.54498289	5.09E-13	GO:0006629	ATSG26580.1	PLA IIA,PLA2A,PLP2	phospholipase A 2A
Sapur.003G198600.1	3.03778397	-1.52450484	0.23188483	-11.3902	5.26E-30	1.96E-29	purple	-0.63807829	2.52E-19		ATSG45570.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.018G087000.1	13.67635053	1.42629188	0.12525312	11.38733	4.84E-30	1.82E-29	purple	-0.62600197	1.86E-18	GO:0016020;GO:0006070	ATSG29110.1	ATGLR2,B,GLR2,B	glutamate receptor 2.8
Sapur.002G171100.1	17984.46984	-0.55231497	0.04852296	-11.3857	4.93E-30	1.85E-29	purple	-0.64755212	4.96E-20	GO:0016020;GO:0009765	ATSG26810.1	LHCB2,LHCB2.1,LHCB2.4	photosystem II light harvesting chlorophyll A/B-binding protein
Sapur.011G050200.1	7.16442277	-2.08383284	0.18355729	-11.3564	5.39E-30	2.02E-29	purple	-0.61885079	1.47E-17	GO:0004587;GO:0005515;GO:0008483	ATSG46180.1	DCS1N-OAT	ornithine-delta-aminotransferase
Sapur.009G052100.1	4390.137778	0.76208409	0.06697556	11.37858	5.35E-30	2.01E-29	purple	-0.65981571	5.57E-21	GO:0030243;GO:0007017;GO:0005874	ATSG12250.1	TUB8	beta-6 tubulin
Sapur.010G313200.1	4.30062077	-2.39447409	0.21861385	-11.3776	5.48E-30	2.05E-29	purple	-0.67844147	1.02E-22	GO:0008295;GO:0006597;GO:0004014	ATSG18930.1	SAMDC4,SAMDC4	Adenosylmethionine decarboxylase family protein
Sapur.010G049500.1	79.22163373	-0.55137932	0.04862817	-11.3629	6.40E-30	2.40E-29	purple	-0.70543431	1.12E-25	GO:0003476	ATSG58470.1	ATRBP1,RBP1	RNA-binding protein 1
Sapur.010G170500.1	1.02597005	-2.27362624	0.20047883	-11.3606	6.61E-30	2.48E-29	purple	-0.66027738	1.08E-22	GO:0016787	ATSG20170.1		AP2/B3-like transcriptional factor family protein
Sapur.017G084100.1	10.33452019	-1.42657266	0.12588228	-11.3479	7.60E-30	2.85E-29	purple	-0.63049353	8.86E-19	GO:0007165;GO:0005515;GO:0043531	ATSG17680.1		disease resistance protein (TIR-NBS-LRR class), putative
Sapur.006G171100.1	39.71127551	-0.67746374	0.14026501	-11.3427	8.08E-30	3.02E-29	purple	0.59206584	2.56E-16				
Sapur.009G136100.1	438.4292487	-0.87587148	0.07729752	-11.3312	9.19E-30	3.46E-29	purple	-0.6912726	1.03E-23		ASG6270.1		hypothetical protein
Sapur.003G075200.1	11.93877958	1.03332734	0.09124396	11.32486	9.88E-30	3.69E-29	purple	0.61939969	1.68E-17	GO:0055737;GO:0000045	ATG8F	ATG8F	Ubiquitin-like superfamily protein
Sapur.010G164900.1	41.05963423	0.91688152	0.08097768	11.32273	1.01E-29	3.78E-29	purple	0.61428285	1.75E-17				Exostosin family protein
Sapur.010G041400.1	1306.149052	0.79304746	0.07015095	11.309	1.18E-29	4.42E-29	purple	0.61393342	7.00E-19	GO:0055114;GO:0016491;GO:0008270	ATSG22440.1		Zinc-binding alcohol dehydrog

Sapur.0086136500.1	441.5947547	0.504168587	0.047183165	-10.6853	1.19E-26	4.17E-26	psmile	-0.644910929	7.85E-20	AT2G37730.2	NAD(P)-linked oxidoreductase superfamily protein	aldo-keto reductase family protein
Sapur.0106016500.1	16.50573909	1.167066874	0.107552384	-10.665	1.48E-26	5.17E-26	psmile	-0.670719786	7.29E-22	GO:0006468,GO:0005524,GO:0004672	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.0106180100.1	9.180893945	2.220422944	0.209211682	-10.609	1.51E-26	5.40E-26	psmile	-0.570130604	6.48E-15	GO:0005975,GO:0004553	beta glucosidase 23	NA
Sapur.0106126500.1	772.7960099	-0.517003067	0.048587982	-10.6597	1.57E-26	5.47E-26	psmile	-0.684801944	4.63E-23	GO:0005515	Leucine-rich repeat (LRR) family protein	LRR receptor-like kinase EXS
Sapur.0106136000.1	157.1653839	-0.543251169	0.050987876	-10.6566	1.61E-26	5.66E-26	psmile	-0.681290318	6.47E-23			hypothetical protein
Sapur.0105138400.1	12.64128687	-0.986082524	0.092620019	-10.6563	1.63E-26	5.68E-26	psmile	-0.661735027	3.90E-21	GO:0016747	HXXXD-type acyl-transferase family protein	taxadien-5-alpha-ol O-acetyltransferase, putative
Sapur.0106077100.1	140.6668294	0.514585193	0.048329959	10.65298	1.69E-26	5.88E-26	psmile	-0.60981725	3.65E-17	GO:0008270	HAD(PFV4/PHD zinc finger superfamily protein	zinc finger protein, putative
Sapur.0106124700.1	207.5648834	0.807166495	0.084248803	10.6491	1.76E-26	6.12E-26	psmile	-0.62074181	4.25E-18			hypothetical protein
Sapur.0108029600.1	3992.843958	-0.710024597	0.066798617	-10.6293	2.18E-26	7.55E-26	psmile	-0.668376988	1.05E-21	GO:0005975,GO:0004553	alpha-xylosidase 1	alpha-xylosidase
Sapur.0106029600.1	1.344584736	-1.278864458	0.120254238	-10.6227	2.36E-26	8.20E-26	psmile	-0.616154574	7.9E-18		arabinogalactan protein 31	pollen protein Che E-like protein
Sapur.0070193400.1	155.4345228	0.866286307	0.07966019	10.6237	2.31E-26	8.02E-26	psmile	-0.597536199	1.44E-16	GO:0008153,GO:0008824	nicotinamidase 1	isochorismatase family protein
Sapur.0106127500.1	241.2512524	-0.495861054	0.135167399	-10.6228	2.34E-26	8.10E-26	psmile	-0.548894624	8.73E-16	GO:0004331	NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.0113125500.1	269.5581161	-0.462357289	0.045353329	-10.6215	2.37E-26	8.20E-26	psmile	-0.662074522	3.68E-21	GO:0055085,GO:0022857,GO:0016021	Major facilitator superfamily protein	polyol/monosaccharide transporter, putative
Sapur.0086298800.1	21.85142772	0.814256611	0.077218388	-10.6449	2.37E-26	9.91E-26	psmile	-0.585616168	4.57E-16	GO:0006950	Adenine nucleotide alpha hydrolases-like superfamily protein	external stress family protein
Sapur.0152029400.1	11.00558854	0.874232544	0.082473626	10.60015	2.98E-26	1.03E-25	psmile	-0.659058818	6.39E-21			NA
Sapur.0105121200.1	103.2205429	0.828209337	0.078491149	10.55576	3.12E-26	1.08E-25	psmile	-0.623843697	1.08E-21			AwPGT-9 rapidly elicited protein, putative
Sapur.0135253200.1	479.8859238	0.420892881	0.039736004	10.59223	3.24E-26	1.12E-25	psmile	-0.604764614	4.96E-17	GO:0006355,GO:0003677	CAB/LHCB/LHCP	Dof zinc finger protein
Sapur.0023107500.1	412.2426992	-0.820278925	0.056916429	-10.5888	3.36E-26	1.16E-25	psmile	-0.667342012	1.38E-21		exocyst complex component sec3A	exocyst complex component Sec3
Sapur.0135107200.1	41.83439799	-0.553895981	0.058022329	-10.5955	4.58E-26	1.58E-25	psmile	-0.628892855	1.58E-21	GO:0000062	acyl-CoA-binding protein	NA
Sapur.7005900.1	301.1644608	0.3688109	0.034934761	10.55713	4.71E-26	1.62E-25	psmile	-0.672306425	4.53E-22		Uncharacterized conserved protein (DUF2215)	transmembrane protein, putative
Sapur.0036284100.1	6.778023867	-1.275132169	0.12452211	-10.5159	4.87E-26	1.68E-25	psmile	-0.618438231	4.17E-21		Plant protein of unknown function (DUF1191)	NA
Sapur.0106111300.1	385.2982531	-0.428469324	0.040599138	10.55366	4.89E-26	1.68E-25	psmile	-0.629266164	2.06E-18			hypothetical protein
Sapur.0113126300.1	10.24577522	-0.990585814	0.093819681	-10.5528	4.93E-26	1.70E-25	psmile	-0.619267157	2.99E-19	GO:0016747	GCL2	lanthionine synthetase C-like protein
Sapur.0146122300.1	1282.239304	0.737725007	0.069942191	10.54764	5.21E-26	1.79E-25	psmile	-0.6485426	4.18E-20			pirin-like protein
Sapur.0106294500.1	145.9258125	0.814256611	0.077218388	-10.5449	5.36E-26	1.84E-25	psmile	-0.614042884	2.11E-17	GO:0016853,GO:0009507	ACC3	allene oxide cyclase
Sapur.0142030000.1	17.19527826	-1.426824046	0.135153837	-10.54225	5.52E-26	1.90E-25	psmile	-0.561752996	1.94E-14		inositol polyphosphate 5-phosphatase 11	NA
Sapur.0146291300.1	3.126561025	-2.822324895	0.1730024621	-10.523	6.09E-26	2.09E-25	psmile	-0.668774223	4.01E-20	GO:0006508,GO:0004190	Eukaryotic aspartyl protease family protein	aspartic proteinase nepenthesin-1 protein
Sapur.0055124500.1	513.8182144	-0.675291258	0.058546479	-10.5243	6.47E-26	2.26E-25	psmile	-0.668079015	1.20E-21	GO:0005515,GO:0006468,GO:0004672	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.0035144800.1	247.7427813	0.976777955	0.092833852	10.52179	6.86E-26	2.35E-25	psmile	-0.589387414	4.64E-16		Protein of unknown function (DUF581)	ethphon-induced protein
Sapur.0010044800.1	24.82820559	-0.737347161	0.078616396	-10.5213	6.88E-26	2.36E-25	psmile	-0.630281513	4.19E-19		nuclear factor Y, subunit C13	histone-like transcription factor, putative
Sapur.7120000.1	7.596029339	1.10418325	0.104973631	10.51864	7.09E-26	2.43E-25	psmile	-0.642509873	1.19E-19		splicing factor-related	NA
Sapur.7063400.1	1.628123898	-2.676232127	0.25468211	-10.5175	7.17E-26	2.46E-25	psmile	-0.618388231	1.98E-18		Plant protein of unknown function (DUF247)	NA
Sapur.0105237900.1	1345.866391	-0.258508351	0.024587799	-10.5137	7.47E-26	2.56E-25	psmile	-0.674011155	8.88E-22	GO:0003676	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA-recognition motif 2 in RNA-binding protein musashi-like musashi protein
Sapur.7103700.1	0.95125434	2.903408624	0.27621659	10.50754	7.97E-26	2.73E-25	psmile	-0.623037515	2.88E-18			NA
Sapur.0170090000.1	1.064101612	-3.056717636	0.291238317	-10.4956	9.05E-26	3.10E-25	psmile	-0.613060924	1.42E-17			hypothetical protein
Sapur.0106294100.1	7.925056511	-1.661257592	0.15771561	-10.4944	9.17E-26	3.14E-25	psmile	-0.614238211	4.32E-21			NA
Sapur.7152100.1	6.40921596	1.181837557	0.1126291	10.49318	9.28E-26	3.17E-25	psmile	-0.657206155	1.68E-20			
Sapur.0036115600.1	11.47605005	1.318882212	0.125781178	10.48689	9.92E-26	3.39E-25	psmile	-0.59046767	3.98E-16	GO:0016887,GO:0005524	ATO	splicing factor-related
Sapur.0106248800.1	28.64215705	-0.633272224	0.060405972	-10.4884	1.01E-25	3.52E-25	psmile	-0.6334682	4.13E-20		MCM9	root determined nodulation protein
Sapur.7157100.1	1.996904916	2.498554739	0.238408884	10.48048	1.06E-25	3.63E-25	psmile	-0.651804657	2.35E-20			NA
Sapur.0118260600.1	15588.73204	-0.266275457	0.097459333	-10.4729	1.15E-25	3.93E-25	psmile	-0.645576202	7.20E-20	GO:0016788	GDSL-like Lipase/Acylhydrolase superfamily protein	NA
Sapur.0016171300.1	1360.515158	-0.514803788	0.049190334	-10.4655	1.24E-25	4.24E-25	psmile	-0.675824254	2.73E-22	GO:0005975,GO:0004553	GTBM/L/KM/14	beta-D-xylosidase/alpha-L-arabinofuranosidase
Sapur.0056233000.1	8.526568884	-1.346125	0.131173092	-10.4623	1.27E-25	4.34E-25	psmile	-0.616791204	2.01E-18	GO:0016758,GO:0008152	UDP-glucuronosyltransferase 85A5	UDP-glucuronosyltransferase family protein
Sapur.0162277800.1	216.7995236	0.478852636	0.045775587	10.46087	1.31E-25	4.45E-25	psmile	-0.556845403	1.70E-16	GO:0007264,GO:0005525	Ras-related small GTP-binding family protein	septum-promoting GTP-binding protein
Sapur.0116164400.1	526.5897718	-0.652287784	0.064804586	-10.4061	1.46E-25	4.96E-25	psmile	-0.62852278	8.36E-19		Pollen Ole e 1 allergen and extensin family protein	pollen ole e 1 allergen and extensin family protein
Sapur.0161186000.1	149.242315	-0.380833604	0.132096576	-10.4532	1.42E-25	4.83E-25	psmile	-0.604540938	5.12E-17	GO:0005515,GO:0006468,GO:0004672	Leucine-rich repeat transmembrane protein kinase	receptor-like kinase, putative
Sapur.0146241400.1	3.674078556	-2.191867693	0.21166447	-10.4462	1.52E-25	5.16E-25	psmile	-0.64188115	1.32E-19		Leucine-rich repeat (LRR) family protein	Serine/Threonine kinase, plant-type protein%2C putative
Sapur.0055185200.1	108.6230614	-0.546255189	0.067869323	-10.44	1.63E-25	5.56E-25	psmile	-0.602213641	3.99E-17	GO:0006355,GO:0003677	BLH11	BELL-like homeodomain 11
Sapur.0086116600.1	150.1042469	-0.598883033	0.057373576	-10.4384	1.68E-25	5.63E-25	psmile	-0.649342411	5.55E-20	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATPSKR1,PSKR1	phytosulfokine receptor 1
Sapur.0060293500.1	26.47434405	-0.633272224	0.060405972	-10.4884	1.01E-25	3.52E-25	psmile	-0.643304743	1.53E-19			Endoplasmic reticulum vesicle transporter protein
Sapur.0096294100.1	85.75244632	-0.029183335	0.008677221	-10.4298	1.81E-25	6.16E-25	psmile	-0.549834137	2.51E-12	GO0005524	BC51	cytochrome BC1 synthesis
Sapur.0118260600.1	366.7989704	-0.425291258	0.05960511	-10.4223	1.96E-25	6.66E-25	psmile	-0.642832171	1.94E-20			Pentatricopeptide (PPR-like) superfamily protein
Sapur.0180284800.1	84.24662219	0.624252895	0.059606151	10.4205	2.00E-25	6.79E-25	psmile	-0.609275789	2.35E-17	GO0005515	SKIP1	SKP1 interacting partner 1
Sapur.0105287500.1	288.1917174	-0.680867025	0.076997337	-10.4196	2.02E-25	6.85E-25	psmile	-0.613267442	1.37E-17			glutamine synthetase, putative
Sapur.0196102500.1	7.861199068	-1.713182093	0.16645628	-10.4185	2.04E-25	6.93E-25	psmile	-0.654880595	1.57E-20			NA
Sapur.0106200500.1	739.6236127	-0.314554607	0.03012324	-10.4148	2.12E-25	7.20E-25	psmile	-0.674067941	3.84E-22		ATSUN1,SUN1	SadU/unc-84 domain protein 1
Sapur.0031467600.1	1.004855211	-2.844327322	0.273372962	-10.4046	2.36E-25	8.01E-25	psmile	-0.664132523	2.51E-21	GO:0042546,GO:0016020,GO:0008107	ATFT1,ATFUT1,FT1,MUR2	fucosyltransferase 1
Sapur.0080237400.1	1208.409115	0.203197018	0.019501855	10.40184	2.43E-25	8.26E-25	psmile	-0.618235881	3.75E-19	GO0005515	PLAT2 transmembrane family protein	LRR-like disease resistance protein
Sapur.0105341000.1	502.6147043	-0.308428261	0.047298305	-10.3928	2.68E-25	9.05E-25	psmile	-0.643341221	1.01E-19		prenylated RAB acceptor 1.B4	prenylated rab acceptor protein, putative
Sapur.0110289400.1	26.18587553	0.80328258	0.077552048	10.39081	2.73E-25	9.24E-25	psmile	-0.62103883	2.92E-18	GO0008168,GO0008168	5-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase domain protein
Sapur.0070283300.1	1.420478355	-2.191867693	0.16768452	-10.3838	2.92E-25	9.87E-25	psmile	-0.618970006	1.58E-19	GO:0016020,GO:0008810,GO:0005215	Major facilitator superfamily protein	MFS transporter
Sapur.0071261000.1	8.798211128	-1.758889895	0.169389196	-10.3849	2.90E-25	9.82E-25	psmile	-0.585459	8.07E-16	GO:0006468,GO:0005524,GO:0004672	PRSK	PRS-like receptor kinase
Sapur.0105618500.1	105.4667606	0.537561631	0.051776178	10.37843	3.12E-25	1.05E-24	psmile	-0.598057482	1.38E-16			Ribosomal L18p/L5e family protein
Sapur.0106060600.1	1827.431662	-0.653482377	0.062992763	-10.3739	3.26E-25	1.10E-24	psmile	-0.661213023	4.31E-21	GO0005524,GO0005515	GO0006508,GO0004190	Eukaryotic aspartyl protease family protein
Sapur.0106296600.1	29.10800314	-1.204224002	0.116142049	-10.3612	3.72E-25	1.26E-24	psmile	-0.562305182	2.32E-14			NA
Sapur.0070209700.1	184.2212002	0.574170340	0.055417135	10.36088	3.74E-25	1.26E-24	psmile	-0.631812984	7.12E-19			cold acclimation protein WCOR413 family
Sapur.0106302200.1	3.423473007	-2.016846427	0.197950431	-10.3572	3.88E-25	1.31E-24	psmile	-0.55682153	1.27E-14			NA
Sapur.0046204200.1	5.308528399	-1.941907495	0.187606561	-10.3511	4.14E-25	1.40E-24	psmile	-0.676372976	8.09E-22			
Sapur.0020392300.1	34.19685068	-0.879692253	0.085091859	-10.3417	4.56E-25	1.54E-24	psmile	-0.633874243	5.00E-19	GO0005515	GT8B6	Pentatricopeptide repeat (PPR) family protein
Sapur.0051124000.1	176.1478474	-0.607947527	0.057808484	-10.3345	4.98E-25	1.65E-24	psmile	-0.607704398	4.16E-17	GO0006468,GO0005524,GO0004672	GT5D	Serine/Threonine kinase domain protein
Sapur.0162803800.1	272.3244617	0.33117783	0.032038365	10.33047	5.13E-25	1.73E-24	psmile	-0.621418807	3.99E-18		VPS22	vacuolar-sorting protein SNF8
Sapur.0046204700.1	11.3097259	1.007819163	0.098126779	10.32955	5.18E-25	1.74E-24	psmile	-0.617248292	7.37E-18			NA
Sapur.0105009500.1	548.7473878	-0.477444356	0.046135434	10.30849	6.45E-25	2.17E-24	psmile	0.60112293	8.52E-17			hypothetical protein
Sapur.0051171200.1	706.6495201	-0.302884513	0.029243523	-10.2684	7.55E-25	2.52E-24	psmile	-0.643417789	6.12E-19	GO0003676	CID11	CTC-interacting domain 11
Sapur.0106095900.1	225.708891	-0.664251119	0.062556621	-10.2917	7.68E-25	2.57E-24	psmile	-0.62608096	1.82E-18		ATHMT-1,HMT-1	Homocysteine S-methyltransferase family protein
Sapur.0051171200.1	688.6981353	-0.307565164	0.045427131	-10.2882	7.97E-25	2.67E-24	psmile	-0.613707406	2.57E-18		PLAT2 transmembrane family protein	MLA2 transcription factor
Sapur.0106106100.1	265.9572115	-2.172462951	0.211364623	-10.2783	8.83E-25	2.95E-24	psmile	-0.777569136	5.44E-33	GO0016758,GO08152	UGT78D2	UDP-glucosyl transferase 78D2
Sapur.0130244800.1	42.13419973	0.597369588	0.058130014	10.273	9.33E-25	3.12E-24	psmile	-0.62302912	2.07E-19			Calcium-binding EF-hand family protein
Sapur.0046139800.1	65.69845495	-1.002485156	0.11611843	-10.2702	9.60E-25	3.21E-24	psmile	-0.6287609	4.71E-24			Protein of unknown function (DUF640 and DUF632)
Sapur.0180100300.1	981.3477161	-0.834200988	0.081938768	-10.2534	1.14E-24	3.81E-24	psmile	-0.598893862	1.18E-16	GO0006055	ATBCL8,BCL5,AAG14	blue-copper-binding protein
Sapur.0106264600.1	739.8021137	-0.521018276	0.051968832	-10.2519	1.16E-24	3.87E-24	psmile	-0.63797661	2.62E-19			Rhodanese/Cell cycle control phosphatase superfamily protein
Sapur.0096139900.1	13.80808707	1.066566679	0.104066736	10.24887	1.20E-24	3.99E-24	psmile	-0.60827879	2.93E-17			alpha/beta-hydrolases superfamily protein
Sapur.0070211900.1	2.208993317	-2.569826338	0.25368259	-10.2479	1.21E-24	4.03E-24	psmile	-0.604105451	1.47E-17	GO0006355,GO0003677	ANACS37,VND1	vascular-related NAC-domain protein 1
Sapur.0162203500.1	12.98508819	-1.669422231	0.164121573	-10.2472	1.22E-24	4.06E-24	psmile	-0.643929004	9.30E-20			Major facilitator superfamily protein
Sapur.0106106100.1	161.2062243	-1.083329941	0.105798605	-10.2384	1.33E-24	4.46E-24	psmile	-0.598918318	1.16E-16	GO0006468,GO0005524,GO0004672	ATNXE6,JBO1,NDX6	NUDIX (nexo or nex-related)6
Sapur.0146144100.1	13.20726653	-1.010661825	0.098739269	-10.2352	1.38E-24	4.59E-24	psmile	-0.633783399	5.16E-19	GO0015121	ATZP4	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.0105265500.1	135.2523904	-0.667106155	0.064117711	-10.2341	1.38E-24	4.61E-24	psmile	-0.590881392	1.94E-16	GO0005515	ABI2,SK10	Leucine-rich repeat (LRR) family protein
Sapur.0151122800.1	319.0797052	0.315877652	0.030888721	10.22598	1.52E-24	5.06E-24	psmile	-0.656545394	1.01E-20	GO0005515		ubiquitin family protein
Sapur.0162079100.1	31.95818806	-1.55051448	0.151669331	-10.2243	1.54E-24	5.13E-24	psmile	-0.623042294	2.95E-18	GO0006810,GO0005525	SAICP,CSP94,FFC,SRP54CF	chloroplast signal recognition particle 54 kDa subunit
Sapur.0050434500.1	2.931378836	-1.767065695	0.173015809	-10.2088	1.66E-24	5.51E-24	psmile	-0.56558125	1.18E-14			Protein of unknown function (DUF167)
Sapur.0106263000.1	107.2568406	-0.836605881	0.081918391	-10.2183	1.72E-24	5.71E-24	psmile	-0.644429614	8.53E-20	GO0008080		GNAT family acetyltransferase
Sapur.0106266500.1	2.545826537	-0.066316088	0.020377483	-10.2112	1.77E-24	5.86E-24	psmile	-0.604209442	5.96E-17		EXO84B	exocyst component 84B
Sapur.0105245900.1	1.213617001	-2.271483229	0.32057863	-10.2049	1.88E-24	6.25E-24	psmile	-0.571605251	3.32E-15	GO0005975,GO0004553	BG1	beta-1,3-glucanase 1
Sapur.0175130400.1	311.2934692	0.706824028	0.069332026	10.19216	2.13E-24	7.12E-24	psmile	-0.62084824	5.17E-18	GO0016788	GLIP1	GDSL lipase/esterase
Sapur.0145122100.1	6.273923906	-1.510323282	0.14829405	10.18465	2.32E-24	7.68E-24	psmile	-0.59125245	2.97E-16	GO0005515,GO0016491	ATP4H-1	PsbH isoform 1
Sapur.0080232600.1	29.01508052	-0.502861707	0.10341476	-10.1832	2.36E-24	7.79E-24	psmile	-0.61269063	1.55E-18	GO0005515		NA
Sapur.0070252900.1	1.447429762	-2.082798044	0.302788425	-10.1816	2.40E-24	7.92E-24	psmile	-0.528478596	1.22E-15	GO0005975,GO0004553		glycosyl hydrolase family protein with chitinase insertion domain
Sapur.0106180000.1	758.4513328	-0.327398286	0.035288063	10.18329	2.46E-24	7.94E-24	psmile	-0.614374658	1.02E-17	GO0016491,GO0006561		Cytochrome P450 family
Sapur.0030680000.1	431.8834644	0.470585950	0.046261684	10.17234	2.64E-24	8.71E-24	psmile	-0.639039191	2.12E-19	GO0006415,GO0003747	Class I peptide chain release factor	immature colon carcinoma transcript 1 protein
Sapur.0162065500.1	1.286563699	-3.205338939	0.315167382	-10.1708	2.68E-24	8.86E-24	psmile	-0.54634704	1.46E-13	GO0080017,GO0070310	microtubule-associated proteins 70-5	myosin II heavy chain-like protein
Sapur.0162645800.1	688.1272155	-0.658380718	0.064913283	-10.1697	2.71E-24	8.97E-24	psmile	-0.611738916	7.91E-18	GO0005975,GO0004650	Pectin lyase-like superfamily protein	polygalacturonase(glycosyle hydrolase family protein
Sapur.0020864600.1	1113.738792	0.309368152	0.030435519	10.16866	2.75E-24	9.09E-24	psmile	-0.619325883	1.68E-17			ubiquitin fold modifier-conjugating enzyme
Sapur.0061277500.1	1.691744882	-2.264267076	0.342041579	-10.1665	2.80E-24	9.25E-24	psmile	-0.605815135	4.34E-17	GO0043565,GO0005635,GO0003700,GO0009408	AT-HSFA6B,HSFA6B	heat shock transcription factor
Sapur.0180280200.1	22.39174502	-1.450804077	0.142755049	-10.1636	2.88E-24	9.51E-24	psmile	-0.623852573	4.03E-18			transmembrane protein, putative
Sapur.0105266700.1	1441.050269	-0.567487856	0.058432123	-10.1614	2.92E-24	9.65E-24	psmile	-0.644896209	9.94E-20	GO0004781	APS3	Pseudouridine synthase/archaeosine transglycosylase-like family protein
Sapur.0106145500.1	231.1566084	0.767789443	0.075175752	10.13908	3.71E-24	1.22E-23	psmile	-0.607136424	3.48E-17	GO0055114,GO0020037,GO0016705,GO0005506	ATR4,CYP450.1,RED1,RNT1	cytochrome P450, family 83, subfamily B, polypeptide 1
Sapur.0070188700.1	984.3088287	0.180347319	0.18657665	10.137	3.76E-24	1.25E-23	psmile	-0.615319014	9.61E-18	GO0055114,GO0020037,GO0006979,GO0004601	RC1,RC1A	Peroxidase superfamily protein
Sapur.0062061300.1	571.938396	-0.346876349	0.034049152	-10.1309	4.03E-24	1.33E-23	psmile	-0.636257084	3.42E-19			RotaGAP/TBC domain protein
Sapur.0070192500.1	6.347318822	1.583983071	0.15762558	10.10426	5.29E-24	1.75E-23	psmile	-0.552803706	6.06E-14			epoxide hydrolase
Sapur.7127200.1	2.496467674	1.831837296	0.180079888	10.09761	5.64E-24	1.85E-23	psmile	-0.700795593	1.64E-24		ATIMH1,FIM1	Fimbrin 1
Sapur.0146127500.1	1.720076431	-2.628254401	0.261453857	-10.0907	6.07E-24	1.99E-23	psmile	-0.559076984	1.04E-16		CLE20	CLAVATA/ESR-RELATED 20
Sapur.0056112000.1	6.718955444	-1.208275	0.120000164	-10.0885	6.21E-24	2.04E-23	psmile	-0.621032622	3.88E-18			Transmembrane protein family protein
Sapur.0010221900.1	217.9461021	-0.276619219	-0.08866	6.336	2.26E-23	2.07E-23	psmile	-0.652080801	2.26E-20			sequence-specific DNA binding transcription factors
Sapur.0105880200.1	28.98023392	-0.867837926	0.080186174	10.8247	2.34E-23	2.14E-23	psmile	-0.64422966	2.52E-20	GO0005885,GO0016020,GO0152997,GO0152338,GO0008855		MATE efflux family protein
Sapur.0180090600.1	88.93162519	-0.774066152	0.076894825	-10.078	6.91E-24	2.26E-23	psmile	-0.573308842	2.55E-15			transmembrane protein, putative
Sapur.0106142300.1	5.832853471	-1.192164	0.118398281	-10.0717	7.27E-24	2.41E-23	psmile	-0.644308308	6.29E-20	GO0006355,GO0003677		Dof-type zinc finger DNA-binding family protein
Sapur.0162749500.1	1293.913014	0.47329979	0.046801066	10.07028	7.48E-24	2.46E-23	psmile	-0.618464999	6.09E-18	GO0016758,GO08152	UGT74E2	UDP-glucosyltransferase family protein
Sapur.0030680000.1	134.2905255	-0.652371386	0.065011573	-10.0371	7.68E-24	2.54E-23	psmile	-0.61794986	4.6E-18			hypothetical protein
Sapur.0020650800.1	141.674804	0.994514052	0.098783421	10.06762	7.68E-24	2.51E-23	psmile	-0.610888887	7.62E-17			NA
Sapur.0162282500.1	7.407262895	-1.13118349	0.112463587	-10.0582	8.45E-24	2.75E-23	psmile	-0.605969601	4.11E-17	GO0043531		NB-ARC domain-containing disease resistance protein
Sapur.7079480.1	2.578556661	-1.8162851	0.180577263	10.05822	8.46E-24	2.75E-23	psmile	-0.679768667	2.26E-22			NA
Sapur.0096200900.1	226.8008029	0.331434412	0.032985118	10.048	9.38E-24	3.05E-23	psmile	-0.593288897	2.67E-16			plant/mmx00-1480 protein, putative
Sapur.0105180800.1	26.61324	-0.667237888	0.065187587	-10.0241	1.01E-23	3.28E-23	psmile	-0.654880389	1.38E-20	GO0005515,GO0006468,GO0005524,GO0004672		LRR receptor-like kinase
Sapur.1590G0730800.1	0.668806056	2.866862946	0.28391947	-10.0274	1.15E-23	3.75E-23	psmile	-0.725328058	6.45E-27	GO0000160	ARR17,RR17	response regulator 17
Sapur.0020387000.1	16.42449969	1.072886169	0.107165386	10.01087	1.23E-23	4.00E-23	psmile	-0.601452272	1.13E-17	GO0003676		RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.0105221400.2	1.546903071	-2.638031898	0.263626764	10.01007	1.38E-23	4.46E-23	psmile	-0.629031618	1.13E-18		RGLG2	RING domain ligase2
Sapur.0106294700.1	139.4828649	-0.662299192	0.067000115	10.00946	1.38E-23	4.46E-23	psmile	-0.624891761	1.14E-18	GO0016788		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.0171061700.1	869.7232394	0.487514467	0.048678732	10.00754	1.41E-23	4.57E-23	psmile	-0.601207122	8.41E-17	GO0016853,GO0005975		Galactose mutarotase-like superfamily protein
Sapur.0070133800.1	13.30449502	0.156704352	0.115863368	-9.98507	1.77E-23	5.72E-23	psmile	-0.650377966	2.84E-20	GO0005881,GO0000398,GO0000387		spliceosome protein-related
Sapur.0145604700.1	8.958881615	-0.997274152	0.09694221	-9.98301	1.81E-23	5.86E-23	psmile	-0.618977294	2.16E-19			ATP binding cassette cell binding/helicases
Sapur.0061317000.4	13.7393931	1.064564065	0.106568634	9.961607	2.24E-23	7.23E-23	psmile	-0.579410702	1.86E-15	GO0016791,GO0006633	FATB	fatty acyl-ACP thioesterases B
Sapur.0071202800.1	132.9341688	0.820446833	0.08816469	9.9302	2.34E-23	7.68E-23	psmile	-0.60664149	3.12E-17	GO0008429	PLA IIA,PLP7	patatin-like protein 6
Sapur.0036203900.1	1724.426257	0.625005439	0.062887434	9.938479	2.83E-23	9.10E-23	psmile	-0.628055663	1.32E-18		JASZ,TTF1S3B	jasmonate-zim-domain protein 6
Sapur.0146389700.1	18.82551173	0.748208663	0.07535142	9.9332	2.91E-23	9.35E-23	psmile	-0.717205376	3.32E-26	GO0005089	RHO guanyl-nucleotide exchange factor 2	Rho guanine nucleotide exchange factor
Sapur.0061339600.1	47.09469612	0.754285429	0.076106117	9.91087	2.73E-23	1.20E-22	psmile	-0.610520255	2.08E-17		Protein of unknown function (DUF668)	DUF3475 domain protein
Sapur.0096012200.1	237.3795617	0.529616011	0.05344086	9.91032	2.76E-23	1.20E-22	psmile	-0.600304191	1.5E-17		BXO protein family	BXO domain protein, putative
Sapur.0080263600.1	640.2147572	-0.645331329	0.065303206	-9.88221	4.97E-23	1.59E-22	psmile	-0.590787419	3.81E-16		Histone superfamily protein	histone H4
Sapur.0070255800.1	560.3265	-0.661331763	0.067000213	-9.87656	5.12E-23	1.64E-22	psmile	-0.614680554	8.6E-17	UBC16	ubiquitin-conjugating enzyme 16	ubiquitin-conjugating enzyme E2
Sapur.0080263000.1	204.3065339	-0.869381784	0.088008057	9.878434	5.16E-23	1.65E-22	psmile	-0.635803114	3.69E-19			hemerythrin HHE cation-binding domain protein
Sapur.0170239300.1	218.252119	0.469231955	0.045556449	9.86797	5.73E-23	1.83

Sapur.01T61132D0.1	140.5920133	-0.56580898	0.062016429	-9.12469	7.19E-20	2.12E-19	psrle	-0.5717027	5.27E-15	GO:0043531	ATG14A170.1	NB-ARC domain-containing disease resistance protein	CC-NBS-LRR resistance protein
Sapur.01G0281600.1	229.369224	-0.79120477	0.086875288	-9.10736	8.44E-20	2.49E-19	psrle	-0.57392705	2.58E-15	GO:0016747	ATG17540.1	HXXXD-type acyl-transferase family protein	benzoyl coenzyme A: benzyl alcohol benzoyl transferase
Sapur.01W0201100.1	2641.110009	-0.17844294	0.06331161	-9.1048	8.64E-20	2.55E-19	psrle	-0.60454854	5.13E-17	GO:0004857,GO:0042545,GO:0030599,GO:0005618	ATG69220.1	Plant invertase/pectin methylesterase inhibitor superfamily	NA
Sapur.01G1285000.1	134.4469733	-0.34483757	0.037881157	-9.10315	8.78E-20	2.58E-19	psrle	-0.60496392	4.86E-17		ATG47360.1	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.01G1274000.1	136.7634006	-0.83731412	0.092069882	-9.0988	9.12E-20	2.68E-19	psrle	-0.59483124	2.13E-16	GO:0006468,GO:0005634,GO:0006472	ATG66933.1	Protein kinase superfamily protein	NA
Sapur.01G1610000.1	3.95417146	-1.54317328	0.169613764	9.098255	9.18E-20	2.70E-19	psrle	-0.56903296	7.55E-15	GO:0003247,GO:0008270,GO:0005515	ATG53132.1	RING/U-box superfamily protein	wall-associated receptor kinase galacturonan-binding protein
Sapur.01G0621700.3	24.23269994	0.61188576	0.067265531	9.096572	9.32E-20	2.74E-19	psrle	-0.59320581	2.70E-16	GO:0016020,GO:0008378,GO:0006486	ATG32120.1	Galactosyltransferase family protein	beta-1%2C3-galactosyltransferase, putative
Sapur.01J0281000.1	282.8521237	-0.60392882	0.076180117	-9.09557	9.41E-20	2.77E-19	psrle	-0.60394114	5.60E-17	GO:0003677	ATG27670.1	histone H2A 7	core histone H2A/H2B/H3/H4
Sapur.01J0281000.1	95.47787879	-0.05132642	0.01558329	-9.09547	9.42E-20	2.77E-19	psrle	-0.56493531	1.26E-14		ATG60710.1	NAD(P)-linked oxidoreductase superfluamily protein	NA
Sapur.01J0281000.1	1.43761939	-0.55321494	0.061251499	-9.0928	9.56E-20	2.81E-19	psrle	-0.60042276	6.23702E-17	GO:0030418,GO:0030410	ATN04626.1	Arginase/agmatinase and	n-carbamoylmethine
Sapur.T07L100.1	12.40295998	-0.82991236	0.091278529	-9.09209	9.72E-20	2.86E-19	psrle	-0.59475132	1.69E-16		ATG16470.1	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.01G0279800.1	1125.115149	-0.01469954	0.00202861	-9.0903	9.89E-20	2.91E-19	psrle	-0.58517284	5.25E-16	GO:0005515	ATG27792.1	Glutathione S-transferase family protein	glutathione S-transferase
Sapur.01G0671500.1	17.62697832	-0.78821831	0.086756025	-9.08546	1.03E-19	3.03E-19	psrle	-0.59287648	2.83E-16		ATG21470.1	Pentatricopeptide repeat (PPR-like) superfamily protein	NA
Sapur.01G1344100.2	2.05975103	-0.90708366	0.10102042	-9.08052	1.08E-19	3.16E-19	psrle	-0.57969124	1.72E-15		ATG54680.1	Tetratricopeptide repeat (TPR)-like superfamily protein	CAAP-like protein
Sapur.01G1165700.2	2.91619547	-1.53248603	0.168999759	-9.06795	1.21E-19	3.56E-19	psrle	-0.52579384	1.54E-12	GO:0005515	ATG19330.1	ARIA	Secretin-type PQ2-like protein
Sapur.01J0288500.1	551.0162837	-0.12135184	0.013839766	-9.06269	1.25E-19	3.67E-19	psrle	-0.5511608	2.68E-14		ATG38200.1	Class I glutamine amidotransferase-like superfamily protein	class I glutamine amidotransferase
Sapur.01B0276800.1	15.58923651	-0.96775908	0.106741666	9.066337	1.23E-19	3.61E-19	psrle	-0.58893024	4.95E-16				hypothetical protein
Sapur.01G1238800.1	141.228755	-0.34270206	0.038239478	-9.05792	1.33E-19	3.90E-19	psrle	-0.60288476	6.76E-17		ATG47360.1	Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.0061117D0.2	43.00018504	-1.91385108	0.206475906	-9.04873	1.45E-19	4.25E-19	psrle	-0.55238599	1.86E-14	GO:0008234,GO:0006508	ATG45102.1	Cysteine proteinases superfamily protein	cysteine protease
Sapur.15W0G0T4200.1	0.64285264	-2.80503716	0.30271069	-9.0396	1.72E-19	5.03E-19	psrle	-0.63743488	2.80E-19	GO:0016747	ATG48930.1	HCT	NA
Sapur.01G1751100.1	92.09720144	-0.19371184	0.021239455	9.027563	1.76E-19	5.15E-19	psrle	-0.58684635	6.31E-16	GO:0005741	ATG47505.1	voltage dependent anion channel 2	porin/voltage-dependent anion-selective channel protein
Sapur.01T0287400.1	25.7042023	-0.42162228	0.157602001	-9.01525	1.96E-19	5.73E-19	psrle	-0.51801499	6.44E-12		ATG25760.1	ATGDU2,GDU2	glutamine dumper 2
Sapur.01T0171400.1	127.0188164	-0.69885827	0.10057714	-9.01024	2.06E-19	6.01E-19	psrle	-0.54198563	1.89E-14	GO:0004683,GO:0006672	ATG24010.1	Protein kinase superfamily protein	receptor-like kinase, putative
Sapur.01H0200600.2	27.28882998	-0.70220482	0.0779388	-9.01	2.06E-19	6.01E-19	psrle	-0.80560258	4.02E-17		ATG22320.2		NA
Sapur.01G1176600.1	24.6047468	-0.97238201	0.108026407	-8.98552	2.63E-19	7.70E-19	psrle	-0.62093144	2.91E-17	GO:0004683,GO:0005634,GO:0006472	ATG23170.1	Protein kinase superfamily protein	NA
Sapur.01G0206400.1	20.68083829	-0.92368127	0.102875483	-8.97831	2.75E-19	8.00E-19	psrle	-0.58515106	6.96E-16		ATG79480.1	Carbohydrate-binding XB domain superfamily protein	carbohydrate-binding module family 43 protein
Sapur.01G0622500.1	166.6449829	-0.77835269	0.08679364	-8.96786	3.02E-19	8.78E-19	psrle	-0.57732494	2.47E-15	GO:0005515,GO:0042531	ATG14470.1	NB-ARC domain-containing disease resistance protein	NA
Sapur.1177G00.1	1.05806169	-2.35492731	0.262785519	8.961256	3.12E-19	9.10E-19	psrle	-0.72026208	2.08E-16		ATGRM1,FIM1	Fimbrin1	NA
Sapur.01G1162300.1	260.3900731	-0.50105798	0.055918815	-8.96077	3.23E-19	9.35E-19	psrle	-0.60699016	3.55E-17		ATG44380.1	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	late embryogenesis abundant protein
Sapur.0062D120.2	14.45391169	-1.91353013	0.21357547	-8.95703	3.13E-19	9.60E-19	psrle	-0.58279925	6.75E-16	GO:0005515,GO:0016491	ATG60520.1	NDB2	external alternative NAD(P)H-ubiquinone oxidoreductase B4
Sapur.0G1187800.1	1.72982922	-2.65067742	0.29624428	-8.94761	3.63E-19	1.05E-18	psrle	-0.55383561	5.92E-14		ATG38230.1		NA
Sapur.0G0280100.1	805.5279548	-0.10795184	0.012673887	-8.94489	3.76E-19	1.15E-18	psrle	-0.56834635	1.98E-16		ATG50120.1	SQD2	glycosyltransferase family protein
Sapur.01G0181400.1	17.0316035	-0.88840899	0.09932282	8.94471	3.73E-19	1.08E-18	psrle	-0.51540663	8.62E-12		ATG21910.1		transmembrane protein, putative
Sapur.01W0160300.1	151.7439418	-0.66408311	0.051946249	-8.94001	3.86E-19	1.12E-18	psrle	-0.5822216	1.32E-15	GO:0006281,GO:0004518	ATG48425.1	DNAse I-like superfamily protein	AP endonuclease DNA glycosylase or apyrimidinic site (lyase) protein, putative
Sapur.0B0G1730D.8	8.44183355	-0.93319399	0.104386413	-8.9398	3.90E-19	1.13E-18	psrle	-0.58431708	9.46E-16	GO:0003676	ATG18830.1	SC1.1B	SC35-like splicing factor 2B
Sapur.01G0281300.1	285.0506201	-0.15284708	0.017108161	-8.93918	3.96E-19	1.15E-18	psrle	-0.60513022	8.98E-17		ATG46180.1	MEE29	helicase domain protein
Sapur.01G0121300.1	145.696623	-0.22710204	0.025427318	-8.93148	4.21E-19	1.22E-18	psrle	-0.58020969	7.28E-16	GO:0003676,GO:0008810,GO:0005622	ATG73140.1	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain	ras GTPase-activating protein-binding protein, putative
Sapur.0G7G0T7000.1	89.43311582	-0.56923724	0.061498023	8.930974	4.23E-19	1.22E-18	psrle	-0.57461226	3.57E-15	GO:0005524	ATG18193.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	P-loop nucleoside triphosphate hydrolase-like protein
Sapur.0D5G0600.3	22.83897675	-0.62329169	0.08686675	-8.92785	4.34E-19	1.26E-18	psrle	-0.57537362	2.08E-15		ATG50560.1	NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase/reductase
Sapur.01G0280600.2	0.81475852	-2.63729917	0.29546891	-8.92641	4.40E-19	1.27E-18	psrle	-0.69227532	1.00E-23	GO:0016020,GO:0008378,GO:0004486	ATG05170.1	Galactosyltransferase family protein	beta-1%2C3-galactosyltransferase, putative
Sapur.0G6G0400.1	9.56694671	-1.04168266	0.12813763	8.9243	4.51E-19	1.30E-18	psrle	-0.57869156	1.59E-15	GO:0005515,GO:0006979,GO:0004602	ATGPR2,GPX2	glutathione peroxidase	glutathione peroxidase
Sapur.0G9G1D70.1	163.4515299	-1.02180882	0.11487839	8.896167	5.78E-19	1.67E-18	psrle	-0.55696482	4.62E-14		ATG21180.1		transmembrane protein, putative
Sapur.0G4G6B200.1	148.5852261	-0.97108112	0.109488113	-8.89577	5.75E-19	1.67E-18	psrle	-0.60507775	2.92E-17	GO:0003247,GO:0006468,GO:0005524,GO:0004672	ATG66880.1	Protein kinase superfamily protein	kinase domain protein
Sapur.0G5G0540.1	12.25757948	-0.91043981	0.120373447	8.884215	6.44E-19	1.85E-18	psrle	-0.52639176	6.17E-14	GO:0003247	ATG53970.1	Protein kinase family protein	wall-associated receptor kinase-like kinase
Sapur.0G6G4A600.1	7.60263704	-1.32790205	0.149469793	8.882784	6.52E-19	1.88E-18	psrle	-0.56077417	2.21E-14		ATG67417.1	TBL7	Pro5/Cys5/Gly5/Glu5/Ser5/Thr5 acyl-acetyltransferase family protein
Sapur.01G0251900.1	114.2019158	-0.60910198	0.068748718	-8.85983	8.01E-19	2.30E-18	psrle	-0.5983271	1.28E-16	GO:0005515	ATG17980.1		C2 calcium/lipid-binding and phosphorribosyltransferase family protein
Sapur.01G0230000.1	70.2969203	-0.71942572	0.08148257	-8.83833	9.72E-19	2.78E-18	psrle	-0.55330883	5.70E-14		ATG30320.1	Remorin family protein	NA
Sapur.01G0167000.1	20.50052894	-1.07251122	0.124896163	8.825075	1.05E-18	3.01E-18	psrle	-0.55685562	4.71E-14		ATG02450.1	NIMIN-1,NIMIN1	NIMIN interactor 1
Sapur.01B1G11300.1	733.4634968	-0.74101247	0.084236432	-8.79682	1.41E-18	4.02E-18	psrle	-0.54897258	9.76E-14	GO:0006355,GO:0005634,GO:0003677,GO:0009725	ATG20730.2	ARF7,BIP,IAA21,IAA23,IAA27	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related
Sapur.01W0241000.1	138.0895081	-0.66418108	0.076188192	-8.7849	1.44E-18	4.16E-18	psrle	-0.10241641	-8.77986	GO:0005515,GO:0030037,GO:0016705,GO:0005506	ATG31181.1	CYP64A1	cytochrome P450, family 64, subfamily A, polypeptide 1
Sapur.0G9G1K500.1	102.9161892	-0.66226603	0.075635882	-8.77385	1.73E-18	4.92E-18	psrle	-0.59346211	2.61E-16		ATG27740.1		transcriptional activator
Sapur.0G5G1B400.1	102.6142047	-0.62182511	0.07097585	-8.77164	1.76E-18	5.02E-18	psrle	-0.54344871	1.56E-14		ATG30120.1	Remorin family protein	NA
Sapur.T03H100.1	77.07076002	-0.53042869	0.060525754	8.76425	1.88E-18	5.35E-18	psrle	-0.55760195	1.39E-14		ATG18150.1	Methyltransferase-related protein	transmembrane protein, putative
Sapur.0G6G1T600.1	71.94471616	-0.82008823	0.092636276	8.764037	1.87E-18	5.36E-18	psrle	-0.56432878	1.96E-14		ATG02180.1	Ribulose-bisphosphate carboxylase 2A kDa subunit, putative	NA
Sapur.01W0240800.1	136.5724502	-0.63880149	0.07224396	8.71126	3.01E-18	8.50E-18	psrle	-0.57863701	-2.06E-02	GO:0055114,GO:0016491	ATG68370.2	PDE181,SPC1,ZDS	zeta-carotene desaturase
Sapur.0G5G1T400.1	40.58146481	-0.80271208	0.10344389	8.70197	3.12E-18	8.80E-18	psrle	-0.56030608	4.38E-16	GO:0006355,GO:0003677	ATG45130.1	ANAC106,AND1	NAC transcription factor
Sapur.0B0G1380B.0	0.94430275	-2.56081312	0.29496739	-8.68169	3.90E-18	1.10E-17	psrle	-0.55739104	3.40E-14	GO:0003824,GO:0006470,GO:0004722	ATG23340.1		Protein phosphatase 2C family protein
Sapur.01W0G0D300.1	113.5390936	-0.81786119	0.094562839	-8.67616	4.09E-18	1.16E-17	psrle	-0.58726751	6.25E-16	GO:0005515	ATG46620.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	chaperone BCS1
Sapur.01T0287000.1	27.70551371	-0.62402617	0.07968737	-8.6747	4.15E-18	1.17E-17	psrle	-0.58191918	1.38E-15		ATG18910.1	HT1	Protein kinase superfamily protein
Sapur.0G5G1K700.1	1058.776374	-0.41742079	0.048145831	-8.66997	4.33E-18	1.22E-17	psrle	-0.58342266	9.43E-16		ATG02050.1	TROL	thylakoid rhodanese-like
Sapur.01J0240200.1	46.93812844	-0.62008224	0.069349933	-8.66808	4.36E-18	1.23E-17	psrle	-0.55185149	4.50E-14	GO:0006189	ATG70190.1	phosphoribosylaminoimidazole carboxylase	phosphoribosylaminoimidazole carboxylase
Sapur.01J0131700.1	401.3224887	-0.41438368	0.05817197	8.668904	4.36E-18	1.23E-17	psrle	-0.5156099	5.70E-14	GO:0009942,GO:0008312,GO:0006414,GO:0005786	ATG30640.1	Signal recognition particle, SRP9/SRP14 subunit	signal recognition particle 14 kDa protein
Sapur.0G5G1T500.1	0.92527135	-2.46025653	0.28758536	-8.65919	4.75E-18	1.34E-17	psrle	-0.56834129	2.31E-15	GO:0005524	ATG20890.1	TCP-1/cpn60 chaperonin family protein	NA
Sapur.01G1178800.1	1488.781705	0.38445605	0.044661924	8.645951	5.34E-18	1.50E-17	psrle	-0.56335428	1.62E-14	GO:0006483,GO:0005524,GO:0004672	ATG60940.1	SNRK2-10,SNRK2.10,SRK2B	SNF1-related protein kinase 2.10	Serine/Threonine kinase domain protein
Sapur.01T0201500.1	31.59878091	-0.62006423	0.08084	8.638084	5.72E-18	1.61E-17	psrle	-0.56246604	1.79E-14	GO:0055114,GO:0008113,GO:0005783,GO:0016671,GO:0006979	ATG18830.2		Peptide methionine sulfoxide reductase family protein
Sapur.0G6G4N100.1	17.22951874	-0.74268676	0.085992463	-8.63665	5.79E-18	1.63E-17	psrle	-0.59614577	7.70E-16		ATG68170.1	DOT4	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.T03J800.1	1.07164977	-2.30186447	0.32798651	8.632112	6.46E-18	1.82E-17	psrle	-0.6417852	6.30E-20		ATG23170.1		NA
Sapur.01G2274300.1	10.03643039	-1.32031679	0.153779737	-8.58791	8.86E-18	2.48E-17	psrle	-0.54331711	1.95E-13	GO:0010872,GO:0042803,GO:0004657,GO:0000774	ATG36390.2	Co-chaperone GrpE family protein	NA
Sapur.01G0271900.1	2.50088152	-2.92587187	0.32464034	-8.58025	9.47E-18	2.66E-17	psrle	-0.60882282	8.91E-17	GO:0005515	ATG44640.1	LRR and NB-ARC domains-containing disease resistance protein	NBS-LRR resistance protein
Sapur.01G2138400.1	3753.127992	-0.28128271	0.031813301	-8.57876	9.59E-18	2.68E-17	psrle	-0.62770507	1.71E-14	GO:0055114,GO:0016491,GO:0008270	ATG59940.1	Gro1/Eve-like dehydrogenase family protein	glutathione-dependent formaldehyde dehydrogenase
Sapur.0G6G1T7100.1	96.98240403	-0.53609007	0.062585162	-8.56577	1.07E-17	2.99E-17	psrle	-0.54307934	1.94E-13	GO:0008270,GO:0005515	ATG02750.1	RING/U-box superfamily protein	zinc finger, C3HC4 type (RING finger) protein
Sapur.0G6G1T600.1	585.9351024	-0.20420825	0.023636276	8.564476	1.09E-17	3.05E-17	psrle	-0.54315651	1.96E-13	GO:0008270,GO:0005515	ATG29510.1	RING/U-box superfamily protein	zinc finger protein, putative
Sapur.01G2610100.1	424.5293892	-0.62470432	0.072959406	8.562625	1.10E-17	3.07E-17	psrle	-0.57234725	2.21E-13	GO:0003824,GO:0006470,GO:0004722	ATG51760.1	AHG1	protein phosphatase 2C
Sapur.01G2291200.1	47.58418861	-0.51752625	0.06046221	8.560105	1.13E-17	3.14E-17	psrle	-0.55283722	2.85E-16	GO:0020037,GO:0000505	ATG68810.1		Cytochrome c1 heme protein
Sapur.01G1230800.1	8.84837393	-2.27837659	0.149573352	-8.54619	1.27E-17	3.54E-17	psrle	-0.54832718	1.07E-13		ATG39160.1	RmlC-like cupins superfamily protein	rhizaldehyde receptor, putative
Sapur.01G0281900.1	161.0296207	-0.39602909	0.03501527	-8.54586	1.28E-17	3.56E-17	psrle	-0.56872713	-8.54586	GO:0003676	ATG24160.1	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 1 in heterogeneous nuclear ribonucleoprotein A subfamily protein, putative
Sapur.01G0251800.1	814.8515761	-0.65709127	0.076931085	-8.54123	1.33E-17	3.69E-17	psrle	-0.51387816	6.39E-12		ATG26740.1	CCR	CCR-like
Sapur.0G6G5L800.1	231.2074875	0.31788777	0.037239504	8.538597	1.36E-17	3.77E-17	psrle	-0.5160531	1.26E-14	GO:0009165,GO:0006749,GO:0000287	ATG35390.2	Phosphoribosyltransferase family protein	ribose-phosphate pyrophosphokinase
Sapur.0G9G8B600.1	100.3889125	-0.97620953	0.113754934	-8.53151	1.57E-17	4.37E-17	psrle	-0.50719616	2.98E-11		ATG19860.1		hypothetical protein
Sapur.01G1794000.1	195.7534637	1.38762813	0.167600208	8.497515	1.94E-17	5.36E-17	psrle	-0.52678822	-2.19E-12		ATG37040.1	ATPAL1,PAL1	PHE ammonia lyase 1
Sapur.01G0280800.1	21.7523816	0.70147613	0.082564428	8.48804	2.08E-17	5.76E-17	psrle	-0.54152114	1.04E-13	GO:0008138,GO:0006470	ATG24010.1	dual specificity protein phosphatase 1	NA
Sapur.01G0241900.1	33.49607709	0.79816312	0.094224755	-8.47084	2.44E-17	6.72E-17	psrle	-0.54554722	1.49E-13	GO:0010312,GO:0008270,GO:0006508,GO:0004222	ATG45040.1	Matrixin family protein	matrix metalloproteinase
Sapur.01G1620800.1	2159.058604	-0.51663329	0.06447567	-8.47029	2.45E-17	6.75E-17	psrle	-0.57347384	4.12E-15	GO:0004566,GO:0005975,GO:0004553	ATG64190.1	glycosyl hydrolases family 32	endo-beta-1%2C6-galactanase
Sapur.1S0G0900.1	155.7869056	-0.78468288	0.092789914	8.456623	2.75E-17	7.58E-17	psrle	-0.61330757	1.36E-17		ATG18230.2	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	NA
Sapur.01W0G4T000.2	41.29700924	-0.56022623	0.067225319	8.452141	2.76E-17	7.61E-17	psrle	-0.53810022	1.44E-13	GO:0016853,GO:0005737	ATG22120.1	phosphoglucose/phosphomannose isomerase family	protein phosphorylation inhibitor 2 containing protein
Sapur.01G2945000.1	1230.178	0.28279627	0.033502046	8.418649	3.81E-17	1.04E-16	psrle	-0.5694302	7.14E-15	GO:0045045,GO:0005742	ATG27390.1	TOM20-2	translocase outer membrane 20-2
Sapur.01W0G4D400.2	0.92735546	-1.48235369	0.19404024	-8.41793	3.83E-17	1.05E-16	psrle	-0.55852185	5.98E-14	GO:0005886	ATG50402.2	ATKORQC1,RQKGE3	Rab guanine nucleotide exchange factor, putative
Sapur.01B0277400.1	7299.069911	0.81762858	0.097116417	8.417041	3.86E-17	1.06E-16	psrle	-0.55282759	6.22E-14	GO:0008295,GO:0006597,GO:0004014	ATG24735.4	SAMDC	S-adenosylmethionine decarboxylase
Sapur.0B0G1030B0.1	1534.511363	0.49332292	0.058807878	8.388722	4.91E-17	1.34E-16	psrle	-0.55302065	7.53E-14	GO:0022781,GO:0006355	ATG70080.1	RNA polymerase II transcription elongation factor	ER-associated factor, putative
Sapur.0G5G1AT200.1	13.86067331	-0.84680992	0.100790608	-8.38182	5.23E-17	1.42E-16	psrle	-0.5011875	2.40E-14		ATG19880.1		NA
Sapur.01G0222300.1	3030.055773	-0.22687046	0.02708428	-8.37645	5.45E-17	1.49E-16	psrle	-0.55931394	2.61E-14	GO:0003676	ATG41060.2	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 1 in heterogeneous nuclear ribonucleoprotein A subfamily protein, putative
Sapur.01W0G1D200.1	0.87267389	-2.07766417	0.36760351	-8.37102	5.75E-17	1.56E-16	psrle	-0.56849055	1.67E-15	GO:0016787	ATNUDT13.ATNUDX13,NUC	nudix hydrolase 13	nudix hydrolase
Sapur.15W0G0T7300.1	1.71895264	-1.67907531	0.20068306	-8.37065	5.73E-17	1.56E-16	psrle	-0.58404288	9.35E-16		ATG65180.1	EN TN/VHS family protein	NA
Sapur.01G1160600.1	1.16407818	-2.88583771	0.34506763	-8.35883	6.33E-17	1.72E-16	psrle	-0.60634524	1.91E-17				hypothetical protein
Sapur.01G0371500.1	4.86214152	-1.43368865	0.171875075	-8.34839	6.92E-17	1.88E-16	psrle	-0.57972391	5.82E-15		ATG51160.1		Esterase/lipase/thioesterase family protein
Sapur.01G1622700.1	24.32553917	-0.79376062	0.10481427	-8.34421	7.17E-17	1.95E-16	psrle	-0.52932252	1.51E-12	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATG31080.1	CYP71B2	cytochrome P450, family 71, subfamily B, polypeptide 2
Sapur.0B0G6H200.1	26.3422967	-0.91987223	0.109377061	-8.33801	7.56E-17	2.05E-16	psrle	-0.54919831	9.58E-14		ATG55560.1	AGF2,AHL15	AT-hook protein of GA feedback 2
Sapur.01G4G4A300.1	44.47375754	-0.82409769	0.098696703	-8.33593	7.68E-17	2.08E-16	psrle	-0.54881445	1.56E-13	GO:0043565,GO:0008270,GO:0006355,GO:0003700	ATG45050.1	GATA2	GATA transcription factor, putative
Sapur.01G1421000.1	8.16385483	-0.70078466	0.120062445	-8.33507	7.75E-17	2.10E-16	psrle	-0.55684397	3.64E-14	GO:0008270,GO:0005515	ATG30400.1	RING/U-box superfamily protein	RING-H2 finger protein
Sapur.0G7G1Z100.1	531.0174185	-0.25432874	0.030569676	-8.3167	9.04E-17	2.45E-16	psrle	-0.56342655	1.98E-14	GO:0015136,GO:0003824	ATG42360.1	BIO2,BIO8	Radical SAM superfamily protein	biotin synthase
Sapur.0G5G8B400.1	111.140756	-0.59535367	0.071954808	-8.31406	9.23E-17	2.50E-16	psrle	-0.54362006	1.12E-13		ATG28090.1		PHF0X peptidase domain family protein	PHF0X peptidase domain protein, putative
Sapur.0G0G0Z200.1	557.7988073	-0.24608746	0.029713551	-8.31228	9.39E-17	2.54E-16	psrle	-0.57470848	3.92E-15	GO:0003677	ATG76510.1		ARID/BRIGHT DNA-binding domain-containing protein	ARID/bright DNA-binding domain protein
Sapur.01G2471200.1	2001.26266	-0.46846756	0.05642231	-8.30582	9.91E-17	2.68E-16	psrle	-0.58507608	1.61E-14	GO:0005515,GO:0006468,GO:0005524,GO:0004672	ATG14640.2	Leucine-rich repeat transmembrane protein kinase	receptor-like kinase, putative
Sapur.01G0260900.1	0.85258514	-2.53888223	0.30587025	-8.30381	1.01E-16	2.73E-16	psrle	-0.54347466	2.45E-13		ATG41760.1		hypothetical protein
Sapur.0G6G1K000.1	1.28026042	-2.32464394	0.1637245	-8.30316	1.01E-16	2.74E-16	psrle	-0.54330679	1.35E-13		ATG43060.1		NA
Sapur.01G0331300.2	4.27422824	-1.50081509	0.180941261	8.296646	1.07E-16	2.90E-16	psrle	-0.68434544	3.39E-23		ATG54570.1		esterase/lipase/thioesterase family protein
Sapur.01G0280500.2	0.61041998	-2.77498698	0.33491452	8.28542	1.18E-16	3.18E-16	psrle	-0.60862061	1.96E-17		ATG73830.1	BEE3	BR enhanced expression 3	transcription factor BEE, putative
Sapur.0G2G1C200.1	8.29491008	-0.95114842	0.114859472	-8.28098	1.23E-16	3.30E-16	psrle	-0.53892718	1.31E-13					hypothetical protein
Sapur.01G0240200.1	39.5343983	-0.95280494	0.115073102	-8.27565	1.28E-16	3.45E-16	psrle	-0.52037819	2.84E-12	GO:0006355,GO:0003700	ATG59-_LEBS-1	ethylene-responsive element binding factor 1	ethylene-responsive transcription factor 2
Sapur.0G5G1T500.1	439.9176236	-0.84806784	0.094165861	-8.2677	1.37E-16	3.88E-16	psrle	-0.51074092	2.62E-12	GO:0004222,GO:0006508,GO:0004190	ATAPLA,ATAPM1	aspartic proteinase family	aspartic proteinase
Sapur.0G5G1AT500.1	447.0104996	-0.83323261	0.04276521	-8.2634	1.42E-16	4.01E-16	psrle	-0.54869605	1.04E-13	GO:0016757	ATG77130.1	GUX2,PGSIP2	plant glycogenin-like starch initiation protein 2	secondary cell wall-related glucuronosyltransferase family 8 protein
Sapur.01G0888800.1	2.56078251	-1.56883223	0.20127156	-8.24815	1.47E-16	4.16E-16	psrle	-0.55854794	2.04E-14	GO:0046891,GO:0008171	ATG56160.1	O-methyltransferase family protein	NA
Sapur.0G6G2070D0.1	62.94937434	-0.52403461	0.063377129	-8.24278	1.68E-16	4.52E-16	psrle	-0.55283091	6.04E-14		ATG01480.1	AtMYB108,MYB108,MOX	myb domain protein 108	MYB74-like 2 MYB transcription factor, putative
Sapur.01G0280700.1	2.96887615	-2.62363277	0.27623584	-8.2401	1.72E-16	4.62E-16	psrle	-0.58966145	4.66E-16		ATG20875.1	EFG1	epidermal patterning factor 1	epidermal patterning factor
Sapur.0B0G4B300.1	154.1232574	-0.82249987	0.100095561	-8.21755	2.08E-16	5.59E-16	psrle	-0.55427001	5.07E-14	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATG24540.1	CYP86C1	cytochrome P450, family 86, subfamily C, polypeptide 1	cytochrome P450 family protein
Sapur.01G0280400.1	174.8165461	-0.58235027	0.071954808	-8.21426	2.12E-16	5.68E-16	psrle	-0.57344984	4.12E-15	GO:0006355	ATG38180.1	FRS3	FAR1 related sequence protein	FAR1 related sequence protein
Sapur.01G0270800.2	2.22001989	-0.45760348	0.300204807	-8.19242	2.56E-16	6.85E-16	psrle	-0.57439148	4.07E-15		ATG31657.3		Plant protein 1589 of unknown function	plant-specific domain TIGR01589 family protein, putative
Sapur.01G0280600.1	2356.646673	0.23710386	0.03136129	8.187664	2.63E-16	7.03E-16	psrle	-0.55834976	1.05E-14	GO:0055114,GO:0050661,GO:0030543,GO:0008883	ATG68280.1	HEMA1	Glutamyl-tRNA reductase family protein	glutamyl-tRNA reductase
Sapur.01G2641500.1	650.1883514	0.40005477	0.04898922	-8.16621	3.18E-16	8.49E-16	psrle	-0.53689166	4.64E-13	GO:0006396,GO:0006364,GO:0000287,GO:0000315	ATG76030.1	EN01	endosa 1	endosa, carboxy-terminal T

Sapur.008G055600.1	0.30748246	-0.546710747	0.37815734	-1.44565	0.148274232	0.188725109	purple	-0.6732855	4.46E-22	GO:0005680	ATSG05560.1	EMB2771	E3 ubiquitin ligase, putative	anaphase-promoting complex subunit 1
Sapur.010G039100.2	4.64567847	0.211165544	0.153622888	1.374512	0.160282705	0.213490383	purple	-0.85327256	8.86E-46		ATSG06340.1		HR-like lesion-inducing protein-related	HR-like lesion-inducing protein
Sapur.019W0105800.2	0.34231961	-0.567702276	0.422969339	-1.34212	0.179017487	0.225488261	purple	-0.173471825	4.76E-15		ATSG06270.1		AAA-type ATPase family protein	DNA polymerase III subunit gamma/tau
Sapur.014G058900.1	9.10747018	0.139082948	0.109389322	-1.27145	0.203569848	0.25366683	purple	-0.763680733	2.92E-31	GO:0005515	ATSG06755.1		F-box family protein	cyclin-like F-box protein
Sapur.001G145400.1	0.38258848	0.746003552	0.593811228	1.257571	0.207773625	0.258327823	purple	-0.594628841	1.20E-16		ATSG02430.1		Protein of unknown function (DUF679)	transmembrane protein, putative
Sapur.002G073100.1	3.48730703	0.200832963	0.166770614	1.204247	0.228694238	0.282238513	purple	-0.648410671	4.27E-20	GO:0006914	ATSG08540.1		DNA-directed RNA polymerase II protein	DNA-directed RNA polymerase II
Sapur.017G101100.2	0.968351667	0.770915859	0.648635345	-1.18852	0.234828763	0.289211081	purple	-0.619262832	5.38E-18	GO:0006418;GO:0000166;GO:0005524;GO:0004812	ATSG16751.1	EMB2247	ATP binding;valine-tRNA ligase;aminoacyl-tRNA ligase;nucleotide binding;ATP binding;aminoacyl-tRNA ligases	valyl-tRNA synthetase
Sapur.019G075300.2	0.155163925	0.711554858	0.609697778	1.166507	0.24049065	0.299315675	purple	-0.641619854	1.38E-19	GO:0016773;GO:0005975	ATSG06920.1	XK-2;XK2	xylulose kinase-2	D-xylulose kinase family protein
Sapur.014G117000.5	0.12859828	0.705736027	0.753027542	0.937168	0.348656536	0.416368307	purple	-0.872648603	4.15E-50		ATSG02070.1		Cysteine proteinases superfamily protein	cysteine-type peptidase
Sapur.010G039200.2	2.38047545	0.157783669	0.179769269	0.877466	0.643403646	0.516500246	purple	-0.649932181	5.56E-19		ATSG04660.1			TGN related, localized DIP41-interacting protein, putative
Sapur.013G161000.2	0.592274875	0.275027617	0.273122708	0.763284	0.457304556	0.531065329	purple	-0.55812786	2.98E-14		ATSG62480.2	ATSNAR2;GRK1	geminivirus rep interacting kinase 1	Serine/Threonine kinase domain protein
Sapur.002G052600.2	0.203833964	0.147515865	0.138217484	1.067349	0.677034459	0.951850213	purple	-0.697032422	3.71E-24	GO:0006468;GO:0005524;GO:0004672	ATSG22260.1	CRK21	cysteine-rich RLK(RECEPTOR-like protein kinase)21	glycosyl hydrolase family 28 protein
Sapur.014G057400.2	1.33316996	-0.134051849	0.209153727	-0.64093	0.521574408	0.596801479	purple	-0.627312302	1.49E-18	GO:0005515	ATSG40880.1		WD-40 repeat family protein / dwd2 protein (DWD2)	F-box and WD40 domain protein, putative
Sapur.013G081300.1	0.139715164	0.128663127	0.128667227	0.999679	0.578768208	0.651863619	purple	-0.532553111	7.08E-13	GO:0005515;GO:0008677;GO:0050975;GO:0004367;GO:0009331;GO:0006072	ATSG40600.1	GLYL1;SFD1	NAD-dependent glycerol-3-phosphate dehydrogenase family protein	glycerol-3-phosphate dehydrogenase (NAD(P)+) protein
Sapur.002G160100.1	55.2379918	0.025185176	0.047486041	0.53037	0.595853159	0.670362615	purple	-0.73515764	6.35E-26		ATSG05700.1		Drought-response family protein	stress-induced protein DI19, carbosy-terminal protein
Sapur.001G158500.1	0.125661238	0.147968532	0.1092532	0.662029	0.642842883	0.716397125	purple	-0.73974114	2.21E-27		ATSG19883.1			transmembrane protein, putative
Sapur.008G031500.3	0.146862147	-0.262658973	0.666167368	-0.39428	0.693375154	0.762791737	purple	-0.763505052	3.06E-31	GO:0006508;GO:0004185	ATSG07980.1	SCPL27	serine carboxypeptidase-like 27	serine carboxypeptidase-like protein
Sapur.010G038800.2	1.718391798	0.353392183	0.193097817	0.276282	0.782331685	0.841458311	purple	0.870537964	1.32E-49		ATSG28240.1		Protein of unknown function (DUF616)	transmembrane protein, putative
Sapur.014G075800.2	0.074185292	0.154373523	0.102747612	0.267815	0.768846021	0.847325951	purple	-0.614607738	1.17E-17	GO:0005515	ATSG07240.1		basic helix-loop-helix (bHLH) family protein	transcription factor BEL putative
Sapur.15W0GW2300.1	1.040823189	-0.070915081	0.334268785	-0.21215	0.831889121	0.881425035	purple	-0.605953968	4.15E-17		ATSG37900.1		Protein of unknown function (duplicated DUF1396)	NA
Sapur.003G025900.1	0.147152878	0.375103183	0.768968625	-0.09569	0.924261001	0.952513341	purple	-0.717097076	4.26E-32		ATSG78830.3	GCS	gelgin-like protein 5	coiled-coil vesicle tethering protein, putative
Sapur.013G106300.1	0.353232665	-0.171317718	1.815306156	-0.09437	0.924812062	0.950832708	purple	0.536207766	4.57E-13	GO:0007264;GO:0005525	ATSG52310.1	ATARL8;LATGR1;GB1	GTP-binding protein 1	ADP-ribosylation factor(Arf)/Arf-like (Arl) small GTPase family protein
Sapur.005G037700.2	0.043228882	0.169392258	2.038885245	-0.83808	0.933787277	NA	purple	-0.852700004	4.06E-24	GO:0006508;GO:0004185	ATSG23120.1	SCPL34	serine carboxypeptidase-like 34	serine carboxypeptidase
Sapur.014G106200.2	0.06611461	0.128661759	0.904833276	0.064392	0.964671295	NA	purple	0.605343481	4.55E-17	GO:0071805;GO:0016020;GO:0015079	ATSG13420.1	ATHAKS;HAKS	high affinity K+ transporter 5	potassium transporter
Sapur.010G039700.2	0.006604848	0.138663127	0.904833276	0.064392	0.964692	NA	purple	-0.681532902	8.91E-23		ATSG18860.1		Ubiquitin-specific protease family C19-related protein	transmembrane protein, putative
Sapur.004G039300.2	0.026739922	0.089319595	2.710535058	0.032952	0.973712558	NA	purple	0.699528975	1.25E-24		ATSG56680.1	bHLH105;ILR3	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	bHLH transcription factor
Sapur.009G023700.1	0.011660284	0.091189802	2.904833276	0.031392	0.974956514	NA	purple	0.72192888	1.44E-26		ATSG07540.1	TRF12	Basic-leucine zipper (bZIP) transcription factor family protein	double-strand telomere-binding protein, putative
Sapur.006G067500.2	0.014075432	0.091189802	2.904833276	0.031392	0.974956514	NA	purple	0.594491212	2.24E-16	GO:0043565;GO:0006355;GO:0003700	ATSG26270.1	ABI5;GIA1	Basic-leucine zipper (bZIP) transcription factor family protein	abscisic acid insensitive protein
Sapur.008G062000.2	0.037819457	-0.058824143	2.063214026	-0.02851	0.97775466	NA	purple	-0.617327415	5.13E-18	GO:0016149;GO:0006415;GO:0005737	ATSG16170.1	ATFHB7;HCT;GI9	high chlorophyll fluorescent 109	peptide chain release factor 2
Sapur.003G156600.4	0.042319643	-0.031891234	1.567569227	-0.01008	0.983739916	NA	purple	-0.578177573	2.21E-14	GO:0005516	ATSG41560.1	ACA4	autoinhibited Ca(2+)-ATPase, isoform 4	calcium-transporting ATPase 4, plasma membrane-type protein
Sapur.002G194200.2	0.007853997	0.055375013	2.904833276	0.01913	0.984737169	NA	purple	-0.918245164	3.16E-64		ATSG12970.1	EPI10;STOMAGEN	stomagen	NA
Sapur.002G026900.2	0.008868233	0.055375013	2.904833276	0.01913	0.984737169	NA	purple	-0.718537497	3.16E-26	GO:0016787	ATSG18280.1	APY2;ATAPY2	apyrase 2	nucleoside diphosphatase
Sapur.012G174400.3	0.005114485	0.055375013	2.904833276	0.01913	0.984737169	NA	purple	-0.72325717	3.18E-26	GO:0006612;GO:0008324	ATSG27250.1		NAD(P)-binding Rossmann-fold superfamily protein	oxidoreductase, short chain dehydrogenase/reductase family protein
Sapur.012G174500.2	0.005090729	0.055375013	2.904833276	0.01913	0.984737169	NA	purple	-0.611312005	7.88E-19	GO:0055114;GO:0016491	ATSG27260.1		Pyridine nucleotide-disulphide oxidoreductase family protein	NADPH:adenoxin oxidoreductase
Sapur.15W0G118800.2	0.004880298	0.055375013	2.904833276	0.01913	0.984737169	NA	purple	-0.656531344	1.01E-20	GO:0016597;GO:0008152	ATSG69040.2	ACA4	ACT domain repeat 4	ACT domain protein, putative
Sapur.003G066800.2	0.010648008	0.05317169	2.904833276	0.01849	0.985439595	NA	purple	-0.625645752	5.21E-18		ATSG01180.1	ATP9RL;PRR1	pinoresinol reductase-like protein	Rossmann-fold NAD(P)-binding domain with glycine-rich motif
Sapur.001G134900.2	0.014192004	0.053717484	2.904833276	0.01849	0.985439595	NA	purple	-0.825027011	2.94E-40		ATSG33680.1		Remorin family protein	remorin/remorin benzylic ether reductase-like protein
Sapur.008G152300.7	0.035284158	-0.021255396	2.618802436	-0.00812	0.993524137	NA	purple	-0.731708657	1.38E-27	GO:0005975;GO:0004650	ATSG60580.1		Pectin lyase-like superfamily protein	polygalacturonase
Sapur.014G115100.1	0.010228869	0.018869013	2.904833435	0.00623	0.995028949	NA	purple	-0.720292183	2.11E-26	GO:0004652	ATSG58750.1	CSY2	citrate synthase 2, peroxisomal protein	citrate synthase 2, peroxisomal protein
Sapur.010G081600.2	0.009556859	0.018869013	2.904833435	0.00623	0.995028949	NA	purple	-0.662899842	3.16E-21		ATSG47530.1		Auxin-responsive family protein	auxin-induced in root cultures protein, putative
Sapur.005T158800.2	0.011541884	0.018869013	2.904833435	0.00623	0.995028949	NA	purple	-0.64193381	1.41E-19		ATSG17790.1		DNA/RNA associated Golgi protein family	NA
Sapur.016G148800.2	0.030680202	0.016222365	2.665767841	0.006085	0.995146517	NA	purple	-0.668952995	1.02E-21		ATSG30898.1			hypothetical protein
Sapur.014G071200.2	0 NA	NA	NA	NA	NA	NA	purple	0.794012212	2.39E-16	GO:0008168;GO:0008152	ATSG09320.1	ATCOQ3;COQ3;EMB3002	coenzyme Q 3	3-demethylubiquinone-9 3-methyltransferase
Sapur.15W0G044000.1	50.33485003	-0.636150779	0.112718567	-81.1305	0	0	purple	-0.890701782	6.12E-55	GO:0008017;GO:0005524;GO:0003777;GO:0005871	ATANACK1;HM;NACK1	ATNACK1,HM,NACK1	ATP binding microtubule motor family protein	kinesin-like protein NACK1
Sapur.001G080100.1	51.58063875	0.302120812	0.084692611	-34.8937	9.94E-247	4.58E-201	purple	-0.92667105	3.27E-68		ATSG40680.1		membrane-associated kinesin-like regulator 2, putative	membrane-associated protein
Sapur.004G167400.1	148.9912455	-1.192595578	0.067373279	-32.5439	2.55E-232	9.41E-231	purple	-0.94051623	1.45E-74		ATSG18370.1		Plant protein of unknown function (DUF827)	weak movement under blue light protein
Sapur.012G188700.1	84.18647656	-0.891578828	0.130216611	-31.3457	1.11E-215	3.61E-214	purple	-0.923188976	2.97E-66	GO:0045454;GO:0015035;GO:0009055	ATSG30630.1		Glutaredoxin family protein	electron transporter, putative
Sapur.003G002300.1	53.07104853	-0.341192125	0.131313389	-30.8885	1.70E-209	5.34E-208	purple	-0.897845656	5.68E-57	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATSG75445.1		Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.008G138800.1	52.50182552	-2.697667124	0.08785377	-30.7063	4.68E-207	1.46E-205	purple	-0.891215407	4.33E-55		ATSG33400.1			hypothetical protein
Sapur.001G188500.1	24.91168600	-0.551000111	0.178117	-30.1368	4.09E-201	9.04E-200	purple	-0.829440104	3.40E-37		ATSG18800.1			transmembrane protein, putative
Sapur.009G092600.1	72.0826644	-1.568173245	0.07698531	-18.1633	1.64E-174	3.94E-173	purple	-0.930404049	1.88E-69		ATSG28150.1		Domain of unknown function (DUF866)	auxin-regulated protein, putative
Sapur.002G179000.1	120.4102508	-2.187153128	0.094616108	-17.9445	7.27E-172	1.71E-170	purple	-0.909317755	7.62E-61		ATSG05151.1			hypothetical protein
Sapur.012G047700.1	99.42656015	-1.149958891	0.112812855	-27.922	1.44E-171	3.38E-170	purple	-0.868605586	3.78E-49	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATSG18550.1		ATP binding microtubule motor family protein	kinesin-like protein KIF19
Sapur.013G088300.1	579.8890047	-5.121322	0.055437865	-27.655	2.41E-168	5.12E-167	purple	-0.921832102	2.87E-66	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATSG27442.1	ATKIC11;KC11;SCRM	Kinesin-like protein for actin-based movement family protein	inducer of CBF expression 1 protein
Sapur.010G153400.1	134.1584217	-2.202564145	0.07089369	-27.5687	2.64E-167	5.93E-166	purple	-0.871638911	8.54E-50	GO:0005089	ATSG05940.1	ATROPGEF5;ROPGEF5	ROP guanine nucleotide exchange factor 5	NA
Sapur.002G047300.1	305.3017556	-3.168128512	0.132698189	-26.3911	1.73E-153	3.50E-152	purple	-0.88632671	5.27E-47		ATSG07725.1		Putative membrane lipoprotein	membrane lipoprotein, putative
Sapur.003G021500.1	127.226897	-2.283763931	0.08709271	-26.222	1.49E-151	2.95E-150	purple	-0.861271708	1.99E-47	GO:0005515	ATSG72670.1	IQD8	IQ-domain 8	IQ calmodulin-binding motif protein
Sapur.016G081600.1	164.0052616	-2.355383987	0.086038831	-26.0556	1.16E-149	2.26E-148	purple	-0.918576391	2.27E-64		ATSG53320.1			hypothetical protein
Sapur.013G139500.1	40.37176132	-0.934564056	0.131818429	-25.9284	3.18E-148	6.14E-147	purple	-0.867645012	7.49E-49	GO:0045454;GO:0015035;GO:0009055	ATSG45260.1		Glutaredoxin family protein (DUF641)	DUF641 family protein
Sapur.014G309500.1	254.4931577	-3.134001443	0.122839649	-25.5199	1.19E-143	2.19E-142	purple	-0.89619854	1.42E-56	GO:0007165	ATSG03100.1		Rho GTPase activating protein with PAK-box/PX1-Rho-binding domain	Rho GTPase-activating protein
Sapur.005G031500.1	89.03973933	-1.643142	0.09974732	-25.4067	2.51E-143	4.61E-142	purple	-0.85064603	5.47E-45		ATLTP8;TLP8	ATLTP8,TLP8	tubby like protein	tubby-like protein
Sapur.013G107300.1	222.5736297	-2.136767124	0.084010919	-25.4344	1.05E-142	1.93E-141	purple	-0.8490766	6.23E-45	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATSG72850.1		Di-glucose binding protein with kinesin motor domain	Di-glucose binding protein with kinesin motor domain protein
Sapur.008G020200.1	435.3358812	-3.823122475	0.07255551	-25.2513	1.10E-140	1.98E-139	purple	-0.845604046	1.46E-44	GO:0006468;GO:0005524;GO:0004672	ATSG70540.1	CDKB2;;1	cyclin-dependent kinase B2;1	cyclin-dependent kinase
Sapur.015G042100.1	52.9962453	-1.468781836	0.217378502	-25.1579	1.16E-139	2.07E-138	purple	-0.55423361	3.93E-14	GO:0003677	ATSG33880.1	HB-13;ZIP;WOX9	homeobox-3	wuschel homeobox protein, putative
Sapur.014G030300.1	69.00272005	-1.566 338 2496	0.122465127	-24.926	1.89E-137	3.76E-136	purple	-0.826428108	6.20E-48	GO:0031225;GO:0016046;GO:0010215	ATSG81120.1	ATSBH1;COB;TJ;SEB1	COBRA like protein-7 precursor	COBRA like protein
Sapur.15W0G029000.1	58.66274567	-1.461758517	0.139485235	-24.8181	5.72E-136	9.84E-135	purple	-0.8909614	9.50E-55	GO:0006236;GO:0032147;GO:0005679;GO:0005819	ATSG70780.2	TPK2	targeting protein for MIK2	NA
Sapur.005G001300.1	33.78078811	-0.312375642	0.095189847	-24.7137	7.61E-135	1.38E-133	purple	-0.842436062	1.06E-48		ATSG40960.1			hypothetical protein
Sapur.010G009200.1	83.14633669	-1.473584877	0.0605491	-24.3364	8.07E-131	1.33E-129	purple	-0.840949895	4.24E-43		ATSG15830.1		ARM repeat superfamily protein	clasp amino-terminal protein
Sapur.006G188200.1	131.7981639	-2.09657507	0.086207219	-24.2505	6.53E-130	1.06E-128	purple	-0.89513748	2.94E-56	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATSG68400.1		leucine-rich repeat transmembrane protein kinase family protein	tyrosine kinase domain protein
Sapur.15W0G151100.1	36.70029948	-0.312312128	0.094606019	-24.1124	1.85E-128	2.97E-127	purple	-0.82800397	3.70E-41		ATSG70510.1			NA
Sapur.016G285400.1	231.6674116	-2.000806619	0.083295931	-24.0312	1.67E-127	2.64E-126	purple	-0.857292221	1.51E-46	GO:0005524;GO:0004252	ATSG20430.1		Subtilase family protein	subtilisin-like protease
Sapur.006G067400.1	217.8518761	-2.406246422	0.102087653	-23.5609	1.29E-127	5.18E-126	purple	-0.854009379	2.87E-46	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATSG27424.1		ATP binding microtubule motor family protein	kinesin-like protein KIF11B, putative
Sapur.007G037700.1	21.66318573	-2.895874877	0.121902145	-23.7885	4.39E-125	6.77E-124	purple	-0.854892893	1.85E-46		ATSG25530.1		Zinc-finger domain of monoamine-oxidase A repressor R1	zinc finger CCCH domain protein, putative
Sapur.003G039700.1	36.88823923	-1.522830996	0.107536828	-23.4626	9.81E-122	1.46E-120	purple	-0.862130895	1.27E-47	GO:0004872	ATSG66840.1		GAP domain containing protein	membrane protein, putative
Sapur.010G029300.1	94.41552587	-2.516883237	0.107939936	-23.3174	3.95E-120	4.33E-119	purple	-0.891479956	3.63E-55		ATSG23790.1		Plant protein of unknown function (DUF936)	DUF936 family protein
Sapur.010G141900.1	124.1196665	-3.503222728	0.073239007	-23.2558	1.24E-119	2.31E-118	purple	-0.858394972	2.02E-47	GO:0006457;GO:0003755;GO:0006413	ATCYP5;CYP19-4;CYP5		cyclophilin 5	peptidyl-prolyl cis-trans isomerase, cyclophilin-type protein
Sapur.019G031300.1	175.4218145	-2.554081356	0.110919633	-23.0264	2.54E-117	3.56E-116	purple	-0.8454672	4.47E-44	GO:0016788	ATLTL1;LTL1		Li-tolerant lipase 1	NA
Sapur.006G089800.1	149.4939027	-4.401368886	0.091187123	-22.9033	4.31E-116	5.96E-115	purple	-0.878329397	1.52E-51	GO:0005515	ATSG49910.1	BUB3.2	Transducin/WD40 repeat-like superfamily protein	mitotic checkpoint protein BUB3
Sapur.009G167600.1	177.7195924	-2.924656143	0.105375545	-22.8386	1.90E-115	2.61E-114	purple	-0.854520297	2.61E-46		ATSG49100.1		ARM repeat superfamily protein	clasp amino-terminal protein
Sapur.001G062300.1	67.10594549	-2.088345881	0.117827232	-22.8159	3.19E-115	4.37E-114	purple	-0.859015092	4.00E-47		ATSG32135.1			transmembrane protein, putative
Sapur.011G072400.1	37.09617951	-2.305401371	0.10125341	-22.7601	9.28E-115	1.27E-113	purple	-0.822867113	5.64E-40	GO:0006468;GO:0005524;GO:0004672;GO:0030246	ATSG18830.1		Concanavalin A-like lectin protein kinase family protein	lectin-domain receptor kinase
Sapur.007G007300.1	264.8676133	-2.341004082	0.09450769	-22.7682	9.47E-115	1.29E-113	purple	-0.897817245	4.40E-57	GO:0005515	ATSG49660.1		Transducin/WD40 repeat-like superfamily protein	WD40 repeat protein, compass complex protein
Sapur.016G142200.1	32.46277333	-1.763802322	0.077052429	-22.7596	1.15E-114	1.57E-113	purple	-0.889969887	5.64E-60	GO:0006284	ATSG27040.1		HHH-GPD superfamily base excision DNA repair protein	AP/5c-specific adenine DNA glycosylase
Sapur.013G111600.1	77.07372145	-2.350564464	0.103378851	-22.7378	1.90E-114	2.58E-113	purple	-0.846295657	2.91E-44		ATSG70510.1			hypothetical protein
Sapur.008G155400.1	58.17799665	-2.346389941	0.103837291	-22.5887	4.46E-113	5.97E-112	purple	-0.89202651	1.34E-56	GO:0005515	ATSG31130.1	ATRANGAP1;RANGAP1	RAN GTPase activating protein 1	Ran GTPase activating protein
Sapur.001G172600.1	164.184554	-3.268577003	0.092779084	-22.5414	1.63E-112	2.17E-111	purple	-0.873170528	3.08E-50		ATSG54630.1			HEC/Hrb1RBP family protein
Sapur.010G042700.1	496.0813534	-5.521445449	0.0677529	-22.4974	6.55E-111	8.69E-110	purple	-0.893432043	4.97E-55		ATSG04760.1		Pentatricopeptide repeat (PPR-like) superfamily protein	PPR containing plant protein
Sapur.013G021300.1	51.13729479	-1.929208688	0.086061602	-22.4178	2.64E-111	3.45E-110	purple	-0.887239779	5.80E-54		ATSG53301.1	ATNJATTAN	cyclin family	microtubule-binding protein TANGLED protein
Sapur.009G068100.1	138.0647775	-3.869022621	0.088985549	-22.3883	4.80E-110	6.17E-109	purple	-0.867642274	2.20E-37		ATSG16630.1			transmembrane protein, putative
Sapur.006G085200.1	76.9318168	-2.252792232	0.101128078	-22.2782	6.01E-110	7.73E-109	purple	-0.848994018	2.72E-45	GO:0005515;GO:0006468;GO:0004672	ATSG67410.1	IMK2	inflorescence meristem receptor-like kinase 2	receptor-like kinase
Sapur.002G016900.1	575.134828	-7.715067982	0.079325186	-22.0099	2.32E-107	2.89E-106	purple	-0.891077622	9.96E-56	GO:0005634;GO:0003950;GO:0004673;GO:0008270;GO:0003677	ATSG31320.1	ATWRP2;PARP2	poly(ADP-ribose) polymerase domain protein	poly(ADP-ribose) polymerase domain protein
Sapur.012G087900.1	642.8302744	-2.272344407	0.104107895	-21.8307	1.19E-105	1.45E-104	purple	-0.892913029	1.31E-55		ATSG19120.1	EIN3	EXORDIUM like 5	plant(kingdom)-specific protein
Sapur.016G232800.1	127.017255	-1.937945906	0.088663221	-21.8077	1.96E-105	2.40E-104	purple	-0.83262053	1.29E-41		ATSG55010.1			NA
Sapur.015G074200.1	55.18011633	-1.874344468	0.086020754	-21.7865	2.92E-105	3.56E-104	purple	-0.851940407	5.20E-46	GO:0005085;GO:0016020;GO:0008810;GO:0005215	ATSG34190.1		Xanthine/uracil permease family protein	nucleobase ascorbate transporter
Sapur.010G081800.1	82.70245792	-1.623992205	0.076157676	-21.7776	3.78E-105	4.60E-104	purple	-0.857150604	1.62E-46		ATSG31480.1	DRP5A	Dynamin related protein 5A	dynamin-like protein
Sapur.010G081300.1	50.15871132	-1.188604243	0.10085501	-21.7119	1.58E-104	1.91E-103	purple	-0.882875906	5.50E-53	GO:0008270;GO:0003676;GO:0006265;GO:0003917;GO:0003677	ATSG42660.1		zinc knuckle (CCHC-type) family protein	GRF zinc finger protein
Sapur.010G089400.1	172.7923388	-3.751019299	0.126788851	-21.6976	2.16E-104	2.60E-103	purple	-0.855161265	2.44E-45		ATSG51260.1			hypothetical protein
Sapur.014G035700.1	55.55194133	-1.246681223	0.075470752	-21.6284	9.71E-104	1.16E-102	purple	-0.87979448	3.30E-52		ATSG65530.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing protein
Sapur.017G096100.1	47.77763363	-1.307966721	0.097952751	-21.519	1.01E-102	1.22E-101	purple	-0.809879396	9.75E-38		ATSG38300.1			hypothetical protein
Sapur.008G161200.1	146.2128803	-4.468825897	0.088519671	-21.4365	6.10E-102	7.13E-101	purple	-0.87548023	8.10E-51		ATSG08868.1			hypothetical protein
Sapur.009G091000.1	193.3825861	-5.263418836	0.093573507	-21.3123	8.73E-101	1.00E-99	purple	-0.829370879	4.24E-37	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATKL;KATA;KATAP	ATKL;KATA;KATAP	kinesin 1	kinesin motor domain protein
Sapur.009G080900.1	16.27597354	-2.904709505	0.137081966	-21.1896	1.19E-99	1.35E-98	purple	-0.854864842	6.17E-46	GO:0003677	ATSG19184.1		AP2/B3-like transcriptional factor family protein	B3 DNA binding domain protein
Sapur.001G203400.1	120.3942471	-2.062366623	0.097812834	-21.061	9.63E-99	1.08E-97	purple	-0.829491261	4.75E-40	GO:0005515	AENODIL17;ENODL17	AENODIL17,ENODL17	early nodulin-like protein 17	blue copper-like protein
Sapur.015G204400.1	75.350438	-2.305338016	0.10208595	-20.903	5.03E-97	5.53E-96	purple	-0.819715318	2.39E-39		ATSG17680.2		Kinase interacting (KIP1-like) family protein	KIP1-like protein
Sapur.015G097500.1	122.6091721	-1.875105377	0.09868602	-20.8248	3.58E-96	2.80E-95	purple	-0.85194504	2.01E-36		ATSG38570.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.004G169700.1	409.8986185	-8.855145509	0.087139134	-20.8247	2.59E-96	2.81E-95	purple	-0.833082845	1.06E-41	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATSG19150.1	PDK2	phosphoglycerate kinase family 2	kinesin motor domain protein
Sapur.007G088900.1	298.3753339	-6.911513802	0.094328714	-20.798	4.51E-96	4.88E-95	purple	-0.864836104	2.07E-48		ATSG16080.1		PRL1-interacting factor, putative	PRL1-interacting factor G
Sapur.011G018500.1	106.7614865	-1.486612889	0.071625856	-20.7553	1.10E-95	1.18E-94	purple	-0.828835859	6.70E-41	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	ATKL;KATA;KATAP	ATKL;KATA;KATAP	kinesin 1	kinesin, putative
Sapur.002G016400.1	30.42956212	-0.985094786	0.081970726	-20.5573	6.63E-94	6.99E-93	purple	-0.813939089	2.46E-38		ATSG19980.1		cytomatrix protein-related	cytomatrix-like protein, putative
Sapur.001G195000.1	41.76787784	-0.925258164	0.064883115	-20.4693	2.54E-93	2.66E-92	purple	-0.822984198	6.21E-40		ATSG29280.1			hypothetical protein
Sapur.005G293800.1	88.3328661	-2.214809384	0.059595027	-20.3844	2.30E-92	2.38E-91	purple	-0.869207775	3.04E-49	GO:0008270	ATSG38440.1		DHHC-type zinc finger family protein	zinc finger protein
Sapur.012G088200.1	182.7919857	-4.263418836	0.059375937	-20.3406	5.62E-92	5.76E-91	purple	-0.894440789	7.96E-52	GO:0005975;GO:0004553	ATGBG2;GIA	ATGBG2;GIA	O-Glycosyl hydrolases family 2 protein	glucan endo-1?,3?,3-beta-glucosidase
Sapur.005G146300.1	445.9340198	-7.2367917	0.053365609	-20.2185	6.73E-91	6.83E-90	purple	-0.846796321	2.42E-44		ATSG02440.1			plant/T23H19-170 protein
Sapur.014G134900.1	34.57661964	-1.353668806	0.136788479	-20.2163	7.04E-91	7.14E-90	purple	-0.822084198	6.45E-40		ATSG20620.1	CHUP1	Hydroxyproline-rich glycoprotein family protein	unusual positioning of chloroplasts 1A
Sapur.005G076900.1	69.11618646	-2.157058232	0.107048845	-20.1502	2.68E-90	2.69E-89	purple	-0.821767723	1.08E-39		ATSG28370.1			transmembrane protein, putative
Sapur.001G082300.1	1180.498087	-8.574007185	0.08486802	-20.1248	3.60E-90	3.24E-87	purple	-0.820437	1.22E-39	GO:0003924;GO:0007017;GO:0005874	ATSG14660.2	TUA6	Tubulin/Tria2 family protein	alpha-tubulin
Sapur.017G102700.1	177.2310024	-0.92610208	0.047002537	-19.6781	3.32E-86	3.16E-85	purple	-0.859034699	6.27E-47		ATSG65510.1			AAR2 protein family
Sapur.003G030000.1	100.4828447	-1.577771169	0.09200589	-19.6517	5.16E-86	4.91E-85	purple	-0.838284657	1.31E-41		ATSG08160.1		Vesicular transport Sec31/Sec31 family protein	COP1 coatomer protein
Sapur.010G042700.1	171.5270881	-2.344264826	0.119312127	-19.648	6.01E-86	5.71E-85	purple	-0.839478847	6.67E-43

Sapur.016G071200.1	285.8623647	8.814546141	0.070188822	-11.6064	3.82E-31	1.47E-30	purple	-0.667939939	1.42E-21	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	AT2G36200.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	125 kDa kinesin-like protein				
Sapur.002G195500.1	604.8640432	-0.538947575	-0.04674288	-11.53	9.31E-31	3.56E-30	purple	-0.713401657	1.03E-25	GO:0005515	AT5G48460.1	Actin binding Calponin homology (CH) domain-containing protein	fimbrin				
Sapur.T036600.1	39.116125	-0.98451728	0.085674358	-11.4873	1.53E-30	5.81E-30	purple	-0.68177451	8.48E-23		AT4G27730.1	Regulator of Ipu4 activity in the MYB pathway protein	NA				
Sapur.002G046400.1	47.96931651	-0.763581746	0.066601068	-11.465	1.98E-30	7.50E-30	purple	-0.648271265	4.38E-20		AT5G50890.1	alpha/beta-Hydrolases superfamily protein	GDSL esterase/lipase				
Sapur.012G028300.1	49.62753203	-0.870961806	0.075475154	-11.3891	4.74E-30	1.78E-29	purple	-0.629012273	1.13E-18		AT4G21540.1		hypothetical protein				
Sapur.T180900.1	54.42716932	-1.129732318	0.099416498	-11.3636	6.35E-30	2.38E-29	purple	-0.612183306	1.61E-17	GO:0006468;GO:0005524;GO:0004672;GO:0008270;GO:0008022;GO:0006625;GO:0005737	APM4,KTP2K12,PEK12	pertein-12	NA				
Sapur.016G111000.1	114.4921818	-1.466424386	0.129381557	-11.1795	5.14E-29	1.89E-28	purple	-0.618808459	4.93E-18		AT5G51680.1	Tautomerase/MIF superfamily protein	macrophage migration inhibitory factor-like protein				
Sapur.007G051100.1	23.92652218	-0.919218646	0.092032392	-11.0756	1.65E-28	6.05E-28	purple	-0.619443007	1.61E-20		EMB2763	ribonuclease III family protein	NA				
Sapur.017G059100.1	16.686271	-1.060900764	0.095819281	-11.0719	1.72E-28	6.26E-28	purple	-0.642818028	1.13E-19	GO:0005515	AT5G34355.1	ATPS1,PS1	forkhead-associated (FHA) domain-containing protein	NA			
Sapur.007G050500.1	55.74797542	-1.368392249	0.126944804	-10.7884	1.16E-26	4.26E-26	purple	-0.596148887	7.22E-17		EMB2763	ribonuclease III family protein	NA				
Sapur.010G061600.1	272.8563946	-1.157417519	0.106948782	-11.0284	2.79E-26	1.01E-27	purple	-0.618256135	6.30E-18	GO:0016887;GO:0005524;GO:0050885;GO:0042626;GO:0016021;GO:0006810	AT3G10080.1	ATMRP3,MRP3	multidrug resistance-associated protein 3	NA			
Sapur.002G195200.1	31.36838604	-0.9182624	0.104956175	-10.8577	1.83E-27	6.51E-27	purple	-0.618543006	1.02E-18	GO:0045454;GO:0015035;GO:0009055	AT5G42620.1	Glutaredoxin family protein	electron transporter, putative				
Sapur.016G176100.1	5.256682661	-1.691215562	0.159410077	-10.6092	2.70E-26	9.35E-26	purple	-0.634089326	4.90E-19				hypothetical protein				
Sapur.011G029200.1	3.598954671	-2.086175888	0.198861161	-10.2836	8.35E-25	2.80E-24	purple	-0.64848616	1.17E-21		AT4G54490.1	PBP1	pinoid-binding protein 1	vacuolar iron transporter-like protein			
Sapur.005G164000.1	25.17543328	-0.094009864	0.107176639	-10.2075	1.83E-24	6.09E-24	purple	-0.6123	2.12E-20	GO:0006396	AT5G07580.1	Small nuclear ribonucleoprotein family protein	small nuclear ribonucleoprotein Sm protein D1				
Sapur.010G058900.1	10.78633663	-1.021031158	0.136183862	-10.1916	2.16E-24	7.16E-24	purple	-0.61431658	2.79E-18		AT5G68550.1	DUF761 domain protein	NA				
Sapur.014G127000.1	251.2426817	-0.495574631	0.04910847	-10.1729	2.62E-24	8.66E-24	purple	-0.637870651	2.61E-19	GO:0070176;GO:0000796	AT3G21590.1		condensin complex subunit 2				
Sapur.016G034200.1	160.4324261	-1.054715628	0.104205168	-10.1109	4.94E-24	1.62E-23	purple	-0.603910856	5.63E-17	GO:0016758;GO:0008195	AT5G21760.1	HYR1	UDP-Glycosyltransferase superfamily protein	UDP-glucose flavonoid 3-O-glucosyltransferase, putative			
Sapur.007G054100.1	11.75064956	-1.262312277	0.137005212	-9.56411	2.13E-21	7.05E-21	purple	-0.596760157	5.61E-16	GO:0016301;GO:0006470;GO:0004722	AT5G18160.1	ribonuclease III family protein	NA				
Sapur.005G110700.1	37.19519762	-1.041185958	0.104776991	-9.93735	2.86E-23	9.21E-23	purple	-0.583983301	9.91E-16		AT5G34355.1	ATPS1,PS1	forkhead-associated (FHA) domain-containing protein	NA			
Sapur.T142600.1	14.82273203	-1.013847	0.129445804	-9.76804	1.15E-22	3.66E-22	purple	-0.645434695	2.70E-20	GO:0016846	TAR2	tryptophan aminotransferase related 2	tryptophan aminotransferase				
Sapur.T177000.1	43.21072639	-1.01834467	0.103943016	-9.79714	1.16E-22	3.67E-22	purple	-0.57827548	2.36E-15		AT5G34355.1	ATPS1,PS1	forkhead-associated (FHA) domain-containing protein	NA			
Sapur.007G054900.1	18.77857611	-0.911398671	0.105107959	-9.62153	6.49E-22	2.02E-21	purple	-0.607107227	1.46E-17		AT4G27730.1	Regulator of Ipu4 activity in the MYB pathway protein	NA				
Sapur.010G016900.1	17.87846426	-0.861693572	0.115569276	-9.61522	6.90E-22	2.14E-21	purple	-0.60884634	8.93E-17				NA				
Sapur.010G039400.1	30.82263659	-0.778677888	0.092501439	-9.38693	3.16E-21	1.88E-20	purple	-0.648881218	1.16E-18	GO:0043531	AT5G52230.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	adenosine-triphosphatase, putative				
Sapur.012G092000.1	4.753562203	-2.295386616	0.138218009	-9.37337	7.03E-21	2.13E-20	purple	-0.616342088	8.49E-18				NA				
Sapur.010G092600.1	3804.555429	-0.954888829	0.102173265	-9.34596	9.11E-21	2.76E-20	purple	-0.54192277	2.55E-13	GO:0055114;GO:0016491	AT4G21880.2	ANS,LDOX,TD54,TT18	leucoanthocyanidin dioxygenase	anthocyanidin synthase			
Sapur.003G130100.1	37.86146785	-0.924760064	0.112911747	-9.25264	2.18E-20	6.54E-20	purple	-0.605737056	4.26E-17		AT4G33180.1	Ribosome biogenesis protein	transmembrane protein, putative				
Sapur.016G299500.1	536.8853868	-0.056393983	0.114600424	-9.21753	3.04E-20	9.06E-20	purple	-0.618147814	6.40E-18		AT4G17030.1	Sec14p-like phosphatidylinositol transfer family protein	patellin 4 protein, putative				
Sapur.T179100.1	19.97507908	-1.029696469	0.112362416	-9.16643	4.89E-20	1.45E-19	purple	-0.52438861	1.02E-12	GO:0006468;GO:0005524;GO:0004672;GO:0008270;GO:0008022;GO:0006625;GO:0005737	APM4,KTP2K12,PEK12	pertein-12	NA				
Sapur.007G056500.1	6.362609988	-1.146733707	0.125278334	-9.15378	5.50E-20	1.63E-19	purple	-0.556878665	9.99E-15		AT4G15730.1	Regulator of Ipu4 activity in the MYB pathway protein	NA				
Sapur.010G056100.1	18.00756617	-0.767173109	0.086406989	-9.11766	7.17E-20	2.12E-19	purple	-0.588420304	1.31E-16	GO:0005515	AT5G48150.1	Leucine-rich receptor-like protein kinase family protein	LRR receptor-like Serine/Threonine-kinase GSO1				
Sapur.005G127800.1	12.24974786	-0.803368874	0.110244488	-9.10111	8.94E-20	2.63E-19	purple	-0.55863805	2.90E-14		AT5G34355.1	ATPS1,PS1	forkhead-associated (FHA) domain-containing protein	NA			
Sapur.T000400.1	4.428149483	-1.78041203	0.197611464	-9.00957	2.07E-19	6.03E-19	purple	-0.532676088	6.93E-14	GO:0016020;GO:0004970	AT2G26120.1	GLR2.7	glutamate receptor 2.7	glutamate-gated kainate-type ion channel receptor subunit GluR5			
Sapur.T042900.1	12.18837837	-0.895176357	0.099692263	-8.97913	2.73E-19	7.94E-19	purple	-0.543945375	1.91E-13	GO:0008270;GO:0008022;GO:0006625;GO:0005779	APM4,KTP2K12,PEK12	pertein-12	NA				
Sapur.T180800.1	8.357615547	-1.25431447	0.140124387	-8.9507	3.52E-19	1.02E-18	purple	-0.551288052	5.74E-14				NA				
Sapur.016G170400.1	115.26289	-0.698049934	0.078076206	-8.94061	3.87E-19	1.12E-18	purple	-0.57478334	3.49E-15		AT4G17000.1		hypothetical protein				
Sapur.002G182100.2	2.979429332	-1.796544866	0.203159012	-8.84304	9.31E-19	2.67E-18	purple	-0.65429457	1.51E-20	GO:0005617;GO:0070716;GO:0005524;GO:0003777;GO:0005871	AT5G23670.1	KINESIN-12B,PAKRP1L	phragmoplast-associated kinesin-related protein, putative	kinesin motor domain protein			
Sapur.013G054700.1	1.635776152	-2.145638278	0.242838314	-8.83039	1.04E-18	2.98E-18	purple	-0.582079773	2.02E-15	GO:0005681;GO:0003196;GO:0003887	AT4G34185.2		ARM repeat protein	ARM repeat protein			
Sapur.007G058800.1	17.94625258	-0.83154465	0.094306747	-8.81427	1.20E-18	3.44E-18	purple	-0.595110694	2.05E-16		AT4G15730.1	Regulator of Ipu4 activity in the MYB pathway protein	NA				
Sapur.T005400.1	12.87628885	-1.02197551	0.110158822	-8.78231	1.60E-18	4.57E-18	purple	-0.54383292	5.12E-13				NA				
Sapur.014G074900.1	14.62043204	-1.142644474	0.130219221	-8.77324	1.74E-18	4.94E-18	purple	-0.56829028	1.08E-14		GO:0032200.1	TRY	Homeodomain-like superfamily protein	MYB-like transcription factor			
Sapur.T002700.1	60.00211084	-0.854964454	0.088816418	-8.61661	4.74E-18	1.33E-17	purple	-0.558125251	1.10E-14	GO:0005515	AT5G34355.1	ATPS1,PS1	forkhead-associated (FHA) domain-containing protein	NA			
Sapur.010G014000.1	2451.451005	-0.008263992	0.116819307	-8.63099	6.08E-18	1.71E-17	purple	-0.574632844	3.56E-15	GO:0016758;GO:0008152	AT5G21790.1		UDP-Glycosyltransferase superfamily protein	NA			
Sapur.T018800.1	4.625062237	-1.853224497	0.217407195	-8.60229	7.81E-18	2.18E-17	purple	-0.546824375	1.12E-13				NA				
Sapur.007G056900.1	2.047516102	-1.531794371	0.178728052	-8.57053	1.03E-17	2.87E-17	purple	-0.654180651	1.54E-20				NA				
Sapur.T176000.1	19.60155504	-0.896059611	0.105488099	-8.51022	1.84E-17	5.10E-17	purple	-0.537531112	1.62E-12		AT5G40840.2	ARIA2D1,L5YN2	Rad21/Rec8-like family protein	NA			
Sapur.T176000.1	5.194705224	-1.199380646	0.141048863	-8.50391	1.85E-17	5.12E-17	purple	-0.525337705	1.62E-12				NA				
Sapur.T041900.1	5.963055602	-1.388420588	0.162396399	-8.50246	1.88E-17	5.14E-17	purple	-0.524991558	1.78E-12				NA				
Sapur.006G047800.2	2.080647831	-1.052283252	0.2421876	-8.47404	2.37E-17	6.54E-17	purple	-0.531467746	7.98E-12		AT3G52110.1		CCP-like protein, putative				
Sapur.005G021100.1	150.2472859	-0.604200462	0.071617324	-8.43651	3.27E-17	8.98E-17	purple	-0.58009783	2.41E-14		GO:0009450.1		Protein kinase superfamily protein	Serine/Threonine-kinase hanpin			
Sapur.005G110500.1	14.75875615	-1.021018809	0.109164275	-8.41078	3.41E-17	9.41E-17	purple	-0.54837425	1.02E-13				NA	NA			
Sapur.014G021900.1	535.9569121	-0.394480457	0.046909118	-8.40946	4.12E-17	1.13E-16	purple	-0.562366786	1.80E-14	GO:0005525;GO:0003924	AT3G60190.1	ADLE,AE,ADA,FD,DLI1E,DI	DYNAMIN-like 1E	dynamin-related protein			
Sapur.003G085400.1	47.27519153	-0.847966064	0.107567526	-8.3956	4.64E-17	1.27E-16	purple	-0.605737056	2.04E-17	GO:0005886;GO:0016021	AT5G26330.2	Integrin-linked protein family (ILK)	Ankyrin-repeat protein	NA			
Sapur.003G133600.1	136.3745177	-0.086104316	0.129815656	-8.36651	5.93E-17	1.62E-16	purple	-0.674194205	3.51E-20	GO:0016747;GO:0008610	AT4G37940.1	Sec14p-like phosphatidylinositol transfer family protein	patellin 4 protein, putative				
Sapur.003G142300.1	247.6631236	-0.614264001	0.073825544	-8.27905	1.24E-16	3.26E-16	purple	-0.58604272	1.61E-15	GO:0005886;GO:0016020;GO:0006810;GO:0015171;GO:0003333	AT4G15180.1	CAT8	chalcone and stilbene synthase family protein	chalcone synthase			
Sapur.007G014000.1	17.9703401	-1.065826884	0.128778839	-8.27667	1.27E-16	3.42E-16	purple	-0.526470074	1.42E-12	GO:0005515	AT4G08850.1		Leucine-rich repeat receptor-like protein kinase family protein	receptor-like kinase			
Sapur.007G055600.1	16.55902053	-1.069312419	0.128637378	-8.18535	2.72E-16	7.35E-16	purple	-0.541172831	2.52E-13		AT4G15730.1	Regulator of Ipu4 activity in the MYB pathway protein	NA				
Sapur.T150600.1	2.158605904	-1.567341563	0.191607951	-8.07457	6.77E-16	1.76E-15	purple	-0.523924634	1.90E-12				NA				
Sapur.006G187000.1	158.8076363	-0.812237595	0.081575885	-7.99546	1.29E-15	3.38E-15	purple	-0.562618868	1.76E-14	GO:0045454;GO:0015035;GO:0009055	AT4G33040.1		Thioredoxin superfamily protein	glutaredoxin			
Sapur.T082500.1	54.21264466	-0.917551174	0.114628277	-7.98508	1.40E-15	3.68E-15	purple	-0.513963931	5.80E-12		AT3G26615.1	CLE25	CLAVATA/ESR-RELATED 25	NA			
Sapur.T065500.1	251.1474759	-0.543317482	0.069152142	-7.81688	5.41E-15	1.39E-14	purple	-0.544583871	6.27E-13		AT5G34355.1	ATPS1,PS1	forkhead-associated (FHA) domain-containing protein	NA			
Sapur.T000100.1	626.4138677	-0.306067927	0.039485566	-7.7463	9.56E-15	2.35E-14	purple	-0.556173387	7.77E-14	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	AT3G16060.1		ATP binding microfilament motor family protein	kinesin motor domain protein			
Sapur.013G078900.1	95.71937701	-0.875519406	0.114257594	-7.69769	1.38E-14	3.32E-14	purple	-0.495248648	4.28E-11		AT4G38730.1		DNA binding ATP binding	saccin			
Sapur.016G096500.1	67.94277776	-0.852845061	0.112029471	-7.61069	2.68E-14	6.37E-14	purple	-0.546419058	1.44E-13	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871	AT4G14150.1	ATNACK1,HIK,NACK1	Kinesin-like protein for mitotic motor family protein	kinesin-like protein NACK1			
Sapur.013G138200.1	50.65712046	-0.946093003	0.085469261	-7.55961	3.04E-14	7.70E-14	purple	-0.511998304	7.20E-12		AT4G38730.1		PLATZ transcription factor family protein	PLATZ transcription factor family			
Sapur.003G056600.1	306.7495853	-0.612802149	0.081132148	-7.54733	4.34E-14	1.09E-13	purple	-0.543230307	1.21E-12	GO:0007165	AT5G38380.1	CIPK10,PKS2,SIP1,SNRK3.8	SOS3-interacting protein 1	CBL-interacting kinase			
Sapur.002G035100.1	465.5868648	-0.492402336	0.065341877	-7.53579	4.85E-14	1.21E-13	purple	-0.514867938	5.25E-12		AT5G43430.1			DUF4378 domain protein			
Sapur.003G078200.1	38.4502195	-0.768793931	0.102126841	-7.52062	5.45E-14	1.36E-13	purple	-0.528546464	1.12E-12	GO:0006355;GO:0003677	AT3G12260.1	ANAC037,EMB2749,NAC037	NAC domain protein	NAC transcription factor			
Sapur.010G139000.1	8.695075943	-1.452807005	0.194291686	-7.47744	7.82E-14	1.94E-13	purple	-0.477085049	2.67E-10	GO:0003247	AT3G17150.1			wall-associated receptor kinase galacturonan-binding protein			
Sapur.T042500.1	6.931837114	-0.875285651	0.117340902	-7.45934	8.70E-14	2.16E-13	purple	-0.47038543	5.10E-10				NA	NA			
Sapur.T042600.1	6.684816464	-0.925760635	0.124263738	-7.45642	8.89E-14	2.20E-13	purple	-0.48867407	6.61E-11		AT3G28455.1	CLE25	CLAVATA/ESR-RELATED 25	NA			
Sapur.006G045000.1	130.5318878	-0.435907754	0.058818275	-7.41262	1.24E-13	3.05E-13	purple	-0.485045752	5.30E-10		AT4G22460.1	PTM,LV14	Sec-independent 4	hypothetical protein			
Sapur.003G142600.1	2.072193827	-1.81510335	0.249808305	-7.3365	1.94E-13	4.75E-13	purple	-0.454675237	7.20E-09	GO:0046983	AT4G22320.1	HEC2	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	bHLH transcription factor			
Sapur.005G127700.1	22.0827988	-0.818664032	0.111367081	-7.35082	1.97E-13	4.83E-13	purple	-0.477155926	2.65E-10		AT5G40840.2	ARIA2D1,L5YN2	Rad21/Rec8-like family protein	NA			
Sapur.005G156000.1	27.60132138	-0.679869352	0.108381883	-7.34836	2.01E-13	4.92E-13	purple	-0.478969152	2.68E-10		AT5G40840.2	ARIA2D1,L5YN2	Rad21/Rec8-like family protein	NA			
Sapur.T042300.1	11.42282239	-0.962379427	0.145191993	-7.31707	2.53E-13	6.18E-13	purple	-0.48899833	8.18E-11		AT3G28455.1	CLE25	CLAVATA/ESR-RELATED 25	NA			
Sapur.T042100.1	2.052696233	-1.395188359	0.177109173	-7.25648	3.97E-13	9.62E-13	purple	-0.534827558	5.47E-13		AT3G28455.1	CLE25	CLAVATA/ESR-RELATED 25	NA			
Sapur.006G120200.1	2.077129974	-1.886881612	0.262490949	-7.20654	5.74E-13	1.38E-12	purple	-0.542977542	1.82E-10		AT2G37370.1		Uncharacterized protein family (UPF0497)	NA			
Sapur.005G127600.1	52.45132779	-0.681181176	0.094829242	-7.18326	6.81E-13	1.64E-12	purple	-0.465172269	8.35E-10		AT5G28370.1			NA			
Sapur.005G127100.1	6.759229991	-0.780288691	0.110725584	-7.04346	1.88E-12	4.46E-12	purple	-0.492088218	1.18E-11		AT5G28370.1			NA			
Sapur.005G126600.1	7.221920795	-0.862898093	0.124140604	-6.95097	3.63E-12	8.51E-12	purple	-0.446543818	4.58E-09		AT5G40840.2	ARIA2D1,L5YN2	Rad21/Rec8-like family protein	NA			
Sapur.004G204200.1	22.13619921	-0.511101112	0.073837853	-6.92163	4.48E-12	9.64E-12	purple	-0.448031543	8.61E-09					hypothetical protein			
Sapur.017G069600.1	714.6025622	-0.217385865	0.031662248	-6.86587	6.61E-12	1.52E-11	purple	-0.486207869	1.08E-10		AT5G51180.1	AtSS2,SS2	starch synthase 2	starch synthase III			
Sapur.005G188700.1	161.0889031	-0.360227447	0.052460776	-6.78765	1.14E-11	2.62E-11	purple	-0.475105663	4.27E-10		AT1G80645.1			cell growth defect factor 2			
Sapur.T177200.1	45.75629029	-0.643872097	0.094954968	-6.78082	1.18E-11	2.75E-11	purple	-0.44760053	5.36E-09		AT3G28370.1			NA			
Sapur.J10G051000.1	3.803673669	-0.611254161	0.100204309	-6.70755	1.51E-11	3.01E-11	purple	-0.492576768	5.54E-11		AT3G28860.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	NA			
Sapur.T155200.1	4.650470496	-0.91871119	0.136275484	-6.74157	1.57E-11	3.59E-11	purple	-0.477437613	2.58E-10		AT3G54750.3			NA			
Sapur.018G020900.1	161.8942083	-0.526875783	0.078916596	-6.67636	2.45E-11	5.57E-11	purple	-0.442875236	6.32E-09	GO:0003968	AT5G49580.1	RDR6,SDE1,SGS2	RNA-dependent RNA polymerase 6	RNA-dependent RNA polymerase			
Sapur.006G083200.2	1.188435938	-0.587406493	0.238738389	-6.6486	2.98E-11	6.71E-11	purple	-0.468810164	5.02E-10					LRR receptor-like			
Sapur.005G079500.1	1.02910051	-1.914824663	0.288176872	-6.64428	3.05E-11	6.90E-11	purple	-0.508302918	1.08E-11	GO:0005634	AT5G30610.1	CYC2,2	Cyclin B2;3	cyclin B2			
Sapur.003G083200.1	0.917802969	-1.760288991	0.283343824	-6.56356	5.25E-11	1.18E-10	purple	-0.464288095	8.91E-10	GO:0004648;GO:0005524;GO:0004672	AT4G21580.1	PEPKR1	phosphoenolpyruvate carboxylase-related kinase 1	calcium-dependent kinase			
Sapur.006G088800.1	77.90937885	-0.502570296	0.076835761	-6.53956	6.17E-11	1.38E-10	purple	-0.503048171	1.89E-11		AT5G09430.1			NA			
Sapur.T056400.1	1.617930654	-1.010461698	0.158058826	-6.52006	7.03E-11	1.57E-10	purple	-0.491197264	3.27E-11		AT5G47520.1			NA			
Sapur.012G028300.2	1.764912874	-1.391440581	0.217473793	-6.3982	1.57E-10	3.47E-10	purple	-0.669182313	9.76E-22		AT5G14230.1			ankyrin 3, ephrin4 protein			
Sapur.T000800.2	1.290994651	-1.511819135	0.243619129	-6.20237	5.56E-10	1.20E-09	purple	-0.44672323	2.62E-09		AT4G27730.1	Regulator of Ipu4 activity in the MYB pathway protein	Regulator of Ipu4 activity in the MYB pathway protein				
Sapur.007G091900.1	144.9320594	-0.436454733	0.075551243	-6.01581	1.79E-09	3.78E-09	purple	-0.417542618	5.31E-08	GO:0016787;GO:0005524;GO:0003677	AT4G35920.1	CHR24	chromatin remodeling 24	chromatin remodeling complex subunit			
Sapur.006G073800.1	969.5278042	-0.312416631	0.054190606	-5.765	8.13E-09	1.68E-08	purple	-0.431038937	4.61E-08	GO:0005515;GO:0004648;GO:0004672	AT2G17180.1		Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase			
Sapur.016G177100.1	55.99456477	-0.405889829	0.071835511	-5.65197	1.59E-08	3.22E-08	purple	-0.43417197	6.96E-08		AT4G48670.1			hypothetical protein			
Sapur.001G161300.1	29.53262746	-0.567832367	0.106153235	-5.33099	9.77E-08	1.92E-07	purple	-0.424835539	2.93E-08	GO:0005515	AT4G16490.1	IQD26	IQ-domain 26	IQ domain protein			
Sapur.T177100.1	43.30051529	-0.50896159	0.09698321	-5.10056	3.36E-07	6.49E-07	purple	-0.350051513	7.01E-05		AT2G39170.1		Conserved in A-thaliana family protein	NA			
Sapur.008G038300.2	0.278904621	-0.967030591	0.459372472	-2.17042	0.029971143	0.041526258	purple	-0.550829819	7.95E-14	GO:0005515	AT5G58190.1		F-box family protein	F-box family protein			
Sapur.006G042200.2	0.316861224	-0.967527257	0.442042837	-2.15418	0.031405186	0.043761631	purple	-0.49914305	2.52E-11		AT1G72120.1	ATCHR2,CHR20	cation/H+ exchger 20	cation/H+ exchger 20			
Sapur.012G107400.2	0.425708887	-0.610042897	0.380758119	-1.6032	0.108889647	0.141054997	purple	-0.550323612	2.34E-11		AT5G07240.1	IQD24	IQ-domain 24	IQ calmodulin-binding motif protein			
Sapur.006G137700.2	0.158026636	-0.256884541	0.9051025	-0.2836	0.776718138	0.858972248	purple	-0.519473304	9.96E-01	GO:0006468;GO:0005524;GO:0004672	AT3G18720.1	EMB3013,RLK	Protein kinase family protein with ARM repeat domain	Serine/Threonine-kinase domain protein			
Sapur.011G144400.2	0.0357611	-0.021399182	2.310400034	-0.00921	0.992656081	NA	purple	-0.749957852	2.29E-20		AT4G04580.1	VPS2.2	SNF7 family protein	charged multivesicular body protein 2a			
Sapur.003G143500.1	48.32736717	-0.616817762	0.147307151	-4.18075	0	0	purple	-0.606704383	5.58E-40	GO:0006355;GO:0003700	AT5G01150.1		Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor			
Sapur.004G112800.1	76.57953763	-1.398849341	0.118028756	-45.7418	0	0	purple	-0.921264291	1.87E-65		AT5G66030.1		Protein of unknown function, DUF547	ternary complex factor MIP1 leucine-zipper protein			
Sapur.005G057500.1	386.4229754	-4.751339416	0.123081762	-38.6201	0	0	purple	-0.84604664	2.60E-44	GO:0055114;GO:0020037;GO:0004879;GO:0004601	AT2G24320.1		Peroxidase superfamily protein	germacrene peroxidase			
Sapur.007G020105.1	207.3748372	-2.562006015	0.067382924	-41.0523	0	0	purple	-0.952601145	1.27E-82		AT4G38520.1		Chaperone DnaJ-domain superfamily protein	auxilin, putative			
Sapur.007G061700.1	61.09554669	-4.969502882	0.179102651	-18.9135	0	0	purple	-0.85751723	1.35E-46	GO:0004857	AT3G12880.1		Plant invertase/pectin methylesterase inhibitor superfamily protein	plant invertase/pectin methylesterase inhibitor domain protein			
Sapur.010G083800.1	89.93633373	-4.750000429	0.251064554	-18.9207	0	0	purple	-0.924050957	2.55E-71		AT2G31361.1	FLO10,YON1,SUP	C2H2 and C2HC zinc fingers superfamily protein	uapsman protein			
Sapur.016G106800.1	116.3318697	-4.27095504	0.078416006	-43.6518	0	0	purple	-0.779023817	0.07E-32		AT5G07080.1		Thioredoxin superfamily protein	gamma-interferon-inducible lysosomal thiol reductase			
Sapur.006G021700.1	60.46656053	-3.363631223	0.138743392	-24.4585	0	0	purple	-0.658840457	1.04E-16		AT5G48450.1		Kinase interacting(KIP1-like) family protein	NA			
Sapur.015W004500.1	60.93613017	-4.777395236	0.158005562	-42.8934	0	0	purple	-0.907405203	3.11E-60	GO:0003247;GO:0006468;GO:0005524;GO:0004672	AT5G18390.2		Protein kinase superfamily protein	wall-associated kinase, putative			
Sapur.015W022600.1	42.23024616	-4.557287287	0.150000149	-40.3925	0	0	purple	-0.826419878	1.65E-40		AT5G57680.2		Kinase interaction (KIN) family protein	KIP1-like protein			
Sapur.009G038300.1	701.2475862	-2.619372071	0.073169326	-36.0293	2.91E-284	1.49E-282	purple	-0.947336234	1.51E-78	GO:0003676	AT5G51950.1		Zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	nucleic acid-binding protein, putative			
Sapur.007G041100.1	186.3980118	-4.313080449	0.123667554	-35.1112	4.55E-270	2.34E-268	purple	-0.94437024	2.96E-77	GO:0005515	AT5G66330.1		Leucine-rich repeat (LRR) family protein				
Sapur.006G094600.1	313.287049	-3.576663533	0.073386972	-35.0844	1.17E-269	5.47E-268	purple	-0.890093183	1.34E-55		AT5G03670.1			hypothetical protein			
Sapur.007G082900.1	97.20548607	-2.364881848	0.065051113	-34.8415	5.72E-266	2.60E-264	purple	-0.929387893	5.57E-69	GO:0005634	AT1G07020.1	ATCYC02;LCYC02,2	Cyclin D2;1	cyclin D2			
Sapur.007G080300.1	1023.165487	-4.164180873	0.041996451	-34.8018	1.61E-265	7.32E-264	purple	-0.943315224	2.30E-76		AT2G28820.1	UVI8B	Regulator of chromosome condensation (RCC1) family protein	UVI4-resistance protein			
Sapur.015W027000.1	136.7737025	-4.129603566	0.103434124	-34.6033	2.26E-262	3.01E-260	purple	-0.81185545	6.71E-38	GO:0016887;GO:0005524;GO:0019138	AT5G74310.1	ATHSP101,HOT1,HSP101	heat shock protein 101	heat shock protein			
Sapur.014G040800.1	108.6116919	-3.962000429	0.114577218	-34.6092	2.29E-262	3.04E-260	purple	-0.928606644	2.24E-68	GO:0005515	AT5G67200.1		Leucine-rich repeat protein kinase family protein	receptor-like protein kinase 9			
Sapur.016G055600.1	49

Sapur.008G140400.1	76.93050665	-3.201353147	0.135064575	-23.7024	3.41E-124	5.19E-123	purple	-0.904778805	2.45E-59	GO:0006355,GO:0005634	AT2G33310.1	IAA13	auxin-induced protein 13	auxin-responsive protein IAA13, putative
Sapur.002G203000.1	449.3995422	-0.620529017	0.0262339	-23.6537	1.08E-123	1.64E-122	purple	-0.879682982	6.73E-52	GO:0008168	AT1G19430.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.013G081500.1	2389.625297	0.647978341	0.02742552	23.62684	2.04E-123	3.09E-122	purple	0.88143297	2.32E-52		AT5G17560.1		BolA-like family protein	BolA superfamily transcriptional regulator, putative
Sapur.006G097700.1	436.3377625	-1.400693139	0.05944838	-23.5615	9.57E-123	1.43E-121	purple	-0.916414591	1.59E-63	GO:0005524,GO:0003678,GO:0043141	AT5G67630.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	TBP-interacting DNA helicase
Sapur.019G045900.1	131.0241204	-0.976297332	0.041439098	-23.5598	9.96E-123	1.49E-121	purple	-0.877922301	1.93E-51		AT5G17690.1	LHP1,TFL2	like heterochromatin protein (LHP1)	chromo domain protein
Sapur.005G049800.1	168.6042162	-1.796084712	0.076575865	-23.455	1.18E-121	1.75E-120	purple	-0.85806783	1.02E-46	GO:0008408,GO:0003677,GO:0000166	AT5G63960.1	EMB2780	DNA binding;nucleotide binding;nucleic acid binding;DNA-directed DNA polymerases;DNA-directed DNA polymera	DNA polymerase
Sapur.010G008000.1	1156.349104	-0.659155376	0.028123875	-23.4376	1.77E-121	2.63E-120	purple	-0.87739006	2.65E-51	GO:0005515	AT4G15900.1	PRL1	pleiotropic regulatory locus 1	PP1/PP2A phosphatase pleiotropic regulator PRL1, putative
Sapur.014G098200.1	236.7204955	-3.172185748	0.135861287	-23.3487	1.42E-120	2.09E-119	purple	-0.73712905	3.57E-28		AT5G49330.1	ATMYB111,MYB111,PFG3	myb domain protein 111	MYB-like DNA-binding domain protein
Sapur.014G075500.1	132.6443569	-1.60123268	0.068714305	-23.3028	4.16E-120	6.09E-119	purple	-0.883717552	5.62E-53		AT4G01030.1		pentatricopeptide (PPR) repeat-containing protein	PPR containing plant protein
Sapur.001G038800.1	170.9825493	-1.475196753	0.063342906	-23.2891	5.72E-120	8.37E-119	purple	-0.894136746	5.90E-56	GO:0006468,GO:0004672	AT1G80640.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.007G106300.1	324.1253512	-1.442958976	0.062017115	-23.2671	9.55E-120	1.39E-118	purple	-0.87769359	2.21E-51		AT1G61730.1		DNA-binding storekeeper protein-related transcriptional regulator	DUF573 family protein
Sapur.004G036700.1	884.2620998	-1.698538114	0.073265098	-23.1835	6.69E-119	9.68E-118	purple	-0.839794056	5.79E-43	GO:0016747	AT1G28680.1		HXXXD-type acyl-transferase family protein	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase
Sapur.014G066300.1	49.62762005	-2.039732533	0.087985023	-23.1827	6.80E-119	9.84E-118	purple	-0.884623344	3.18E-53	GO:0006260,GO:0005634,GO:0000808	AT4G29910.1	ATORC5,ORC5	origin recognition complex protein 5	origin recognition complex 5 subunit
Sapur.010G051300.1	178.3678684	-1.087742781	0.0469349	-23.1756	8.03E-119	1.16E-117	purple	-0.878835055	1.12E-51	GO:0005643	AT1G24310.1			nuclear pore complex protein Nup54
Sapur.009G118100.1	1235.286836	-0.936960637	0.040431167	-23.1742	8.29E-119	1.20E-117	purple	-0.893083387	1.22E-55		AT5G22640.1	emb1211	MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein	MORN repeat protein, putative
Sapur.001G109000.1	2586.573175	0.933698903	0.040312251	23.16167	1.11E-118	1.60E-117	purple	0.875525243	7.92E-51		AT5G45550.1		Mob1/phocein family protein	Mps one binder kinase activator-like protein 1A
Sapur.006G109500.1	168.8180108	-1.396862954	0.060312758	-23.1603	1.14E-118	1.65E-117	purple	-0.861169908	2.09E-47		AT5G02830.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.016G157500.1	180.1475417	-2.141779604	0.092510276	-23.1518	1.39E-118	2.01E-117	purple	-0.882066802	1.57E-52	GO:0005515	AT5G26960.1		Galactose oxidase/kelch repeat superfamily protein	F-box/kelch-repeat plant protein
Sapur.002G183400.1	67.7686391	-1.927162564	0.083376818	-23.1139	3.36E-118	4.80E-117	purple	-0.875615379	7.52E-51	GO:0006281,GO:0005524,GO:0003676	AT3G02060.1		DEAD/DEAH box helicase, putative	NA
Sapur.003G044200.1	23.85554451	-3.145319335	0.136134726	-23.1045	4.18E-118	5.96E-117	purple	-0.844537421	6.85E-44		AT1G31040.1		PLATZ transcription factor family protein	PLATZ transcription factor
Sapur.003G031700.1	76.78504247	-1.715278152	0.074277549	-23.0928	5.47E-118	7.78E-117	purple	-0.877553896	2.41E-51		AT1G15510.1	ATECB2,ECB2,VAC1	Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.013G026800.1	2035.011401	-2.444283276	0.105904221	-23.0801	7.33E-118	1.04E-116	purple	-0.869841698	2.01E-49	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT5G06900.1	CYP93D1	cytochrome P450, family 93, subfamily D, polypeptide 1	NA
Sapur.007G041300.1	131.3962905	-1.998324121	0.086612334	-23.0721	8.84E-118	1.25E-116	purple	-0.760947107	6.33E-31		AT5G67020.1			hypothetical protein
Sapur.013G128900.1	264.6496757	-1.865551308	0.080878915	-23.066	1.02E-117	1.44E-116	purple	-0.846926048	2.27E-44	GO:0042254,GO:0001522	AT1G03530.1	ATNAF1,NAF1	nuclear assembly factor 1	Gar1/NAF1 RNA-binding region protein
Sapur.008G028800.1	193.2786121	-1.538546475	0.066714956	-23.0615	1.13E-117	1.59E-116	purple	-0.784366909	5.79E-34	GO:0003677,GO:0009725,GO:0006355,GO:0005634	AT4G30080.1	ARF16	auxin response factor 16	auxin response factor, putative
Sapur.003G091000.1	374.3486654	-0.968915784	0.042036083	-23.0496	1.48E-117	2.09E-116	purple	-0.848317586	1.19E-44	GO:0006468,GO:0004672	AT1G63500.1		Protein kinase protein with tetratricopeptide repeat domain	tyrosine kinase family protein
Sapur.15WG019100.1	130.0022213	-1.894415292	0.082328831	-23.0104	3.67E-117	5.15E-116	purple	-0.871703189	7.08E-50		AT5G52910.1	ATIM	timeless family protein	timeless protein carboxy-terminal region protein
Sapur.T058400.1	134.8737416	-1.23968025	0.05388989	-23.0039	4.26E-117	5.97E-116	purple	-0.895950171	1.66E-56	GO:0016779,GO:0043631,GO:0003723,GO:0004652,GO:0005634	AT1G17980.1	PAPS1	poly(A) polymerase 1	NA
Sapur.019G031800.1	477.692873	-1.710725168	0.07443245	-22.9836	6.80E-117	9.51E-116	purple	-0.905489203	1.41E-59		AT3G04260.1	PTAC3	plastid transcriptionally active 3	PPR containing protein
Sapur.016G310600.1	110.6276404	-1.65051071	0.07187682	-22.963	1.09E-116	1.52E-115	purple	-0.866195747	1.47E-48		AT3G58660.1		Ribosomal protein L1p/L10e family	NA
Sapur.009G083000.1	59.46473764	-1.197154312	0.052335716	-22.8745	8.33E-116	1.15E-114	purple	-0.877070625	3.20E-51		AT5G39710.1	EMB2745	Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.005G065000.1	365.5386171	-0.930650411	0.040706121	-22.8627	1.09E-115	1.51E-114	purple	-0.877094575	3.16E-51	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT3G50020.1		Leucine-rich receptor-like protein kinase family protein	inactive receptor kinase, putative
Sapur.007G030400.1	556.8201755	-0.954756853	0.041878722	-22.7981	4.78E-115	6.55E-114	purple	-0.883159948	7.97E-53		AT3G50780.1			BTB/POZ domain plant protein
Sapur.012G010600.1	32.09178401	-3.520573205	0.154749426	-22.7502	1.43E-114	1.95E-113	purple	-0.886120378	1.23E-53	GO:0005515	AT5G24330.1	ATXR6,SDG34	ARABIDOPSIS TRITHORAX-RELATED PROTEIN 6	histone-lysine N-methyltransferase ATXR6, putative
Sapur.007G031800.1	756.8799771	-0.725642686	0.031922386	-22.7315	2.19E-114	2.97E-113	purple	-0.879457566	7.71E-52		AT4G37210.1		Tetratricopeptide repeat (TPR)-like superfamily protein	TPR protein, putative
Sapur.017G057400.1	508.7171364	-0.883344318	0.038860348	-22.7313	2.20E-114	2.99E-113	purple	-0.897721845	4.71E-57	GO:0005515	AT5G14170.1	CHC1	SWIB/MDM2 domain superfamily protein	chromatin remodeling complex subunit
Sapur.001G118900.1	183.8830861	-1.514062057	0.066631786	-22.7228	2.67E-114	3.62E-113	purple	-0.88263443	1.10E-52		AT4G17950.1		AT hook motif DNA-binding family protein	AT hook motif DNA-binding family protein, putative
Sapur.002G141000.1	132.4957653	-1.176883693	0.051811594	-22.7147	3.21E-114	4.35E-113	purple	-0.881309182	2.50E-52		AT3G49730.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.013G000100.1	2083.685916	-1.11195638	0.048992151	-22.6811	6.89E-114	9.31E-113	purple	-0.892383065	1.97E-55	GO:0016787,GO:0005524,GO:0003677,GO:0008270,GO:0003676,GO:0005634,GO:000438	AT5G26742.2	emb1138	DEAD box RNA helicase (RH3)	DEAD-box ATP-dependent RNA helicase
Sapur.004G071900.1	242.5767683	-1.588762287	0.070057695	-22.6779	7.40E-114	9.99E-113	purple	-0.869914255	1.93E-49	GO:0005515	AT5G15550.1		Transducin/WD40 repeat-like superfamily protein	ribosome biogenesis WDR12-like protein
Sapur.001G013400.1	253.5624379	-1.741727838	0.077021243	-22.6136	3.18E-113	4.27E-112	purple	-0.883516714	6.38E-53	GO:0016758,GO:0008152	AT5G12890.1		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase, putative
Sapur.013G072700.2	101.3124511	-2.094358294	0.092729999	-22.5856	6.01E-113	8.03E-112	purple	-0.866027522	1.61E-48	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	AT1G33110.1		MATE efflux family protein	NA
Sapur.013G028700.1	382.1113647	-1.927103855	0.085450554	-22.5523	1.28E-112	1.70E-111	purple	-0.848825289	9.34E-45		AT5G27330.1		Prefoldin chaperone subunit family protein	ubiquitin-protein ligase BRE1A, putative
Sapur.013G137500.1	358.5734533	-1.084652552	0.048111002	-22.5448	1.51E-112	2.01E-111	purple	-0.881625275	2.06E-52	GO:0003676,GO:0017069,GO:0000398	AT2G30260.1	U2B\'\'	U2 small nuclear ribonucleoprotein B	U2 small nuclear ribonucleoprotein B 2
Sapur.011G046000.1	219.0255415	-1.545336928	0.068550371	-22.5431	1.57E-112	2.09E-111	purple	-0.870905945	1.11E-49	GO:0030036,GO:0005856	AT4G18600.1	ATSCAR-LIKE.SCARL.WAVES	SCAR family protein	SCAR3, putative
Sapur.15WG091500.1	574.1477949	-1.179563018	0.052388372	-22.5157	2.91E-112	3.85E-111	purple	-0.880535361	4.01E-52	GO:0005515	AT5G40200.1	DegP9	DegP protease 9	NA
Sapur.018G020400.1	302.6836543	-1.956321681	0.086971464	-22.4938	4.77E-112	6.29E-111	purple	-0.898399013	2.89E-57					hypothetical protein
Sapur.008G071400.1	159.9042098	-1.353061951	0.060166603	-22.4886	5.37E-112	7.08E-111	purple	-0.873057889	3.28E-50	GO:0005515	AT1G14030.1		Rubisco methyltransferase family protein	ribulose-1%2C5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase
Sapur.018G040300.1	158.2530373	-1.432641467	0.06372794	-22.4806	6.43E-112	8.46E-111	purple	-0.881430722	2.32E-52	GO:0006355,GO:0003677	AT4G32980.1	ATH1	homeobox gene 1	BEL1-like homeodomain protein
Sapur.005G039400.1	104.1765846	-1.997520854	0.088883535	-22.4735	7.55E-112	9.91E-111	purple	-0.867472618	7.38E-49		AT3G22780.1	ATTSO1,TSO1	Tesmin/TSO1-like CXC domain-containing protein	TSO1, putative
Sapur.017G069500.1	38.68870531	-1.36231323	0.060657067	-22.4593	1.04E-111	1.36E-110	purple	-0.878352164	1.50E-51		AT2G36730.1		Pentatricopeptide repeat (PPR) superfamily protein	cell division protein ftsH, putative
Sapur.016G257800.1	498.947167	-1.157575551	0.051550839	-22.455	1.14E-111	1.50E-110	purple	-0.886823403	7.81E-54	GO:0006468,GO:0005524,GO:0004672	AT1G53050.1		Protein kinase superfamily protein	Serine/Threonine kinase cdk9
Sapur.008G139600.1	1404.15483	-0.801808625	0.035822095	-22.3831	5.75E-111	7.49E-110	purple	-0.888970103	1.93E-54	GO:0016567,GO:0004842,GO:0005515	AT2G33340.1	MAC3B	MOS4-associated complex 3B	ubiquitin-protein ligase, PUB59
Sapur.007G110300.1	78.53233386	-1.298103371	0.058232278	-22.2918	4.44E-110	5.71E-109	purple	-0.885928179	1.39E-53		AT1G06710.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.013G103300.1	97.04534421	-2.539981074	0.114038176	-22.2731	6.74E-110	8.66E-109	purple	-0.881344078	2.45E-52		AT1G72040.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	deoxynucleoside kinase
Sapur.007G034100.1	327.5484446	-0.893058818	0.040123885	-22.2575	9.53E-110	1.22E-108	purple	-0.85659661	2.14E-46	GO:0006913,GO:0005643	AT4G37130.1		hydroxyproline-rich glycoprotein family protein	nucleoporin, putative
Sapur.007G024100.1	278.3798131	-1.609069648	0.072460406	-22.2062	2.99E-109	3.82E-108	purple	-0.838359797	1.09E-42	GO:0016787,GO:0005524,GO:0003677	AT5G66750.1	ATDDM1.CHA1.CHR01.CHR	chromatin remodeling 1	chromatin-remodeling complex ATPase chain, putative
Sapur.012G029700.1	407.1406763	-1.400477361	0.063072723	-22.2042	3.13E-109	4.00E-108	purple	-0.894809534	3.70E-56	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT1G48480.1	RKL1	receptor-like kinase 1	NA
Sapur.009G093400.1	831.243952	-1.373763196	0.061949695	-22.1755	5.93E-109	7.54E-108	purple	-0.857115913	1.65E-46	GO:0032259,GO:0008168,GO:0006364,GO:0005634,GO:0001510,GO:0031167,GO:000864	AT4G25730.1		FtsJ-like methyltransferase family protein	AdoMet-dependent rRNA methyltransferase spb1
Sapur.014G083400.1	376.770062	-1.542083791	0.069719032	-22.1185	2.10E-108	2.65E-107	purple	-0.871623608	7.40E-50	GO:0003676	AT1G01080.1		RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif, a.k.a. RRM%2C RBD protein
Sapur.004G091000.1	1118.504282	-0.769395213	0.034889555	-22.0523	9.08E-108	1.14E-106	purple	-0.88361849	5.98E-53	GO:0016773,GO:0016020,GO:0005524	AT3G50530.1	CRK	CDPK-related kinase	CDPK-related kinase
Sapur.005G076600.1	370.9739079	-1.714926209	0.077803272	-22.0418	1.14E-107	1.43E-106	purple	-0.856678332	2.06E-46		AT1G79150.1		binding	nucleolar complex-associated protein
Sapur.006G146300.1	216.0046781	-1.196041867	0.054413903	-21.9804	4.43E-107	5.52E-106	purple	-0.903741808	5.44E-59		AT4G30840.1		Transducin/WD40 repeat-like superfamily protein	NA
Sapur.008G108500.1	61.77036639	-2.100760201	0.095618486	-21.9702	5.55E-107	6.90E-106	purple	-0.850938693	3.42E-45		AT2G01660.1	PDLP6	plasmodesmata-located protein 6	salt stress response/antifungal domain protein
Sapur.15WG102500.1	89.61521099	-1.293765168	0.058918678	-21.9585	7.18E-107	8.92E-106	purple	-0.848492339	1.09E-44		AT4G24710.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	thyroid receptor-interacting protein
Sapur.005G087700.1	133.3879168	-1.422716842	0.064987305	-21.8922	3.08E-106	3.80E-105	purple	-0.879756097	6.44E-52		AT3G51320.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.15WG001500.1	284.4708406	-1.404871284	0.064212834	-21.8784	4.18E-106	5.14E-105	purple	-0.848591402	1.04E-44	GO:0005515,GO:0000160	AT5G24470.1	APRR5,PRR5	pseudo-response regulator 5	PRR response regulator
Sapur.001G189300.1	1733.661133	1.362088339	0.06235476	21.84418	8.83E-106	1.08E-104	purple	0.820580063	1.71E-39	GO:0008289	AT5G49800.1		Polyketide cyclase/dehydrase and lipid transport superfamily protein	START domain protein
Sapur.019G039400.1	226.4723833	-1.858350088	0.085281781	-21.7907	2.84E-105	3.47E-104	purple	-0.873765865	2.19E-50	GO:0003723,GO:0006396,GO:0000175,GO:0003676,GO:0006402,GO:0004654	AT3G03710.1	PNP,RIF10	polyribonucleotide nucleotidyltransferase, putative	polyribonucleotide nucleotidyltransferase
Sapur.15WG106600.1	714.4537539	-0.876304106	0.040255171	-21.7687	4.59E-105	5.58E-104	purple	-0.876174022	5.42E-51		AT3G48430.1	REF6	relative of early flowering 6	lysine-specific demethylase
Sapur.15WG139600.1	96.78317844	-1.286470058	0.059151142	-21.7489	7.08E-105	8.59E-104	purple	-0.874704923	1.28E-50		AT1G12380.1			hypothetical protein
Sapur.004G169200.1	577.5022143	-0.736542429	0.033917156	-21.7159	1.45E-104	1.75E-103	purple	-0.864900135	2.95E-48		AT1G29690.1	CAD1	MAC/Perforin domain-containing protein	MAC/perforin domain protein
Sapur.011G084200.1	615.0546203	-0.848296016	0.039087266	-21.7026	1.94E-104	2.34E-103	purple	-0.872988385	3.42E-50		AT3G15380.1		Plasma-membrane choline transporter family protein	plasma-membrane choline transporter
Sapur.005G046700.1	95.32550167	-1.63143612	0.075254988	-21.6788	3.25E-104	3.91E-103	purple	-0.852173525	1.89E-45	GO:0005515	AT4G05410.1	YAO	Transducin/WD40 repeat-like superfamily protein	U3 small nucleolar RNA-interacting protein, putative
Sapur.007G001300.1	63.26453198	-1.657321704	0.076455849	-21.6768	3.39E-104	4.08E-103	purple	-0.858522717	8.13E-47	GO:0006355,GO:0005739,GO:0003690	AT1G78930.1		Mitochondrial transcription termination factor family protein	mTERF protein
Sapur.010G058300.1	116.813588	-1.445482207	0.066714214	-21.6668	4.22E-104	5.07E-103	purple	-0.887447373	5.22E-54		AT5G19300.1			RNA methyltransferase, putative
Sapur.007G106900.1	485.9963906	-1.273212986	0.05880523	-21.6514	5.90E-104	7.06E-103	purple	-0.869540253	2.37E-49		AT1G61730.1		DNA-binding storekeeper protein-related transcriptional regulator	NA
Sapur.007G016400.1	243.0678122	-1.028704683	0.047514265	-21.6504	6.02E-104	7.20E-103	purple	-0.898778027	2.20E-57	GO:0006412,GO:0003735	AT4G36420.1		Ribosomal protein L12 family protein	50S ribosomal protein L7/L12, putative
Sapur.012G060100.1	79.192479	-1.80498799	0.083378732	-21.6481	6.34E-104	7.58E-103	purple	-0.877453418	2.55E-51	GO:0006355,GO:0003677	AT5G62940.1	DOF5.6,HCA2	Dof-type zinc finger DNA-binding family protein	NA
Sapur.012G070300.1	130.2940913	-1.038693605	0.048067565	-21.609	1.48E-103	1.76E-102	purple	-0.871329779	8.73E-50		AT5G50350.1			hypothetical protein
Sapur.012G019000.1	144.0143797	-1.147256167	0.053275848	-21.5343	7.44E-103	8.78E-102	purple	-0.890322714	7.88E-55		AT5G16420.1		Pentatricopeptide repeat (PPR-like) superfamily protein	PPR containing plant protein
Sapur.012G054800.1	126.9601831	-1.180001831	0.054895652	-21.4954	1.72E-102	2.02E-101	purple	-0.879156354	9.24E-52	GO:0005515,GO:0030071,GO:0005680	AT3G48150.1	APC8,CDC23	anaphase-promoting complex subunit 8	anaphase-promoting complex subunit
Sapur.002G150400.1	253.3097164	-1.204303047	0.056069779	-21.4786	2.47E-102	2.89E-101	purple	-0.86214213	1.26E-47	GO:0055114,GO:0051287	AT1G01510.1	AN	NAD(P)-binding Rossmann-fold superfamily protein	angustifolia protein
Sapur.003G073200.1	237.4020703	-1.993596347	0.093128061	-21.407	1.15E-101	1.34E-100	purple	-0.854552917	5.91E-46	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT5G61480.1	PXY	Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase
Sapur.012G053300.1	246.8347842	-0.673756167	0.031557169	-21.3503	3.87E-101	4.47E-100	purple	-0.857544465	1.33E-46		AT5G11010.3		Pre-mRNA cleavage complex II protein family	polynucleotide 5'-hydroxyl-kinase NOL9
Sapur.006G032000.1	44.8061175	-1.71259466	0.080335351	-21.3181	7.72E-101	8.88E-100	purple	-0.882968579	8.98E-53	GO:0006397	AT5G04050.1		RNA-directed DNA polymerase (reverse transcriptase)	reverse transcriptase
Sapur.003G157400.1	423.7195261	-1.010904676	0.047584954	-21.2442	3.73E-100	4.25E-99	purple	-0.881444453	2.30E-52	GO:0019867	AT5G19620.1	ATOEP80.EMB213.OEP80.T	outer envelope protein of 80 kDa	outer envelope protein
Sapur.012G013100.1	394.2128127	-1.511411526	0.071185069	-21.2321	4.82E-100	5.49E-99	purple	-0.881153046	2.75E-52		AT3G49240.1	emb1796	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.016G011000.1	468.4170728	-0.979036727	0.046180132	-21.2004	9.47E-100	1.08E-98	purple	-0.836115046	2.89E-42	GO:0005515	AT4G22360.1		SWIB complex BAF60b domain-containing protein	SWIB/MDM2 domain protein
Sapur.001G103200.1	1090.022687	-0.823953704	0.038896986	-21.183	1.37E-99	1.56E-98	purple	-0.866607545	1.18E-48		AT3G24080.1		KRR1 family protein	KRI1 family carboxy-terminal protein
Sapur.009G104900.1	2041.71612	-1.522588073	0.072003405	-21.1461	3.00E-99	3.39E-98	purple	-0.805060661	5.55E-37	GO:0008270,GO:0003676,GO:0006355,GO:0003677	AT4G38680.1	ATCSP2,CSDP2,CSP2,GRP2	glycine rich protein 2	cold-shock DNA-binding domain protein
Sapur.007G032800.1	145.020014	-1.080308006	0.051108415	-21.1376	3.59E-99	4.05E-98	purple	-0.870778252	1.19E-49		AT2G23470.1	RUS4	Protein of unknown function, DUF647	DUF647 domain protein
Sapur.008G090700.1	45.19970908	1.855109832	0.087813717	21.12551	4.64E-99	5.23E-98	purple	0.841256059	3.02E-43	GO:0046983	AT1G68920.3		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	BHLH transcription factor, putative
Sapur.016G253100.1	716.826027	-1.553194983	0.073554652	-21.1162	5.65E-99	6.36E-98	purple	-0.866748624	1.09E-48		AT3G15000.1		cobalt ion binding	hypothetical protein
Sapur.016G281200.1	201.7949048	-1.507757754	0.071417061	-21.112	6.17E-99	6.94E-98	purple	-0.849924507	5.55E-45	GO:0016787,GO:0005524,GO:0003677	AT5G54910.1		DEA(D/H)-box RNA helicase family protein	DEAD-box ATP-dependent RNA helicase
Sapur.013G107100.1	103.3465964	-1.979950433	0.093821895	-21.1033	7.42E-99	8.34E-98	purple	-0.828427292	7.37E-41		AT1G71850.1		Ubiquitin carboxyl-terminal hydrolase family protein	plant organelle RNA recognition domain protein
Sapur.009G069400.1	522.3833473	-0.974739619	0.046234562	-21.0825	1.15E-98	1.29E-97	purple	-0.854278484	6.76E-46		AT3G19650.1		cyclin-related	hypothetical protein
Sapur.016G122800.1	189.8920359	-1.307605191	0.062249573	-21.0059	5.80E-98	6.44E-97	purple	-0.866678752	1.13E-48		AT1G04945.2		HIT-type Zinc finger family protein	HIT-type zinc finger protein
Sapur.017G077300.1	274.5820061	-1.288960275	0.061440584	-20.979	1.02E-97	1.13E-96	purple	-0.860175642	3.50E-47	GO:0005515	AT5G15550.1		Transducin/WD40 repeat-like superfamily protein	ribosome biogenesis WDR12-like protein
Sapur.003G054700.1	124.0087824	-1.603863453	0.076579812	-20.9437	2.14E-97	2.36E-96	purple	-0.852572139	1.56E-45	GO:0006397	AT5G46920.1		Intron maturase, type II family protein	NA
Sapur.010G068100.1	53.32702946	-1.460466661	0.069802207	-20.9229	3.31E-97	3.64E-96	purple	-0.879161131	9.21E-52		AT3G23020.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.005G167300.1	181.9289451	-1.179781943	0.056448077	-20.9003	5.32E-97	5.84E-96	purple	-0.862688163	9.50E-48	GO:0005515	AT1G03110.1		Transducin/WD40 repeat-like superfamily protein	WD40 domain protein
Sapur.016G031600.1	1255.463374	0.803005617	0.038428177	20.89627	5.79E-97	6.35E-96	purple	0.846575826	2.68E-44	GO:0008138,GO:0006470	AT4G18593.1		dual specificity protein phosphatase-related	dual specificity phosphatase domain protein
Sapur.007G005800.1	328.9521611	-0.927714078	0.044402613	-20.8932	6.17E-97	6.76E-96	purple	-0.856644529	2.09E-46	GO:0005525	AT3G49725.1		GTP-binding protein, HflX	NA
Sapur.006G123000.1	254.1612371	-0.917171557	0.043917599	-20.8839	7.50E-97	8.21E-96	purple	-0.852808359	1.39E-45	GO:0009432,GO:0006281,GO:0005524,GO:0003697	AT2G19490.1		recA DNA recombination family protein	DNA repair protein RecA, putative
Sapur.003G051400.1	55.66465949	-1.241610665	0.05949873	-20.8679	1.05E-96	1.15E-95	purple	-0.857780873	1.18E-46					hypothetical protein
Sapur.002G124800.1	30.16375976	-3.291054614	0.157720369	-20.8664	1.08E-96	1.18E-95	purple	-0.81635607	8.69E-39		AT4G00770.1			hypothetical protein
Sapur.005G086700.1	311.8461657	-1.37788733	0.066073086	-20.854	1.40E-96	1.53E-95	purple	-0.841397517	2.84E-43	GO:0005634	AT3G01160.1			Pre-rRNA-processing protein ESF1, putative
Sapur.001G170900.1	286.4558683	-0.693105502	0.033310608	-20.8074	3.71E-96	4.02E-95	purple	-0.873386699	2.72E-50	GO:0003824	AT2G13840.1		Polymerase/histidinol phosphatase-like	PHP domain protein
Sapur.008G138200.1	723.2874222	-1.202826214	0.058072767	-20.7124	2.68E-95	2.87E-94	purple	-0.874978109	1.09E-50		AT1G32580.1		plastid developmental protein DAG, putative	plastid developmental protein DAG, putative
Sapur.002G054800.1	85.61490686	-1.412777141	0.068367676	-20.6644	7.24E-95	7.75E-94	purple	-0.850775452	3.70E-45	GO:0006468,GO:0004672	AT4G38470.1		ACT-like protein tyrosine kinase family protein	tyrosine kinase family protein
Sapur.002G020800.1	115.1213216	-1.809379763	0.087611119	-20.6524	9.29E-95	9.92E-94	purple	-0.832756666	1.21E-41		AT3G49990.1			Low temperature viability protein, putative
Sapur.002G058900.1	121.1407797	-2.25410161	0.109299574	-20.6232	1.70E-94	1.81E-93	purple	-0.706987425	4.32E-25		AT5G55570.1			transmembrane protein, putative
Sapur.002G203100.1	628.5343073	-0.789267871	0.038278453	-20.6191	1.85E-94	1.97E-93	purple	-0.866824042	1.05E-48	GO:0051536,GO:0003824,GO:0010181	AT1G75200.1		flavodoxin family protein / radical SAM domain-containing protein	tRNA wybutosine-synthesizing-like protein
Sapur.010G134700.1	69.38710989	-1.256243405	0.060987121	-20.5985	2.83E-94	3.01E-93	purple	-0.871447637	8.17E-50	GO:0008168	AT1G54310.2		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosylmethionine-dependent methyltransferase
Sapur.15ZG033500.1	17.35255883	-3.154437471	0.153379851	-20.5662	5.51E-94	5.83E-93	purple	-0.749984973	1.28E-29	GO:0016021,GO:0016020				NA
Sapur.019G099200.1	96.55797551	-1.2385608	0.0602328	-20.5629	5.90E-94	6.23E-93	purple	-0.878519959	1.35E-51		AT1G03560.1		Pentatricopeptide repeat (PPR-like) superfamily protein	NA
Sapur.001G154900.1	1042.909211	-0.741166465	0.036066757	-20.5499	7.72E-94	8.15E-93	purple	-0.865089252	2.67E-48	GO:0005643,GO:0046907	AT1G52380.1		NUP50 (Nucleoporin 50 kDa) protein	Ran-binding domain protein
Sapur.006G039000.1	66.89440409	-1.893713465	0.092327568	-20.5108	1.72E-93	1.81E-92	purple	-0.81057173	7.56E-38					NA
Sapur.003G057300.1	772.4455229	-1.165736788	0.056891822	-20.4904	2.62E-93	2.75E-92	purple	-0.872910695	3.57E-50		AT5G46580.1		pentatricopeptide (PPR) repeat-containing protein	PPR containing plant protein
Sapur.016G296000.1	50.20302512	-1.840188235	0.089933301	-20.4617	4.73E-93	4.94E-92	purple	-0.812772111	3.35E-38	GO:0016747	AT5G39050.1		HXXXD-type acyl-transferase family protein	anthocyanin 5-aromatic acyltransferase, putative
Sapur.007G066000.1	68.56537716	-1.293329033	0.063289001	-20.4353	8.12E-93	8.47E-92	purple	-0.843205365	1.26E-43		AT5G23120.1	HCF136	photosystem II stability/assembly factor, chloroplast (HCF136)	NA
Sapur.003G041100.1	67.4155708	-3.726517106	0.182467449	-20.4229	1.05E-92	1.09E-91	purple	-0.807767232	2.10E-37					NA
Sapur.001G181600.1	169.9632419	-1.414060028	0.069245917	-20.4208	1.09E-92	1.14E-91	purple	-0.868427337	4.38E-49	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT5G65700.2	BAM1	Leucine-rich receptor-like protein kinase family protein	LRR receptor-like kinase
Sapur.003G030900.1	616.0879049	-0.818144678	0.040103224	-20.401	1.64E-92	1.70E-91	purple	-0.866488406	1.26E-48		AT2G15690.1		Tetratricopeptide repeat (TPR)-like superfamily protein	DYW nucleic acid deaminase family protein
Sapur.004G117200.1	745.1611288	0.920682993	0.045151374	20.39103	2.01E-92	2.08E-91	purple	0.845539336	4.32E-44	GO:0046983	AT4G34530.1	CIB1	cryptochrome-interacting basic-helix-loop-helix 1	helix loop helix protein
Sapur.016G294200.1	981.4862985	-1.700767199	0.083486798	-20.3717	2.98E-92	3.08E-91	purple	-0.814614552	1.68E-38	GO:0016747	AT5G39050.1		HXXXD-type acyl-transferase family protein	anthocyanin 5-O-glucoside 6-O-malonyltransferase, putative
Sapur.016G006300.1	428.499942	-1.629880747	0.080226082	-20.3161	9.27E-92	9.52E-91	purple	-0.877965586	1.88E-51		AT4G16390.1		pentatricopeptide (PPR) repeat-containing protein	67 kDa RNA-binding protein, P67.1
Sapur.007G096600.1	124.3105527	-1.758591982	0.086636674	-20.2985	1.33E-91	1.36E-90	purple	-0.824160988	4.15E-40	GO:0005515	AT4G05410.1	YAO	Transducin/WD40 repeat-like superfamily protein	U3 small nucleolar RNA-interacting protein, putative
Sapur.006G025100.1	101.8042549	-1.472209915	0.072565151	-20.2881	1.64E-91	1.68E-90	purple	-0.825293599	2.63E-40	GO:0009378,GO:0006310,GO:0006281,GO:0005524	AT3G56690.1	CIP111	Cam interacting protein 111	AAA family ATPase
Sapur.002G195300.1	205.2199773	-1.085485989	0.053591614	-20.2548	3.22E-91	3.29E-90	purple	-0.856055783	2.81E-46		AT5G48470.1			hypothetical protein
Sapur.011G084000.1	57.73925894	-1.527843663	0.075504117	-20.2352	4.79E-91	4.88E-90	purple	-0.848605459	1.04E-44		AT4G21705.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.003G146100.1	85.41129306	-1.512559524	0.074809125	-20.2189	6.67E-91	6.78E-90	purple	-0.891264971	4.19E-55		AT1G11290.1	CRR22	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.002G088200.1	300.018969	-0.954422618	0.047262051	-20.1943	1.10E-90	1.11E-89	purple	-0.849024492	8.50E-45		AT1G09900.1		Pentatricopeptide repeat (PPR-like) superfamily protein	NA
Sapur.001G001300.1	2488.245947	-0.848492559	0.042065143	-20.1709	1.76E-90	1.78E-89	purple	-0.862410468	1.10E-47		AT3G13460.1	ECT2	evolutionarily conserved C-terminal region 2	YTH domain protein
Sapur.15WG003600.1	61.45742238	-2.234877672	0.110856322	-20.1601	2.19E-90	2.21E-89	purple	-0.856633244	2.11E-46		AT5G24510.1		60S acidic ribosomal protein family	NA
Sapur.016G280600.1	75.68188223	-1.104131669	0.05481361	-20.1434	3.08E-90	3.09E-89	purple	-0.862379812	1.12E-47		AT5G54880.1		DTW domain-containing protein	DTW domain protein
Sapur.006G033700.1	402.6741552	-0.77038859	0.038272658	-20.129	4.12E-90	4.13E-89	purple	-0.844347977	7.47E-44	GO:0005515	AT2G41500.1	EMB2776,LIS	WD-40 repeat family protein / small nuclear ribonucleoprotein Prp4p-related	U4/U6 small nuclear ribonucleoprotein PRP4, putative
Sapur.016G234500.1	226.7326854	-1.485458514	0.073797753	-20.1288	4.13E-90	4.14E-89	purple	-0.852331115	1.75E-45	GO:0046983,GO:0006351,GO:0003899	AT1G60620.1	ATRPAC43,RPAC43	RNA polymerase I subunit 43	DNA-directed RNA polymerase subunit
Sapur.15WG072800.1	449.7309831	-2.125833664	0.105728966	-20.1064	6.48E-90	6.47E-89	purple	-0.889916936	1.03E-54	GO:0003676,GO:0006260,GO:0005634,GO:0003677	AT5G08020.1	ATRPA70B,RPA70B	RPA70-kDa subunit B	replication protein A 70 kDa DNA-binding subunit
Sapur.005G187600.1	450.7496805	-1.02381484	0.050929422	-20.1026	7.00E-90	6.98E-89	purple	-0.872682358	4.07E-50		AT3G49990.1			Low temperature viability protein, putative
Sapur.005G208000.1	75.99869947	-2.833693323	0.140994455	-20.0979	7.70E-90	7.68E-89	purple	-0.844664759	6.46E-44		AT1G21050.1		Protein of unknown function, DUF617	DUF617 family protein
Sapur.016G089800.1	102.2689683	-1.076924008	0.053669795	-20.0657	1.47E-89	1.46E-88	purple	-0.863547035	6.05E-48		AT5G03800.1	EMB166,EMB175,emb1899	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.010G192500.1	227.5028453	-1.269186468	0.063369636	-20.0283	3.12E-89	3.09E-88	purple	-0.845801574	3.83E-44		AT1G30240.2			rRNA processing/ribosome biogenesis protein
Sapur.002G105400.1	122.7673758	-1.383337235	0.06907795	-20.0257	3.29E-89	3.25E-88	purple	-0.828195656	8.10E-41	GO:0000723	AT4G09680.1	ATCTC1,CTC1	conserved telomere maintenance component 1	NA
Sapur.003G117200.1	567.0923311	-0.708915725	0.03540465	-20.0232	3.46E-89	3.42E-88	purple	-0.867922168	5.77E-49	GO:0005515	AT1G09760.1	U2A\'	U2 small nuclear ribonucleoprotein A	U2 small nuclear ribonucleoprotein A
Sapur.001G103900.1	120.7871812	-2.183947084	0.109091473	-20.0194	3.73E-89	3.69E-88	purple	-0.810240853	8.54E-38	GO:0005515,GO:0006468,GO:0005524,GO:0004672	AT5G61480.1	PXY	Leucine-rich repeat protein kinase family protein	receptor-like kinase
Sapur.016G038900.1	869.3309414	-1.457109118	0.072785526	-20.0192	3.75E-89	3.70E-88	purple	-0.861006677	2.28E-47	GO:0006396,GO:0003723,GO:0009982,GO:0009451,GO:0001522	AT3G57150.1	AtCBF5.AtNAP57.CBF5.NAP	homologue of NAP57	tRNA pseudouridine synthase
Sapur.008G137400.1	164.6463714	-1.580322576	0.07908359	-19.9829	7.75E-89	7.62E-88	purple	-0.810547354	7.63E-38		AT4G14310.1		Transducin/WD40 repeat-like superfamily protein	transducin/WD40 domain-like protein
Sapur.15WG152900.1	422.4678275	-1.534280268	0.076802279	-19.977	8.73E-89	8.57E-88	purple	-0.834713581	5.29E-42		AT3G58660.1		Ribosomal protein L1p/L10e family	NA
Sapur.016G114900.1	1124.534492	-1.171437009	0.058658355	-19.9705	9.94E-89	9.76E-88	purple	-0.853904459	8.12E-46		AT2G27230.1	LHW	transcription factor-related	bHLH-MYC/R2R3-MYB transcription factor amino-terminal protein
Sapur.003G154900.1	301.9060918	-1.1177444	0.056009977	-19.9562	1.32E-88	1.30E-87	purple	-0.828503129	7.14E-41		AT1G63780.1	IMP4	Ribosomal RNA processing Brix domain protein	U3 small nucleolar ribonucleoprotein IMP4
Sapur.15WG149800.1	127.8279352	-0.787426914	0.039500279	-19.9347	2.03E-88	1.99E-87	purple	-0.866429561	1.30E-48		AT1G55630.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.010G046500.1	57.17422527	-2.386670011	0.11982332	-19.9182	2.83E-88	2.76E-87	purple	-0.783123602	8.58E-34	GO:0006355,GO:0005634	AT2G33310.3	IAA13	auxin-induced protein 13	auxin-responsive protein IAA13, putative
Sapur.004G063300.1	242.5606608	-0.776221048	0.038976434	-19.9151	3.01E-88	2.93E-87	purple	-0.842256406	1.93E-43	GO:0006468,GO:0005524,GO:0004672	AT5G37790.1		Protein kinase superfamily protein	kinase domain protein
Sapur.012G050100.1	266.3890321	-1.349178619	0.067773371	-19.9072	3.52E-88	3.43E-87	purple	-0.873793505	2.16E-50	GO:0006334,GO:0005634	AT1G18800.1	NRP2	NAP1-related protein 2	nucleosome/chromatin assembly factor group protein, putative
Sapur.016G202600.1	3784.25973	1.740547486	0.08750049	19.89186	4.79E-88	4.65E-87	purple	0.839857354	5.63E-43	GO:0016491,GO:0008152	AT3G01980.1		NAD(P)-binding Rossmann-fold superfamily protein	short-chain alcohol dehydrogenase, putative
Sapur.019G084100.1	918.9117217	-1.347310654	0.067749206	-19.8867	5.30E-88	5.15E-87	purple	-0.802262047	1.49E-36		AT4G12600.1		Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	60S ribosomal protein L7aA
Sapur.019G109600.1	19.34039946	-2.943671702	0.148073099	-19.8799	6.08E-88	5.90E-87	purple	-0.776416892	6.85E-33	GO:0016747	AT2G25150.1		HXXXD-type acyl-transferase family protein	anthranilate N-benzoyltransferase, putative
Sapur.002G030800.1	79.94476447	-1.187311954	0.059727763	-19.8787	6.22E-88	6.04E-87	purple	-0.821714758	1.09E-39		AT2G31270.1	ATCDT1A,CDT1,CDT1A	homolog of yeast CDT1 A	DNA replication factor CDT1-like protein
Sapur.005G028600.1	42.86553576	-1.626580532	0.081983468	-19.8403	1.34E-87	1.29E-86	purple	-0.857723365	1.22E-46		AT1G74630.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.007G025300.1	423.7978586	-0.742855701	0.037455552	-19.833	1.55E-87	1.49E-86	purple	-0.854868521	5.06E-46	GO:0003676	AT2G18510.1	emb2444	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in splicing factor 3B subunit 4 (SF3B4)-like protein
Sapur.006G037600.1	74.68052412	-1.239147945	0.062482335	-19.832	1.58E-87	1.52E-86	purple	-0.868973985	3.24E-49		AT1G79540.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.005G041100.1	1926.347873	-0.786824201	0.03967805	-19.8302	1.63E-87	1.58E-86	purple	-0.809288432	1.21E-37		AT5G28840.1	GME	GDP-D-mannose 3\',5\'-epimerase	GDP-D-mannose-3'%2C5'-epimerase
Sapur.017G062800.1	32.99755374	-1.554600614	0.078396385	-19.83	1.64E-87	1.58E-86	purple	-0.848190464	1.26E-44		AT5G39980.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.018G013700.1	252.6913507	-1.713568884	0.086590662	-19.7893	3.68E-87	3.54E-86	purple	-0.814996699	1.45E-38	GO:0005515,GO:0060918,GO:0048513,GO:0004871	AT4G31820.1	ENP,MAB4,NPY1	Phototropic-responsive NPH3 family protein	BTB/POZ domain protein
Sapur.014G034300.1	61.511442	-1.18138793	0.059718948	-19.7825	4.22E-87	4.05E-86	purple	-0.867570138	6.99E-49	GO:0006355,GO:0005739,GO:0003690	AT3G60400.1		Mitochondrial transcription termination factor family protein	NA
Sapur.006G117600.1	43.99916155	-1.736745531	0.087934042	-19.7505	7.94E-87	7.60E-86	purple	-0.823827533	4.74E-40		AT2G06040.1			Rad7, putative
Sapur.001G137000.1	132.0586554	-1.319974077	0.066836312	-19.7494	8.12E-87	7.78E-86	purple	-0.843024901	1.36E-43	GO:0003723,GO:0005525	AT1G30960.1		GTP-binding family protein	GTP-binding protein ERG
Sapur.005G073800.1	4197.223749	-1.191149894	0.060339495	-19.7408	9.62E-87	9.22E-86	purple	-0.859045875	6.23E-47	GO:0003676	AT3G18610.1	ATNUC-L2,NUC-L2,PARLL1	nucleolin like 2	RNA recognition motif 2 in nucleolin-like mainly protein
Sapur.010G186100.1	364.1544566	-1.283947576	0.065182244	-19.6978	2.25E-86	2.14E-85	purple	-0.839659207	6.15E-43		AT3G10530.1		Transducin/WD40 repeat-like superfamily protein	U3 small nucleolar RNA-associated protein, putative
Sapur.001G171500.1	146.6055506	-1.518356086	0.077230541	-19.66	4.74E-86	4.51E-85	purple	-0.890499528	7.00E-55		AT3G26410.1		methyltransferases;nucleic acid binding	tRNA guanosine-2'-O-methyltransferase TRM11-like protein
Sapur.016G114500.1	312.7829403	-1.157386232	0.05895617	-19.6313	8.36E-86	7.91E-85	purple	-0.866957689	9.76E-49	GO:0006396	AT5G22100.1		RNA cyclase family protein	RNA 3'-terminal phosphate cyclase-like protein, putative
Sapur.004G149000.1	227.1170705	-1.273935047	0.064929512	-19.6203	1.04E-85	9.81E-85	purple	-0.853652223	9.19E-46	GO:0032040	AT2G34570.1	MEE21	PIN domain-like family protein	rRNA-processing UTP23-like protein
Sapur.007G005400.1	27.75934953	-4.244900194	0.216382665	-19.6176	1.09E-85	1.03E-84	purple	-0.748458673	1.92E-29	GO:0006355,GO:0005634,GO:0005524,GO:0032502,GO:0006351	AT2G22840.1	AtGRF1,GRF1	growth-regulating factor 1	growth-regulating factor, putative
Sapur.012G026500.1	36.01671196	-1.437087386	0.073279508	-19.611	1.24E-85	1.17E-84	purple	-0.859467507	5.03E-47		AT5G16860.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.005G104700.1	42.18911183	-1.356636246	0.069239119	-19.5935	1.76E-85	1.66E-84	purple	-0.861021047	2.26E-47		AT3G50420.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.002G091500.1	28.75037392	-1.670661387	0.085310962	-19.5832	2.15E-85	2.02E-84	purple	-0.794865266	1.88E-35	GO:0016798,GO:0005975,GO:0004553	AT1G58370.1	ATXYN1,RXF12	glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein	glycosyl hydrolase family 10 protein
Sapur.008G126600.1	198.6308305	-0.914329326	0.046693767	-19.5814	2.23E-85	2.10E-84	purple	-0.864170796	4.35E-48	GO:0005515	AT1G04190.1		Tetratricopeptide repeat (TPR)-like superfamily protein	heat shock protein STI
Sapur.009G058700.1	236.9601352	-1.14951329	0.058758149	-19.5635	3.17E-85	2.97E-84	purple	-0.791284584	6.19E-35		AT2G30100.1		pentatricopeptide (PPR) repeat-containing protein	PPR containing plant protein
Sapur.013G032900.1	67.10040281	-1.029231311	0.052611583	-19.5628	3.21E-85	3.00E-84	purple	-0.828143345	8.28E-41		AT1G12700.1		ATP binding;nucleic acid binding;helicases	PPR domain protein
Sapur.009G107100.1	57.48554092	-1.383314751	0.070801155	-19.538	5.22E-85	4.87E-84	purple	-0.828427681	7.37E-41	GO:0006260,GO:0005634	AT2G20980.1	MCM10	minichromosome maintenance 10	minichromosome maintenance protein
Sapur.018G034700.1	513.36219	1.146680192	0.058808432	19.49857	1.13E-84	1.05E-83	purple	0.838975471	8.32E-43		AT5G11600.1			hypothetical protein
Sapur.004G126800.1	290.3912195	-1.691658053	0.086766546	-19.4967	1.17E-84	1.09E-83	purple	-0.789775803	1.02E-34		AT4G30150.1			Urb2/Npa2 family protein
Sapur.007G062000.1	199.6206786	-1.244072918	0.0638259	-19.4917	1.29E-84	1.20E-83	purple	-0.830568948	3.04E-41	GO:0005524,GO:0003676	AT5G60990.1		DEA(D/H)-box RNA helicase family protein	DEAD-box ATP-dependent RNA helicase
Sapur.010G065700.1	319.7515759	-1.157480844	0.059451284	-19.4694	2.00E-84	1.85E-83	purple	-0.776174854	7.37E-33		AT5G43860.1	ATCLH2,CLH2	chlorophyllase 2	chlorophyllase
Sapur.010G107400.1	65.07992523	-1.473634454	0.075744321	-19.4554	2.62E-84	2.43E-83	purple	-0.810396352	8.06E-38		AT1G13630.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein, putative
Sapur.T132000.1	58.42145172	-1.469073065	0.075515773	-19.4539	2.70E-84	2.50E-83	purple	-0.879511701	7.46E-52		AT2G20710.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.006G120900.1	179.9195836	-1.390275382	0.071551899	-19.4303	4.28E-84	3.95E-83	purple	-0.867408373	7.64E-49		AT2G19385.1		zinc ion binding	cell growth-regulating nucleolar protein, putative
Sapur.002G189900.1	38.67487354	-1.475586697	0.075983249	-19.4199	5.24E-84	4.84E-83	purple	-0.851923801	2.13E-45		AT1G06440.1		Ubiquitin carboxyl-terminal hydrolase family protein	plant organelle RNA recognition domain protein
Sapur.014G059900.1	964.028009	-1.217736015	0.06274362	-19.4081	6.59E-84	6.07E-83	purple	-0.855384879	3.92E-46	GO:0003677,GO:0008289	AT4G00730.1	AHDP,ANL2	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein	homeobox leucine zipper protein
Sapur.010G048200.1	327.778105	-1.076686462	0.055492249	-19.4025	7.36E-84	6.77E-83	purple	-0.82999996	3.85E-41	GO:0005524,GO:0003676	AT3G16840.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.009G034200.1	639.6846809	-1.1183208	0.057653532	-19.3973	8.14E-84	7.49E-83	purple	-0.839623412	6.25E-43	GO:0005524,GO:0003676	AT3G18600.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein	DEAD-box ATP-dependent RNA helicase
Sapur.010G199400.1	397.7327018	-1.272108273	0.065615403	-19.3873	9.87E-84	9.07E-83	purple	-0.841565963	2.63E-43		AT5G18440.1			nuclear fragile X mental retardation-interacting protein
Sapur.009G087300.1	210.8075678	-0.721865869	0.037266861	-19.3702	1.38E-83	1.26E-82	purple	-0.829526497	4.68E-41		AT2G16070.2	PDV2	plastid division2	plastid division protein PDV2
Sapur.003G035300.1	40.07640265	-2.495288678	0.129092773	-19.3294	3.04E-83	2.77E-82	purple	-0.712710678	1.20E-25		AT3G13980.1			hypothetical protein
Sapur.012G098900.1	280.7412121	-1.57145277	0.081448007	-19.2939	6.04E-83	5.49E-82	purple	-0.805952614	4.04E-37	GO:0006457	AT4G25340.1	ATFKBP53,FKBP53	FK506 BINDING PROTEIN 53	peptidyl-prolyl cis-trans isomerase FKBP53
Sapur.15WG147900.1	67.15371258	-1.357245816	0.070379796	-19.2846	7.24E-83	6.57E-82	purple	-0.830816084	2.74E-41		AT4G33495.1	RPD1	Ubiquitin carboxyl-terminal hydrolase family protein	plant organelle RNA recognition domain protein
Sapur.004G022400.1	770.6347973	-0.717392814	0.037207313	-19.281	7.76E-83	7.04E-82	purple	-0.844989579	5.57E-44		AT5G28740.1		Tetratricopeptide repeat (TPR)-like superfamily protein	protein prenylyltransferase
Sapur.016G153200.1	112.1735626	-1.865388721	0.096749848	-19.2805	7.83E-83	7.10E-82	purple	-0.675056462	3.17E-22	GO:0006355,GO:0003700	AT5G12840.2	ATHAP2A.EMB2220.HAP2A.	nuclear factor Y, subunit A1	CCAAT-binding transcription factor
Sapur.004G139600.1	218.085656	-1.120932552	0.058164072	-19.2719	9.25E-83	8.38E-82	purple	-0.870397667	1.47E-49		AT4G21900.1	PRORP3	proteinaceous RNase P 3	multidrug resistance pump protein, putative
Sapur.003G078600.1	1752.35425	-1.011388224	0.052538039	-19.2506	1.40E-82	1.26E-81	purple	-0.77908709	3.02E-33	GO:0005525	AT1G62750.1	ATSCO1.ATSCO1/CPEF-G.SC	Translation elongation factor EFG/EF2 protein	NA
Sapur.003G130600.1	263.0238296	-1.198841819	0.062360015	-19.2245	2.31E-82	2.08E-81	purple	-0.879468202	7.66E-52	GO:0045040,GO:0005742	AT1G27390.1	TOM20-2	translocase outer membrane 20-2	import receptor subunit TOM20
Sapur.013G124300.1	40.68508656	-1.558292791	0.081063287	-19.2232	2.37E-82	2.13E-81	purple	-0.846367929	2.95E-44		AT2G20710.2		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.15WG139900.1	556.0217972	-1.438174532	0.074904899	-19.2	3.70E-82	3.32E-81	purple	-0.829073533	5.65E-41		AT3G22660.1		rRNA processing protein-related	rRNA-processing protein EBP2, putative
Sapur.002G078500.1	147.1910729	-1.145231221	0.059765507	-19.1621	7.67E-82	6.86E-81	purple	-0.862473373	1.06E-47		AT4G08940.1		Ubiquitin carboxyl-terminal hydrolase family protein	plant organelle RNA recognition domain protein
Sapur.016G142400.1	318.299931	-1.19635606	0.062489781	-19.1448	1.07E-81	9.54E-81	purple	-0.830703671	2.87E-41	GO:0005524	AT2G29970.1		Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein	ATP-dependent Clp protease ATP-binding subunit clpL, putative
Sapur.009G053200.1	295.2312247	-1.190187215	0.062192658	-19.1371	1.24E-81	1.11E-80	purple	-0.870726023	1.23E-49		AT2G26810.2		Putative methyltransferase family protein	NA
Sapur.15WG150100.1	485.2634001	0.645453377	0.033730923	19.13536	1.28E-81	1.14E-80	purple	0.849388448	7.15E-45		AT5G23850.1		Arabidopsis thaliana protein of unknown function (DUF821)	glycosyltransferase family 90 protein
Sapur.011G011900.1	302.4645295	-0.880242268	0.046017971	-19.1282	1.47E-81	1.31E-80	purple	-0.832811126	1.19E-41		AT4G05520.2	ATEHD2,EHD2	EPS15 homology domain 2	calcium-binding EF hand protein
Sapur.008G096600.1	91.27796428	-1.612063283	0.08433877	-19.1141	1.93E-81	1.71E-80	purple	-0.817074434	6.61E-39					transmembrane protein, putative
Sapur.011G054800.1	134.4736634	-0.949536451	0.049693699	-19.1078	2.18E-81	1.93E-80	purple	-0.833900773	7.48E-42		AT1G30290.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing protein, putative
Sapur.016G168300.1	578.6293403	-1.368072842	0.071706342	-19.0788	3.79E-81	3.35E-80	purple	-0.81384277	2.25E-38	GO:0006351,GO:0003887,GO:0003677	AT5G64420.1		DNA polymerase V family	NA
Sapur.007G025400.1	278.2481671	-1.299569986	0.068120504	-19.0775	3.88E-81	3.44E-80	purple	-0.875993587	6.03E-51		AT4G36680.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.006G017100.1	49.50739988	-1.634105804	0.085765944	-19.0531	6.19E-81	5.47E-80	purple	-0.831215101	2.32E-41		AT5G41920.1		GRAS family transcription factor	GRAS family transcription factor
Sapur.016G142600.1	2809.458835	-1.089668748	0.057195473	-19.0517	6.37E-81	5.62E-80	purple	-0.774557115	1.20E-32	GO:0055114,GO:0016717,GO:0006629	AT5G05580.1	FAD8	fatty acid desaturase 8	omega-3 fatty acid desaturase, endoplasmic reticulum protein%2C putative
Sapur.005G053200.1	35.61672456	-1.656978618	0.087160257	-19.0107	1.39E-80	1.22E-79	purple	-0.810016704	9.27E-38		AT5G08770.1			hypothetical protein
Sapur.014G142400.1	218.4145479	-1.406662016	0.073997282	-19.0096	1.42E-80	1.25E-79	purple	-0.81996577	2.17E-39	GO:0003677	AT4G12750.1		Homeodomain-like transcriptional regulator	homeodomain transcriptional regulator
Sapur.016G002300.1	1120.897535	0.567496795	0.029897918	18.98115	2.44E-80	2.14E-79	purple	0.852116422	1.94E-45	GO:0005525	AT1G07410.1	ATRAB-A2B.ATRABA2B.RAB	RAB GTPase homolog A2B	Rab-related GTPase family protein
Sapur.005G192300.1	70.34026289	-1.059731644	0.055842293	-18.9772	2.63E-80	2.30E-79	purple	-0.808240112	1.77E-37					hypothetical protein
Sapur.014G109700.1	252.1265065	-1.633200916	0.086149752	-18.9577	3.81E-80	3.33E-79	purple	-0.8115258	5.32E-38	GO:0005515,GO:0006364,GO:0005730	AT2G47990.1	EDA13,EDA19,SWA1	transducin family protein / WD-40 repeat family protein	U3 small nucleolar RNA-associated protein, putative
Sapur.012G023200.1	229.6044562	-1.097373013	0.057929633	-18.9432	5.02E-80	4.38E-79	purple	-0.825847417	2.11E-40	GO:0030688,GO:0006364	AT5G20600.1			nucleolar protein,Nop52 protein
Sapur.15WG058300.1	154.2878397	-1.149257712	0.060727188	-18.9249	7.11E-80	6.20E-79	purple	-0.833063024	1.07E-41		AT1G18450.1	ARP4,ATARP4	actin-related protein 4	NA
Sapur.013G109200.1	166.3607492	-1.297980552	0.068624328	-18.9143	8.70E-80	7.56E-79	purple	-0.793282135	3.20E-35	GO:0046983	AT1G68810.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH30, putative
Sapur.005G138300.1	564.8938269	-1.113123104	0.058916486	-18.8932	1.30E-79	1.12E-78	purple	-0.867563332	7.02E-49		AT1G21880.2	LYM1	lysm domain GPI-anchored protein 1 precursor	LysM domain GPI-anchored protein
Sapur.003G089600.1	475.7573133	-1.078210629	0.057071544	-18.8923	1.32E-79	1.15E-78	purple	-0.84508881	5.32E-44		AT5G41190.1			RNA-binding protein NOB1, putative
Sapur.007G110000.1	148.3369099	-0.818743212	0.043373888	-18.8764	1.78E-79	1.54E-78	purple	-0.830965012	2.58E-41		AT3G07040.1	RPM1,RPS3	NB-ARC domain-containing disease resistance protein	disease resistance protein RPM1, putative
Sapur.005G187100.1	111.2722132	-1.008197683	0.053422748	-18.8721	1.94E-79	1.67E-78	purple	-0.813348047	2.70E-38	GO:0005515	AT3G54350.3	emb1967	Forkhead-associated (FHA) domain-containing protein	microspherule protein
Sapur.016G033500.1	486.061691	-0.783841426	0.041556127	-18.8622	2.33E-79	2.01E-78	purple	-0.834812131	5.07E-42	GO:0005634	AT3G56990.1	EDA7	embryo sac development arrest 7	nucleolar protein
Sapur.008G029700.1	1671.998147	-2.208747787	0.117101512	-18.8618	2.35E-79	2.03E-78	purple	-0.7196464	2.46E-26	GO:0016020,GO:0006810,GO:0005215	AT2G37170.1	PIP2;2,PIP2B	plasma membrane intrinsic protein 2	plasma membrane intrinsic protein
Sapur.013G068300.1	419.8321389	0.781575304	0.041496495	18.83473	3.92E-79	3.37E-78	purple	0.835231331	4.24E-42	GO:0016020,GO:0008375	AT3G03690.1	UNE7	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	core-2/I-branching beta-1%2C6-N-acetylglucosaminyltransferase family protein
Sapur.006G099400.1	371.4534469	-1.426822967	0.075762585	-18.8328	4.07E-79	3.49E-78	purple	-0.798086338	6.32E-36	GO:0005515	AT3G21540.1		transducin family protein / WD-40 repeat family protein	transducin family protein
Sapur.011G087200.1	354.0264598	-1.490330102	0.079147575	-18.8298	4.31E-79	3.70E-78	purple	-0.821570111	1.16E-39		AT3G15460.1		Ribosomal RNA processing Brix domain protein	ribosome biogenesis BRX1-like protein
Sapur.001G059600.1	115.4173301	-1.274334675	0.067792312	-18.7976	7.90E-79	6.76E-78	purple	-0.855196729	4.30E-46		AT3G57430.1	OTP84	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.013G065600.1	355.844334	-1.325772667	0.070548631	-18.7923	8.73E-79	7.46E-78	purple	-0.811942774	4.56E-38	GO:0032040,GO:0006364,GO:0005515	AT5G16750.1	TOZ	Transducin family protein / WD-40 repeat family protein	U3 small nucleolar RNA-associated protein, putative
Sapur.002G086700.1	724.183114	-1.357842513	0.072353734	-18.7667	1.41E-78	1.21E-77	purple	-0.778365986	3.77E-33		AT5G49665.1		Zinc finger (C3HC4-type RING finger) family protein	NA
Sapur.004G069700.1	956.4852418	-1.177704144	0.062777101	-18.7601	1.60E-78	1.37E-77	purple	-0.830893491	2.66E-41	GO:0042254,GO:0005730	AT5G14520.1		pescadillo-related	pescadillo protein

Sapur.01G1286800.1	104.5895066	-1.31607491	0.070154891	-18.7598	1.61E-78	1.37E-77	ppile	-0.845733579	3.95E-44	ATG23710.1	Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.01T0227400.1	176.13095	-0.87386444	0.046424028	-18.7415	2.27E-78	1.93E-77	ppile	-0.823202204	6.57E-40	GO:0005681,GO:0000398,GO:0000387	ATG42510.2	survival motor neuron interacting protein
Sapur.01G0204900.1	201.3096039	-0.32962021	0.076304022	-18.7325	2.69E-78	2.29E-77	ppile	-0.823008821	8.60E-41	GO:0008168,GO:0006479	ATG12270.1	arginine N-methyltransferase, putative
Sapur.01G1311300.1	69.41253827	-1.68001182	0.089699498	-18.7296	2.84E-78	2.41E-77	ppile	-0.817475688	5.67E-39	GO:0008168,GO:0008033,GO:0006364,GO:0003723	ATB82,FIB2	fibrillarin 2	NA
Sapur.01G0611300.1	2581.163988	-0.66105632	0.035288887	-18.7317	3.38E-78	2.86E-77	ppile	-0.832970337	1.11E-41	GO:0006334,GO:0005634	NAP1,2,NAP1KD,NK42	nucleosome assembly protein 1-2	nucleosome assembly protein
Sapur.15WG1050200.1	600.0478296	-1.29810030	0.09045767	-18.6863	6.40E-78	5.40E-77	ppile	-0.86643018	1.30E-48		PDE312,PTAC10	Nucleic acid-binding, OB-fold-like protein	constans interacting-like protein
Sapur.01W2079400.1	441.1028176	-1.40132801	0.075080561	-18.6644	9.65E-78	8.13E-77	ppile	-0.870823463	9.32E-49			P-loop containing nucleoside triphosphate hydrolases superfamily protein	deoxynucleoside kinase
Sapur.01W1644001.1	41.99556576	-1.33642472	0.071627982	-18.6583	1.08E-77	9.11E-77	ppile	-0.81627534	2.52E-46		PDE275,TAK	Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.01G0619900.1	65.5867185	-1.33485901	0.071543414	-18.658	1.09E-77	9.15E-77	ppile	-0.832847602	2.71E-41		ATG60310.1		hypothetical protein
Sapur.01G0533600.1	799.5959864	-0.35962109	0.047128128	-18.6446	1.40E-77	1.17E-76	ppile	-0.815414086	1.42E-45		ATG27090.1	glycine-rich protein	hypothetical protein
Sapur.01G1009600.1	7.96575424	-3.32953571	0.124661127	-18.642	1.47E-77	1.23E-76	ppile	-0.831002216	1.81E-44	ADNT1	ATG60100.1	adenine nucleotide transporter 1	NA
Sapur.01G0204800.1	44.64889344	-1.75174259	0.09527612	-18.6081	3.24E-77	2.76E-76	ppile	-0.599600102	1.05E-16	UBC14	ATG61180.2	ubiquitin-conjugating enzyme E2	ubiquitin-conjugating enzyme E2
Sapur.01G1619300.1	277.0912201	-1.00335571	0.053691671	-18.5903	3.85E-77	3.22E-76	ppile	-0.826390936	1.70E-40	GO:0008033	ATG16260.1	TR24	tRNAse Z4	zinc phosphodiesterase, putative
Sapur.01G1338800.1	70.87181836	-2.21366422	0.118004147	-18.5364	6.07E-77	5.06E-76	ppile	-0.84966207	1.29E-45	GO:0006355,GO:0003700,GO:0007275	ANT,CIC,CVC,LDRG	ATG27030.1	ANT,CIC,CVC,LDRG	DUF domain transcription factor
Sapur.01G2204800.1	81.61286086	-1.66588754	0.089682501	-18.536	1.06E-76	8.80E-76	ppile	-0.832729392	1.20E-41		ATG30700.1	AtODD2,ODD2	indeterminate(ID)-domain 2	nucleic acid-binding protein, putative
Sapur.01G0250100.1	446.2135225	-0.65209884	0.060137262	-18.5296	1.38E-76	1.15E-75	ppile	-0.837888244	5.02E-39		ATG27120.1			SWI/SNF,carboxy-terminal domain protein
Sapur.01G0143900.1	2537.214858	-1.45164369	0.078604369	-18.5125	1.64E-76	1.36E-75	ppile	-0.825212132	2.82E-40	GO:0006508,GO:0004190	ATG01300.1	Eukaryotic aspartyl protease family protein	aspartyl protease family protein
Sapur.00T0241900.1	80.74024642	-1.34281377	0.0725369	-18.5124	1.64E-76	1.36E-75	ppile	-0.83193566	1.74E-41		ATG54350.2	Forkhead-associated (FHA) domain-containing protein	RNA domain protein
Sapur.01G2341300.1	1369.152804	-0.68385424	0.033292161	-18.4997	2.08E-76	1.72E-75	ppile	-0.814481822	1.82E-38	GO:0003676	ATG15010.1	RNA-binding (RRM/RBD/RNP motifs) family protein	heterogeneous nuclear ribonucleoprotein G-RNA recognition motif protein
Sapur.00B1140900.1	557.5952511	-0.54786183	0.036275857	-18.4615	4.21E-76	3.47E-75	ppile	-0.82364995	7.56E-40	GO:0005515	ATG10580.1	Transducin/WD40 repeat-like superfamily protein	WD40 domain protein
Sapur.00G1117000.1	28.6413003	-1.05456468	0.06968	-18.4358	6.78E-76	5.57E-75	ppile	-0.85318656	5.57E-47		ATG70550.1	Protein of unknown function (DUF239)	carboxy-terminal proteinase-like protein
Sapur.01D0201100.1	195.7580762	-1.42225454	0.07363	-18.4316	7.33E-76	6.02E-75	ppile	-0.832554691	1.22E-41	GO:0008270	ATG48570.1	zinc finger (Ran-binding) family protein	2o-finger in Ran-binding protein, putative
Sapur.01G1307700.1	320.2200016	-0.15489397	0.06270527	-18.4186	9.32E-76	7.64E-75	ppile	-0.87871526	6.46E-50	GO:0009821,GO:0009451,GO:0003723,GO:0005622	ATG23070.1	Pseudouridine synthase family protein	tRNA pseudouridine synthase
Sapur.01G1298300.1	553.7555134	-1.13379367	0.061601129	-18.4054	1.18E-75	9.73E-75	ppile	-0.85017848	4.92E-45	GO:0042254,GO:0005622	ATG25260.1	Ribosomal protein L10 family protein	ribosomal protein L10 family protein
Sapur.01G1298500.1	782.1656777	-0.91000242	0.05463623	-18.4013	1.28E-75	1.05E-74	ppile	-0.84079457	2.05E-48		ATG27130.1	Sec61p/Ssh1p family	something about silencing protein sas10, putative
Sapur.01G2283001.1	223.4414705	-1.26586308	0.068807441	-18.3972	1.38E-75	1.13E-74	ppile	-0.86493106	2.81E-48	GO:0005515	ATG25120.1	Transducin/WD40 repeat-like superfamily protein	telomerase capt body protein
Sapur.01G0120700.1	320.9408892	-1.05295383	0.06269279	-18.3904	1.57E-75	1.28E-74	ppile	-0.81624153	8.80E-39		ATG61770.3	PPAN	PETER PAN-like protein	peter Pan-like protein
Sapur.00N0200900.1	286.8783351	-1.34179612	0.069223955	-18.3879	1.64E-75	1.34E-74	ppile	-0.81468159	2.58E-38	GO:0006310,GO:0006281,GO:0003910,GO:0003677,GO:0005524	ATG18130.1	ATG18G,LIG1	DNA ligase 1	ATP-dependent DNA ligase
Sapur.01G1312300.1	342.9258651	-1.21262514	0.069370136	-18.379	1.94E-75	1.58E-74	ppile	-0.82511866	7.98E-40	GO:0008168,GO:0008033,GO:0006364,GO:0003723	ATG27640.1		ARM repeat superfamily protein	importin beta-4, putative
Sapur.00G1127900.1	2231.543913	-0.73846024	0.040280272	-18.3651	2.50E-75	2.05E-74	ppile	-0.825167217	2.77E-40	GO:0007165,GO:0000160,GO:0000160	ATG27120.1	AHK1,HK3	histidine kinase 3	histidine kinase
Sapur.01G0275500.1	167.0041617	-1.20025088	0.065391631	-18.3548	3.02E-75	2.45E-74	ppile	-0.84893321	5.82E-44		ATG33940.1		Mitochondrial substrate carrier family protein	substrate carrier family protein
Sapur.01G1311500.1	164.7224017	-1.34239789	0.068026783	-18.3401	3.81E-75	3.09E-74	ppile	-0.836734399	2.91E-42	GO:0005975,GO:0004553,GO:0043169,GO:0003824	ATG20440.2	BE1,EMB2729	Alpha amylase family protein	1%2C4-alpha-glucan-binding enzyme
Sapur.01G0505600.1	62.07102445	-0.90329705	0.049369036	-18.2965	8.83E-75	7.11E-74	ppile	-0.84153587	6.86E-44		ATG31530.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.01G0250400.1	747.762068	-0.81122266	0.044664419	-18.2862	1.07E-74	8.57E-74	ppile	-0.85202021	1.57E-45		ORP10	OSBPlikeprotein family protein	oxysterol-binding protein-related protein 3C	
Sapur.01G0251500.1	2252.74651	-0.77568232	0.042432027	-18.28497	1.08E-74	8.76E-74	ppile	-0.81232379	2.31E-41		ATG76890.2	Duplicated homeodomain-like superfamily protein	Myb/SANT-like DNA-binding domain protein	
Sapur.01G0307300.1	130.1761646	-0.59170853	0.039262238	-18.2739	1.32E-74	1.07E-73	ppile	-0.86135169	2.26E-49		ATG27150.1	basic helix-loop-helix (bHLH) superfamily protein	transcription factor, putative	
Sapur.01G0689100.1	126.8035852	-1.05091793	0.057522489	-18.2703	1.43E-74	1.16E-73	ppile	-0.834709063	1.30E-42	GO:0016787,GO:0005524,GO:0003677	ATG7810.1	DEAD/H(D/H)-box RNA helicase family protein	DEAD-box ATP-dependent RNA helicase, putative
Sapur.15WG1452200.1	98.7337903	-0.05380552	0.057808405	-18.265	1.57E-74	1.26E-73	ppile	-0.84976526	6.80E-45		ATG51910.1	TCP family transcription factor	TCP transcription factor
Sapur.00N0280300.1	194.9274269	-0.97287623	0.053335526	-18.2492	2.10E-74	1.68E-73	ppile	-0.85065739	4.41E-45	GO:0005819	ATG75010.1	OTF51	endonuclease	PPR containing plant protein
Sapur.01G0869600.1	261.9126151	-2.45652243	0.132714491	-18.2019	4.99E-74	3.97E-73	ppile	-0.83628988	9.58E-23		ATG53750.1		CBS domain-containing protein	CBS domain protein CDS5
Sapur.01G0400100.1	602.9235514	-0.79636438	0.043218445	-18.1947	5.68E-74	4.52E-73	ppile	-0.85085804	3.55E-45		ATG54590.1	ARR9,RR2,RGR1	Response regulator family protein	alpha/beta-hydrolase family protein
Sapur.01G2031400.1	29.18703526	-1.58148003	0.087067627	-18.1576	1.12E-73	8.88E-73	ppile		-0.83879804	8.99E-43	GO:0006355,GO:0005739,GO:0003690	ATG37900.1		Mitochondrial transcription termination factor family protein	mTERF protein
Sapur.01W2620700.1	317.1407521	-0.56117269	0.05617769	-18.1568	1.13E-73	9.00E-73	ppile	-0.84160608	1.07E-48		ATG61870.1	PPR336	pentatricopeptide repeat 336	membrane-associated salt-inducible protein, putative
Sapur.01G1341200.1	22.37058245	-3.30591445	0.073515171	-18.1566	1.14E-73	9.04E-73	ppile	-0.83681666	2.10E-42		ATG08530.1		Pentatricopeptide repeat (PPR) superfamily protein	pentatricopeptide (PPR) repeat protein
Sapur.00G0261100.1	525.5809904	-0.54680418	0.03827573	-18.1344	2.05E-73	1.62E-72	ppile	-0.837908514	3.41E-42		ATG61670.1			pre-mRNA-splicing factor of RES complex protein
Sapur.01G1150200.1	162.1099576	-1.24998941	0.09009437	-18.113	2.52E-73	1.99E-72	ppile	-0.86434661	3.95E-48	GO:0005515	ATG42790.1		Transducin/WD40 repeat-like superfamily protein	NA
Sapur.01G0201300.1	48.84953987	-0.37431351	0.059102262	-18.1098	2.67E-73	2.10E-72	ppile	-0.85231661	1.76E-45		ATG44880.1		Pentatricopeptide repeat (PPR)-like superfamily protein	PPR containing plant protein
Sapur.01G1661700.1	28.36015151	-2.07431263	0.076135412	-18.0878	6.21E-73	4.88E-72	ppile	-0.854717176	6.44E-46	GO:0005515	ATG59760.1	OTF81	Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein, putative
Sapur.00T0605800.1	1980.614963	-1.47735841	0.081872893	-18.0845	8.71E-73	6.82E-72	ppile	-0.826495468	1.52E-40	GO:0003676	ATG18610.1	ATNUC-1.2,NUC-1.2,PARL1	nuclease like 2	RNA recognition motif (RRM) superfamily protein
Sapur.00G1117200.1	227.7388067	-1.02192227	0.054247248	-18.0404	8.88E-73	6.96E-72	ppile	-0.83017305	3.58E-41		ATG26000.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.01G0209400.1	831.9151118	-0.65622443	0.036462748	-18.0002	1.94E-72	1.51E-71	ppile	-0.832682988	1.25E-41	GO:0003565,GO:0005070	ATG60700.1	BZIP17	Basic-leucine zipper (bZIP) transcription factor family protein	CBS domain-containing CBSX3
Sapur.01G0250300.1	600.5857303	-0.96152027	0.03606451	-17.9969	2.16E-72	1.76E-71	ppile	-0.84347431	2.38E-48	GO:0005515	ATG61630.1	ARR3,ARR4,TRR1,THO3	Transducin/WD40 repeat-like superfamily protein	alpha/beta-hydrolase family protein
Sapur.00G1167500.1	99.00631611	-1.06105412	0.059209075	-17.9904	2.32E-72	1.81E-71	ppile	-0.82039142	1.81E-39	GO:0006260,GO:0003887,GO:0003677	ATG42120.2	POLD2	DNA polymerase delta small subunit	DNA polymerase delta small subunit
Sapur.01W1629400.1	362.8181574	-0.79376422	0.04361657	-17.9375	3.04E-72	2.38E-71	ppile	-0.84602877	2.53E-44		ATG47125.2	Hydatrosin / mRNA binding family	DOMAIN OF UNKNOWN FUNCTION 724 6		
Sapur.01W1526000.1	661.5736664	-0.41806152	0.078066725	-17.9603	3.77E-72	2.94E-71	ppile	-0.822161047	9.17E-40	GO:0008168,GO:0008033,GO:0006364,GO:0003723	ATB82,FIB2	FIB2	fibrillarin 2	rRNA 2'-O-methyltransferase fibrillarin
Sapur.01G2301000.1	570.7638303	-1.02763189	0.043425444	-17.9565	4.27E-72	3.32E-71	ppile	-0.81235164	3.41E-38	GO:0005515	ATG41360.1		Galactose oxidase/kelch repeat superfamily protein	F-box/kelch-repeat protein	
Sapur.00G1115000.1	403.3921655	-0.62184176	0.034664866	-17.9387	5.88E-72	4.56E-71	ppile	-0.83059246	1.55E-41	GO:0005515,GO:0006355,GO:0006334,GO:0016568,GO:0003151	ATG46530.2	HIRA	homology of histone chaperone HIRA	histone transcription regulator HIRA protein
Sapur.01G2194000.1	62.1658936	-1.12872759	0.092661877	-17.9329	6.52E-72	5.06E-71	ppile	-0.834945851	5.81E-42		ATG60360.2		Ribosomal RNA adenine dimethylase family protein	ribosomal RNA adenine dimethylase family protein
Sapur.01G0502700.1	51.15576853	-1.61291615	0.09005654	-17.9313	6.92E-72	5.36E-71	ppile	-0.80407956	6.36E-27	GO:0008270	ATG50640.1		zinc finger (Ran-binding) family protein	DNA polymerase, putative
Sapur.01G0607400.1	127.5056539	-1.53283783	0.086699931	-17.9105	9.77E-72	7.55E-71	ppile	-0.803953741	8.21E-37	GO:0000380	ATG57940.1		Domain of unknown function (DUF1736) ;Putative ATPase (DUF699)	GRAT acetyltransferase
Sapur.00G1615000.1	224.3832604	-0.75021028	0.07270148	-17.9104	9.78E-72	7.56E-71	ppile	-0.825703683	2.22E-40	GO:0003723,GO:0000178	ATB8P4,RRP4	ATB8P4,RRP4	Transducin/WD40 repeat-like superfamily protein	exosome complex exonuclease Rrp4
Sapur.00G0642000.1	684.0327374	-1.21133722	0.070804267	-17.8991	1.38E-71	1.07E-70	ppile	-0.831291866	1.78E-45		ATG60940.1		transducin family protein / WD-40 repeat family protein	WD-repeat membrane protein, putative
Sapur.01G1661900.1	492.1048864	-1.27350664	0.071186363	-17.8759	1.83E-71	1.41E-70	ppile	-0.843357151	5.2E-45		ATG60830.1		Protein of unknown function, DUF239	transmembrane protein, putative
Sapur.01G0255600.1	151.2568854	-0.90816889	0.050815119	-17.8712	1.98E-71	1.52E-70	ppile	-0.82867384	6.66E-41		ATG57680.1		Restriction endonuclease, type II-like superfamily protein	NA
Sapur.01G0266500.1	450.9213192	-0.56768409	0.033319919	-17.8686	2.03E-71	1.56E-70	ppile	-0.832476201	1.37E-41		ATG62610.1			pozn, putative
Sapur.01G0728001.1	638.9142478	-0.05683071	0.059221133	-17.8467	3.12E-71	2.39E-70	ppile	-0.84060044	4.61E-43		ATG15000.1		cobalt ion binding	hypothetical protein
Sapur.01G0603100.1	179.8346165	-0.60023249	0.03604851	-17.8203	4.92E-71	3.76E-70	ppile	-0.79659187	1.36E-35		ATG51881.1		ENTH/VHS family protein	RNA polymerase II binding domain protein
Sapur.01G0254500.1	112.6374937	-0.84621144	0.047573963	-17.7873	8.87E-71	6.76E-70	ppile	-0.828265911	7.89E-41	GO:0005524	ATG33960.1		Transducin/WD40 repeat-like superfamily protein	TCP-1/cpn60 chaperonin family protein
Sapur.15WG0674000.1	91.94007543	-0.62879624	0.059102448	-17.7777	1.05E-70	8.01E-70	ppile	-0.854515295	5.90E-46	GO:0006355,GO:0005739,GO:0003690	ATG27600.1	OTF82	Mitochondrial transcription termination factor family protein	mitochondrial transcription termination factor family protein
Sapur.01W1928800.1	64.10571204	-1.26846377	0.09058584	-17.7738	1.13E-70	8.58E-70	ppile	-0.831790205	1.82E-41		ATG38070.1		Pentatricopeptide repeat (PPR) superfamily protein	nuppelle transport protein complex protein
Sapur.01G0941200.1	2362.863373	-0.77035669	0.043382007	-17.7627	1.37E-70	1.04E-69	ppile	-0.837470566	1.61E-42	GO:0005524	ATTCP,_TCP-1	ATTCP,_TCP-1	T-complex protein 1 alpha subunit	TCP-1 (CTT or eukaryotic type II) chaperonin family, alpha subunit
Sapur.01G1272200.1	2569.300663	-0.77976322	0.04361657	-17.7537	1.61E-70	1.22E-69	ppile	-0.841898292	2.7E-43		ATG47520.1	Hydatrosin / mRNA binding family	DOMAIN OF UNKNOWN FUNCTION 724 6	nuclear RNA-binding protein	
Sapur.01G1664000.1	440.128828	-2.38816674	0.072570542	-17.7506	1.71E-70	1.29E-69	ppile	-0.82647334	3.38E-40		ATG60360.1		Ribosomal protein S8e family protein	ribosomal protein S8e
Sapur.01G0420100.1	108.0150807	-1.20838181	0.068080808	-17.7492	1.75E-70	1.31E-69	ppile	-0.829164433	5.05E-41		ATG28440.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.00B2689500.1	25.60683123	-1.17969898	0.066499399	-17.7454	1.87E-70	1.42E-69	ppile	-0.826320065	1.76E-40		ATG29760.1	OTF81	Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.01G0586300.1	393.7291365	-0.98816924	0.056277496	-17.7376	2.15E-70	1.63E-69	ppile	-0.84157602	1.11E-44		ATG39600.1		Small GTP-binding protein family	translation factor GUF1-like protein
Sapur.00G1020900.1	213.0623852	-0.79710859	0.044947316	-17.7343	2.28E-70	1.72E-69	ppile	-0.82516928	2.31E-40		ATG34340.1	TAF8	TBP-associated factor 8	bromodomain associated protein
Sapur.15WG0319800.1	12.61175128	-2.39938288	0.129688193	-17.7312	2.41E-70	1.82E-69	ppile	-0.75378831	2.66E-30		ATG18420.3		CCT motif family protein	zinc finger constans-like protein
Sapur.01G1638800.1	376.5456589	-0.47455652	0.060716522	-17.7026	4.08E-70	3.05E-69	ppile	-0.851792265	2.28E-45		ATG34930.1		Metal-dependent phosphohydrolase	metal-dependent protein hydrolase
Sapur.00T0111100.1	421.7470539	-0.71487872	0.040413707	-17.6899	5.02E-70	3.78E-69	ppile	-0.82418658	1.23E-39		ATG42235.1			transmembrane protein, putative
Sapur.01G1638300.1	175.5018659	-1.30739822	0.07391582	-17.6881	5.18E-70	3.90E-69	ppile	-0.83561124	1.4E-42	PHP1	ATG32140.1	PHP1	phosphoglycerate interacting protein 1	RNA recognition motif (RRM) superfamily protein
Sapur.15WG0050800.1	300.722186	-0.59156545	0.03467889	-17.6873	5.25E-70	3.95E-69	ppile	-0.83669818	2.45E-39		ATG62370.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.00G0105200.1	30.32117536	-1.49879325	0.084821145	-17.6689	7.15E-70	5.47E-69	ppile	-0.82489495	3.56E-40		ATG20120.2	ATORC4,ORC4	origin recognition complex subunit 4	origin recognition complex subunit 4
Sapur.15WG1196800.1	89.51216328	-1.47568114	0.085159998	-17.6576	8.90E-70	6.67E-69	ppile	-0.80416628	7.63E-27	GO:0016779,GO:0006396,GO:0003723	ATG33690.1		Polynucleotide adenylyltransferase family protein	
Sapur.01W1268600.1	431.8420795	-0.64168421	0.051853708	-17.6553	9.24E-70	6.94E-69	ppile	-0.83054454	1.56E-41	GO:0008168,GO:0008175,GO:0006396,GO:0003723	ATG19870.1		tRNA/RNA methyltransferase, putative	tRNA methyltransferase, putative
Sapur.01G1514500.1	40.20829838	-1.39683866	0.079135051	-17.6513	9.94E-70	7.45E-69	ppile	-0.81347044	3.02E-38	GO:0005750	ATG05990.1		Mitochondrial glycoprotein family protein	glycoprotein
Sapur.01G0207800.1	25.06762	-1.69180739	0.092468088	-17.6434	1.14E-69	8.56E-69	ppile	-0.83221027	9.8E-42		ATG28310.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein, putative
Sapur.01G0948000.1	27.81227218	-1.47347213	0.081326042	-17.6416	1.18E-69	8.83E-69	ppile	-0.81692259	9.61E-39		ATG12735.1	MEE22	mitochondrial editing factor 22	PPR containing protein
Sapur.00G1135800.1	513.179804	-0.81008514	0.045970583	-17.625	1.33E-69	9.91E-69	ppile	-0.85246257	1.64E-45	GO:0006412,GO:0005840,GO:0005622,GO:0003735	ATG88620.1		55/S6?62, RNA binding protein	NA
Sapur.01G0138800.1	48.85165456	-1.24585164	0.07050275	-17.6312	1.43E-69	1.06E-68	ppile	-0.78016424	2.21E-33	GO:0032264,GO:0008168,GO:0003150	ATG18830.1		Fru-like endonuclease family protein	ribosomal RNA large subunit methyltransferase E
Sapur.01G0701000.1	473.2627259	-1.16892974	0.06628381	-17.6307	1.43E-69	1.07E-68	ppile	-0.82339146	8.58E-40	GO:0007165,GO:0005515,GO:0005102	AHK4,ATCRE1,CRE1,WOL,W	AHK4,ATCRE1,CRE1,WOL,W	CHASE domain containing histidine kinase protein	histidine kinase cytokinin receptor
Sapur.01G1352700.1	318.3618664	-1.25142282	0.068939211	-17.6304	1.44E-69	1.08E-68	ppile	-0.84329935	1.20E-43	GO:0005515,GO:0005622,GO:0004672			Leucine-rich repeat protein kinase family protein	LRR receptor-like kinase,Thioredoxin-like,kinase, putative
Sapur.15WG1053800.1	103.8547868	-0.07970751	0.061249508	-17.6293	1.47E-69	1.09E-68	ppile	-0.82851873	6.18E-41	GO:0008270,GO:0003676	ATG21380.1		VASCULAR-RELATED NAC-DOMAIN 6	actin-depolymerizing factor, putative
Sapur.00T0269400.1	138.6292154	-0.71768884	0.04071559	-17.6273	1.52E-69	1.14E-68	ppile	-0.81256205	1.91E-38		ATG20560.1		SWIM zinc finger family protein	zinf DRL5-10 protein
Sapur.15WG1001000.2	8.11327016	-2.95370498	0.167560073	-17.6239	1.61E-69	1.20E-68	ppile	-0.713032328	1.52E-27		ATG40390.1	SIP1	Raffinose synthase family protein	Raffinose synthase family protein
Sapur.01G0270200.1	33.69462081	-1.88408052	0.103788624	-17.6171	1.82E-69	1.36E-68	ppile	-0.81970166	2.2E-39		ATG22010.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.01G0143300.1	1122.196811	-1.70075823	0.097730445	-17.6108	2.04E-69	1.52E-68	ppile	-0.70302015	4.29E-25	GO:0055114,GO:0016491,GO:0005507	ATG40370.1	LACS	laccase 5	laccase
Sapur.01G1233800.1	31.57529766	-1.03928563	0.059001943	-17.5965	2.48E-69	1.85E-68	ppile	-0.82970563	4.5E-41		ATG20710.1		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.01G1275001.1	1566.498823	-0.43607731	0.024607742	-17.599	2.51E-69	1.86E-68	ppile	-0.81658283	8.36E-39	GO:0003676,GO:0006418,GO:0005524,GO:0004812,GO:0000166	EMB2755,SYNC1,SYNC1	AtS	Class II aminoacyl-tRNA and biotin synthetases superfamily protein	cytoplasmic asparaginyl-tRNA synthetase
Sapur.01G2014300.1	55.44321771	-1.39465586	0.07362025	-17.5855	3.18E-69	2.36E-68	ppile	-0.82158477	1.15E-39		ATG12260.1	CRR22	Pentatricopeptide repeat (PPR) superfamily protein	organelle transcript processing protein, putative
Sapur.01G0227100.1	191.9729275	-1.06381949	0.059185037	-17.5615	4.08E-69	3.48E-68	ppile	-0.84491237	1.81E-42		ATG24481.1		Protein of unknown function (DUF1220)	DUF1220 family protein
Sapur.01T0210100.1	38.86549225	-1.06388689	0.060692011	-17.5627	4.75E-69	3.52E-68	ppile	-0.829052223	5.76E-41		ATG20710.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.01G1202400.1	531.6262398	-0.61367889	0.054884209	-17.56	4.99E-69	3.66E-68	ppile	-0.80305457	1.12E-36	GO:0042254,GO:0005634	ATG24441.1		Pentatricopeptide repeat (PPR) superfamily protein	pre-rRNA-processing TSR1-like protein
Sapur.01G0245900.1	44.66431185	-1.34064251	0.065002219	-17.5478	6.19E-69	4.57E-68	ppile	-0.82239575	8.36E-40		ATG12770.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein, putative
Sapur.01W2689100.1	16.79315462	-2.35192712	0.160656935	-17.4969	1.43E-68	1.05E-67	ppile	-0.82927367	7.85E-41		ATG29120.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.01G2317000.1	425.5479867	-0.79074632	0.052251143	-17.4846	1.88E-68	1.38E-67	ppile	-0.82435131	3.94E-40		ATG55900.1	emb1860,TIM50	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	import inner membrane translocase subunit TIM50
Sapur.01G1930600.1	199.5647863	-1.20032496	0.07037863	-17.4819	1.94E-68	1.44E-67	ppile	-0.83455463	1.78E-38	GO:0008168,GO:0008152	ATG31740.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	methyltransferase-like protein
Sapur.01G0233900.1	36.25914554	-1.24478273	0.071253621	-17.4697	2.44E-68	1.79E-67	ppile	-0.81533742	1.28E-38		ATG27070.1		5'-AMP-activated protein kinase-related	NA
Sapur.01G0884100.1	4.80293996	-4.53841414	0.259780543	-17.4696	2.44E-68	1.79E-67	ppile	-0.6843956	5.22E-23					hypothetical protein
Sapur.01G1579200.1	260.8135555	-0.88232612	0.050507056	-17.4689	2.47E-68	1.80E-67	ppile	-0.8076903	2.05E-27		ATG38970.1		Zinc finger (C3HC4-type RING finger) family protein	zinc finger (C3HC4-type RING finger) family protein
Sapur.01G0251100.1	250.3418029	-0.57381906	0.03306371	-17.469	2.47E-68	1.81E-67	ppile	-0.815042236	1.43E-38	GO:0006303,GO:0004003,GO:0016877,GO:0016817	ATKU8B,KU80	ATKU8B,KU80	Ku80 family protein	ATP-dependent DNA helicase 2 subunit KU80
Sapur.01G0291000.1	661.329292	-0.70164109	0.041215978	-17.4679	2.49E-68	1.82E-67	ppile	-0.82889728	2.9E-40		ATG60600.1		Zinc finger, RING-type; Transcription factor jumonji/aspartyl/beta-hydroxylase	transcription factor jumonji/jmj domain protein
Sapur.01G1002000.1	148.1525742	-3.36692614	0.078027472	-17.4584	2.97E-68	2.17E-67	ppile	-0.81821692	8.93E-39	GO:0003676	ATG18510.1	emb2444	RNA-binding (RRM/RBD/RNP motifs) family protein	RNA recognition motif 2 in splicing factor 3B subunit 4 (SF3B4) like protein
Sapur.01G0250900.1	258.4150964	-0.80422342	0.049538209	-17.4567	3.12E-68	2.28E-67	ppile	-0.81263005	5.8E-39	GO:0003723	ATG27190.1		RNA-binding (RRM/RBD/RNP motifs) family protein	YAT-like transposase
Sapur.01G0127700.1	366.6118843	-0.85829309	0.049168429	-17.4547	3.29E-68	2.40E-67	ppile	-0.82173288	1.09E-39		ATG25050.1		Actin-binding FH2 (Formin Homology) protein	formin-like protein
Sapur.01G0289800.1	38.23123576	-0.90628908	0.05137272	-17.4503	3.45E-68	2.51E-67	ppile	-0.80804163	1.92E-37	GO:0055114,GO:0020037,GO:0016705,GO:0005506	ATG

Sapur.01Qb04180.1	277.1935362	2.18176809	0.080113457	-15.999	1.33E-57	8.06E-57	purple	-0.79329411	1.48E-35	ATSG43310.2	COP1-interacting protein-related
Sapur.15WG104200.1	1121.363082	-1.518965298	0.095006852	-15.9883	1.54E-57	9.57E-57	purple	-0.79987682	3.40E-36	GO:0003674	31-kDa RNA binding protein
Sapur.03G130100.1	581.5477257	-0.894726476	0.056045884	-15.9641	2.27E-57	1.41E-56	purple	-0.81508454	1.19E-38	GO:0006418;GO:0005524;GO:0004812;GO:0000166	glycyl-tRNA synthetase
Sapur.03Qb117500.1	496.6247633	-0.899449429	0.05648858	-15.9227	4.41E-57	2.72E-56	purple	-0.78973416	1.03E-34	GO:0042254	ribosome biogenesis protein RLP24
Sapur.03G131000.1	375.1342371	-0.758884059	0.047678789	-15.9166	4.86E-57	2.98E-56	purple	-0.79656588	1.21E-35		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01G235600.1	36.6845285	-1.742755067	0.109631099	-15.8965	6.70E-57	4.11E-56	purple	-0.71707235	1.51E-25	GO:0046872	RING membrane-anchor 1
Sapur.04G256700.1	49.6201735	-1.95328424	0.123253074	-15.864	1.13E-56	6.88E-56	purple	-0.74902823	1.65E-29		Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain
Sapur.09G114045.1	560.547944	-0.664772158	0.042018773	-15.8216	2.21E-56	1.35E-55	purple	-0.76062195	6.86E-31	EMB2762	CCAAT-binding factor
Sapur.09G107900.1	162.9575259	-1.00721487	0.063685671	-15.8154	2.44E-56	1.48E-55	purple	-0.78194473	1.24E-33		ARM repeat superfamily protein
Sapur.09G098100.1	52.5883776	-2.56598887	0.163175758	-15.716	2.75E-56	2.77E-55	purple	-0.78728848	-34.37		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.03Bc127900.1	473.148768	-2.53388796	0.16204552	-15.7741	4.68E-56	2.84E-55	purple	-0.55755485	3.32E-14	GO:0009507	Chlorophyll A-B binding family protein
Sapur.01Wg058200.1	611.6042042	-0.818358269	0.05468623	-15.7624	5.60E-56	3.42E-55	purple	-0.82175091	1.13E-39	GO:0051087;GO:0042803;GO:0006457;GO:0000774	Co-chaperone GrpE family protein 2
Sapur.01G003500.1	194.6573482	0.808730455	0.051130634	15.76146	5.73E-56	3.47E-55	purple	-0.73329043	9.30E-28	GO:0016021;GO:0004252	1S4 family peptidase
Sapur.01G232300.1	185.9432009	-0.834777268	0.05298176	-15.7568	6.68E-56	4.03E-55	purple	-0.78988693	8E-34		Hypothetical protein
Sapur.04G018000.1	336.5993025	-1.007781703	0.063982447	-15.7509	6.77E-56	4.09E-55	purple	-0.82308753	9.46E-40		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01G305100.1	34.7929835	-2.105145165	0.134000145	-15.7312	1.08E-55	6.51E-55	purple	-0.78947471	5.60E-34		PPR containing protein
Sapur.03G228900.1	506.2186661	-0.984367881	0.062675011	-15.7059	1.38E-55	8.26E-55	purple	-0.78884059	1.38E-34		PENTATRICOPEPTIDE REPEAT 596
Sapur.01Qb047000.1	27.67527678	-1.140772429	0.072731258	-15.6848	1.93E-55	1.15E-54	purple	-0.80691705	2.86E-37		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.03Wc110800.1	156.4596227	-0.656798652	0.05169095	-15.6758	2.21E-55	1.33E-54	purple	-0.78949272	1.14E-34	GO:0005525	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.03Bc073900.1	27.22294162	-1.187328809	0.075763328	-15.6689	2.47E-55	1.48E-54	purple	-0.80762785	2.21E-37		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01G026100.1	62.7385454	-1.625671218	0.098187021	-15.5897	8.65E-55	5.14E-54	purple	-0.79875796	-16.36		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01G021700.1	151.914668	0.723307023	0.046565576	15.65192	3.22E-55	1.93E-54	purple	-0.78803873	1.59E-34		Mannose-P-dolichol utilization defect 1 protein
Sapur.01G298400.1	1861.824969	-0.714522926	0.045616715	-15.64388	3.65E-55	2.18E-54	purple	-0.77543021	1.00E-32		cytochrome c oxidase,electron carriers
Sapur.09G094200.1	360.1947655	-0.661345469	0.042293931	-15.6369	4.08E-55	2.46E-54	purple	-0.80027262	2.88E-36	GO:0006468;GO:0004672;GO:0005524	Protein kinase superfamily protein
Sapur.09G098300.1	8.034470656	-2.834777268	0.181309797	-15.6355	4.17E-55	2.49E-54	purple	-0.71757882	8E-24	GO:0005515;GO:0005491;GO:0016209	Nucleotide binding
Sapur.09G156100.1	283.6123589	-0.618900653	0.039588357	-15.6342	4.24E-55	2.54E-54	purple	-0.77248415	2.4E-32		Hypothetical protein
Sapur.01G020800.1	201.8268803	-0.803724416	0.051463711	-15.6171	5.57E-55	3.32E-54	purple	-0.80660931	3.19E-37		Zinc finger, RING-type;Transcription factor jumonji/jarid;Jmj/arid;Jmj-hydroxylase
Sapur.03G134045.1	672.0513913	-0.56111962	0.076028884	-15.6132	5.92E-55	3.52E-54	purple	-0.81539218	1.25E-38	GO:0008168;GO:0008033;GO:0006364;GO:0003723	Fibrillarin 2
Sapur.01Qb081300.1	377.0677249	-0.778653947	0.049656215	-15.6084	6.39E-55	3.80E-54	purple	-0.81405916	2.07E-38	GO:0008033;GO:0004809;GO:0003723	N(2,N(2)-dimethylguanosine tRNA methyltransferase, putative
Sapur.09G027700.1	43.11637369	-1.911332207	0.072776143	-15.6062	6.68E-55	3.96E-54	purple	-0.81524895	1.10E-38		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01Qb079000.1	509.6598663	-0.01761901	0.002346362	-15.5969	7.64E-55	4.54E-54	purple	-0.8065563	3.75E-37		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.09G092300.1	975.6403425	-0.525671218	0.034018871	-15.5897	8.65E-55	5.14E-54	purple	-0.78815765	6E-34	ATSCP2,SCP2	sterol carrier protein 2
Sapur.03G060900.1	789.0305304	-1.122364434	0.072109777	-15.5633	1.29E-54	7.66E-54	purple	-0.71231173	1.05E-25	GO:0055114;GO:0016616;GO:0006694;GO:0003854	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.03Wc114000.1	181.05489	-0.765551885	0.05086861	-15.5405	1.84E-54	1.09E-53	purple	-0.81178562	4.83E-38		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.04G076600.1	67.21473564	-1.125883369	0.072518597	-15.5255	2.33E-54	1.38E-53	purple	-0.77434486	1.28E-32		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.03G058800.1	710.5313389	-0.629228604	0.041325776	-15.5135	2.81E-54	1.66E-53	purple	-0.74665724	1.29E-29	GO:0006397;GO:0005634;GO:0003676	pre-mRNA processing protein Prp5
Sapur.03G155500.1	126.6605927	-1.056803431	0.068262696	-15.509	3.03E-54	1.78E-53	purple	-0.71452603	7.91E-26		GRAS family transcription factor
Sapur.03G135100.1	96.2829785	-1.460804265	0.093009987	-15.4897	4.07E-54	2.40E-53	purple	-0.66527139	1.89E-21		Protein of unknown function (DUF3133)
Sapur.01G032000.1	332.1649719	-1.122328275	0.072537005	-15.4732	5.26E-54	3.08E-53	purple	-0.77930042	3.56E-32		Nce2p family
Sapur.01G107100.1	684.768737	-0.835822381	0.054035351	-15.4688	5.64E-54	3.31E-53	purple	-0.78214969	8.51E-34	GO:0008536;GO:0006886	ARM repeat superfamily protein
Sapur.04G026700.1	28.4595323	-2.462321238	0.081620449	-15.4625	6.37E-54	3.46E-53	purple	-0.73197214	2.61E-25		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.05G187000.1	156.3048193	-1.339478473	0.086576106	-15.4546	7.03E-54	4.11E-53	purple	-0.73729534	1.41E-28		SRI-related sequence 5
Sapur.01G213500.1	546.3152969	-0.687248894	0.045000874	-15.4445	8.27E-54	4.81E-53	purple	-0.80051728	2.76E-36	GO:0006379;GO:0006378;GO:0005847	Cleavage and polyadenylation specificity factor subunit 2
Sapur.09G094100.1	28.805187	-1.411663781	0.091428093	-15.4402	8.79E-54	5.14E-53	purple	-0.74887422	1.72E-29	GO:0005515	WD-40 repeat family protein / notchless protein, putative
Sapur.01G118400.1	241.3038058	-1.519621842	0.10181389	-15.4378	9.12E-54	5.32E-53	purple	-0.70029235	1.85E-24		DNA binding protein
Sapur.01G146900.1	8.2469156	-2.21277587	0.208284852	-15.4297	1.03E-53	6.03E-53	purple	-0.64360765	9.75E-20	GO:0016747;GO:0008610;GO:0016020;GO:0006633	3-ketoacyl-CoA synthase 19
Sapur.01G000300.1	296.4601759	-0.854966214	0.055409482	-15.4296	1.04E-53	6.04E-53	purple	-0.77442279	1.25E-32	GO:0005634;GO:0003889;GO:0003677	nuclear RNA polymerase C1
Sapur.09G136200.1	1281.919625	-0.603159938	0.039096107	-15.4276	1.07E-53	6.23E-53	purple	-0.78259737	1.01E-33	GO:0003676;GO:0006418;GO:0005524;GO:0000166	lysyl-tRNA synthetase 1
Sapur.01G028300.1	966.8687821	0.663675672	0.04315566	15.39291	1.83E-53	1.06E-52	purple	-0.76085728	6.55E-31	GO:0005635;GO:0005634;GO:0003677	SUFA-like DNA-binding protein
Sapur.15WG010180.1	233.7936317	-0.970375924	0.06305464	-15.3884	1.58E-53	9.12E-53	purple	-0.77452171	1.20E-32		MAK16 protein
Sapur.01G297700.1	2.18065227	-4.607843405	0.299457575	-15.3852	2.06E-53	1.20E-52	purple	-0.67308733	4.01E-22	GO:0055114;GO:0050660;GO:0016491	FAD-binding Berberine family protein
Sapur.04G035000.1	8.543498228	-2.638405003	0.142255282	-15.3731	2.48E-53	1.44E-52	purple	-0.76025183	1.38E-31		
Sapur.09G192300.1	190.108668	-0.816162627	0.052348836	-15.3349	4.47E-53	2.59E-52	purple	-0.78200022	1.22E-33		
Sapur.09G138000.1	29.53096622	-2.054448894	0.161682633	-15.3105	6.57E-53	3.81E-52	purple	-0.58709263	1.54E-15		
Sapur.01G193700.1	243.7259867	-0.967219913	0.069629736	-15.3271	5.04E-53	2.91E-52	purple	-0.76905537	6.17E-32		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01G273000.1	324.6287844	-1.015731005	0.074178111	-15.2783	1.75E-52	1.01E-51	purple	-0.77664236	3.87E-32	GO:0032940	PPR domain-like family protein
Sapur.01Bc062900.1	1618.22194	-0.413880815	0.027028785	-15.311	6.46E-53	3.72E-52	purple	-0.78619846	1.22E-34	GO:0005681;GO:0000398	chromatin protein family
Sapur.01Bc025400.1	1319.149657	-0.730851592	0.047825816	-15.2812	1.03E-52	5.87E-52	purple	-0.76110343	6.94E-31	GO:0006457;GO:0003755;GO:0000413	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family
Sapur.09G094045.1	272.0683842	-0.574161159	0.070188182	-15.266	1.29E-52	7.38E-52	purple	-0.81739377	-57.39		Hypothetical protein
Sapur.01G016600.1	21.39493791	-1.157726893	0.075837962	-15.2658	1.29E-52	7.42E-52	purple	-0.77271274	2.09E-32		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01G042300.1	1250.73432	-0.845811225	0.05541	-15.2543	1.54E-52	8.84E-52	purple	-0.75345318	1.02E-30	GO:0017056;GO:0005643	Nup1-like carboxy-terminal region protein
Sapur.09G104000.1	496.4544421	-0.635369001	0.041681305	-15.2433	1.83E-52	1.05E-51	purple	-0.77814713	3.02E-32		Pyridoxal phosphate (PLP)-dependent transferases superfamily protein
Sapur.09G100300.1	79.22108874	-1.125180614	0.073934232	-15.2211	2.54E-52	1.46E-51	purple	-0.77284268	1.59E-32		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01Bc005100.1	173.757729	-0.556316888	0.036555527	-15.2205	2.59E-52	1.48E-51	purple	-0.78083474	1.76E-33	GO:0070461	transcriptional regulator of RNA pol II, SAGA, subunit
Sapur.01G265600.1	158.017954	-1.187166154	0.07795183	-15.2155	2.79E-52	1.59E-51	purple	-0.78252107	1.03E-33	GO:0005515	histone lysine-N-methyltransferase ASH1
Sapur.01G027100.1	806.4352746	-0.485957563	0.031960912	-15.2047	3.29E-52	1.87E-51	purple	-0.79640607	-12.35		Ems-interacting protein
Sapur.09G147900.1	17.23658661	-2.305318144	0.185577208	-15.2043	3.31E-52	1.89E-51	purple	-0.77553625	8.94E-33		transmembrane protein, putative
Sapur.01G139100.1	302.383785	-0.84202609	0.055410966	-15.2031	3.37E-52	1.92E-51	purple	-0.77060032	3.91E-32		DNA/ heat shock N-terminal domain-containing protein
Sapur.01G075400.1	14.35511003	-3.471082207	0.096861223	-15.1919	4.00E-52	2.28E-51	purple	-0.76908484	6.22E-32		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01G029600.1	21.23739398	-2.364562251	0.156406604	-15.189	4.13E-52	2.38E-51	purple	-0.78245172	1.06E-33		conserved peptide upstream open reading frame 53
Sapur.03G132800.2	7.070055542	-2.139827536	0.140904206	-15.1823	4.63E-52	2.63E-51	purple	-0.74161392	7.67E-29		Pectin lyase-like superfamily protein
Sapur.01G024700.1	87.06638884	-0.927855158	0.060568805	-15.1773	5.05E-52	2.86E-51	purple	-0.75231658	6.82E-30	GO:0005515;GO:0034968;GO:0018024;GO:0008270;GO:0005634;GO:0042393	SUV4H1/3 homologs
Sapur.08Bc042900.1	190.8031788	-0.985465588	0.064904735	-15.1727	5.36E-52	3.04E-51	purple	-0.76905537	6.17E-32		chromatin assembly factor-1 (DASCIATA1) (FAS1)
Sapur.03G176100.1	381.4917608	-0.525604934	0.03452125	-15.1609	6.47E-52	3.22E-51	purple	-0.76914586	1.01E-32	GO:0005515;GO:0006508;GO:0004222	AKAP
Sapur.01G079900.1	256.4945659	-0.834480661	0.054959616	-15.1653	6.00E-52	3.40E-51	purple	-0.81671879	7.59E-39	GO:0008097;GO:0006412;GO:0005840;GO:0003735	Ribosomal protein L35/Gln-tRNA synthetase, anti-codon-binding domain
Sapur.03G202700.1	115.4317425	-1.376789169	0.090800708	-15.1618	6.33E-52	3.58E-51	purple	-0.81943843	2.49E-38		Zinc finger domain of monoamine-oxidase A repressor R1
Sapur.05G167100.1	124.8587847	-0.798225729	0.05268881	-15.1566	6.96E-52	3.94E-51	purple	-0.78491354	2.46E-33		Hypothetical protein
Sapur.15WG082600.1	1808.457005	0.419180932	0.027670256	15.14582	8.07E-52	4.56E-51	purple	-0.7611759	6.03E-31	GO:0005524	ubiquitin-conjugating enzyme 2
Sapur.03Bc147400.1	257.6347055	-0.765620707	0.05253836	-15.1453	8.38E-52	4.73E-51	purple	-0.80051904	1.29E-37	GO:0005515	TCP-1 (CT or eukaryotic type II) chaperonin family, epsilon subunit
Sapur.01G057400.1	1380.680955	-0.79134803	0.052397384	-15.1028	1.55E-51	8.71E-51	purple	-0.77455413	1.20E-32	GO:0019867	translocon at the outer envelope membrane of chloroplasts 75-III
Sapur.03Wc138200.1	110.6729245	-0.832657219	0.055177739	-15.0918	1.83E-51	1.03E-50	purple	-0.80851128	2.60E-37	GO:0005515;GO:0003682;GO:0005524	Mitochondrial transcription termination factor family protein
Sapur.01Bc024300.1	2424.711694	-0.651127788	0.043429682	-15.0848	2.04E-51	1.14E-50	purple	-0.74604869	6.10E-29	GO:0016787;GO:0005524;GO:0003677	DEAD/DEAH box RNA helicase family protein
Sapur.01G121400.1	236.0077366	-1.539602223	0.103934469	-15.0174	5.61E-51	3.15E-50	purple	-0.77432329	1.29E-32		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01G136200.1	842.4781245	-0.477365429	0.031821305	-15.0154	5.82E-51	3.25E-50	purple	-0.76883896	6.48E-32	GO:0006397	splicing factor PWI domain-containing protein
Sapur.03G208100.1	17.36847522	-3.121500243	0.2078409	-15.0151	5.85E-51	3.26E-50	purple	-0.77721402	1.36E-32		Hypothetical protein
Sapur.01G022200.1	29.15205942	-1.991486128	0.079614357	-14.9657	1.23E-50	6.82E-50	purple	-0.76423057	2.49E-31		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.09G152600.1	135.2890227	-0.963204183	0.106445759	-14.9649	1.25E-50	6.91E-50	purple	-0.68725958	1.28E-23		
Sapur.04G021100.1	1459.114014	-0.807413957	0.053985831	-14.956	1.42E-50	7.88E-50	purple	-0.76435671	2.40E-31	GO:0005515	F-box/RNI-like superfamily protein
Sapur.05Q047500.1	477.6275296	-1.006127975	0.074098117	-14.9278	2.17E-50	1.20E-49	purple	-0.76704231	1.11E-31	GO:0000080	Domain of unknown function (DUF1726) ;Putative ATPase (DUF699)
Sapur.01Q084200.1	82.42802288	-1.962832234	0.131624457	-14.9169	2.86E-50	1.58E-49	purple	-0.66842494	9.95E-21	GO:0016491;GO:0020037;GO:0016705;GO:0005506	cytochrome P450 family protein
Sapur.03G008600.1	464.7941995	-0.822761113	0.055495521	-14.8258	9.98E-50	5.45E-49	purple	-0.78659311	2.86E-34		Hypothetical protein
Sapur.03Bc000200.1	189.3451141	-0.604705388	0.040793024	-14.8253	1.00E-49	5.46E-49	purple	-0.77883006	2.60E-32	GO:0005515;GO:0003682;GO:0005524	ORC3/CDC1/CDC6 ATPase
Sapur.01G050100.1	41.7152311	-1.157022243	0.078188277	-14.8084	1.27E-49	6.95E-49	purple	-0.75116289	9.36E-30	GO:0005515;GO:0046422;GO:0009507	origin recognition complex 1
Sapur.09G189100.1	65.73889121	-1.502735116	0.148161852	-14.7692	1.48E-49	8.08E-49	purple	-0.66050744	1.61E-22	GO:0005515;GO:0006468;GO:0005524;GO:0004672	ATP-dependent protein kinase family protein
Sapur.03G169200.1	31.42079859	-1.196021283	0.080832462	-14.7979	1.51E-49	8.20E-49	purple	-0.77785597	4.41E-32		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.03G240700.1	42.68819723	-1.424882279	0.09699132	-14.7976	1.52E-49	8.27E-49	purple	-0.76230204	2.4E-31		mitochondrial MATH domain family
Sapur.01G129800.1	19.98592286	-1.691604948	0.114312484	-14.7968	1.54E-49	8.36E-49	purple	-0.75149797	8.52E-30	GO:0005515;GO:0003676	Arginosuccinate family protein
Sapur.05Q047500.1	66.3476286	-1.112484037	0.0752181	-14.7904	1.68E-49	8.05E-49	purple	-0.80093236	1.38E-36		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01Q007800.1	204.1473445	-0.94686836	0.064206024	-14.7912	1.67E-49	9.07E-49	purple	-0.73688867	3.87E-28	GO:0005515	nucleotide binding,protein binding
Sapur.04G082100.1	40.75691192	-1.156295721	0.078240549	-14.7787	2.01E-49	1.09E-48	purple	-0.80873892	1.48E-37		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.09G054900.1	75.55631322	-1.859896456	0.092065412	-14.7714	2.24E-49	1.21E-48	purple	-0.74703954	-14.689	GO:0005515	Calcium-dependent lipid-binding(C2 domain) family protein
Sapur.01G027200.1	55.26255344	-1.11602153	0.075263439	-14.7695	2.30E-49	1.25E-48	purple	-0.79927661	3.85E-36		Pentatricopeptide repeat (PPR)-like superfamily protein
Sapur.01W024080.1	148.4551135	-0.610288851	0.07397819	-14.7515	2.93E-49	1.58E-48	purple	-0.78870498	-44.34		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.15WG147500.1	208.3280594	-1.051365513	0.111964985	-14.7489	3.13E-49	1.69E-48	purple	-0.79408174	2.45E-35	GO:0005515;GO:0006468;GO:0004672	Leucine-rich repeat transmembrane protein kinase
Sapur.09G230100.1	49.86147154	-1.814284343	0.168820466	-14.7383	3.24E-49	1.88E-48	purple	-0.77514488	1.02E-32		
Sapur.09G032500.1	218.2206404	-0.646288462	0.043802491	-14.7244	4.56E-49	2.42E-48	purple	-0.76364805	2.95E-31		Myb transcription factor, putative
Sapur.09G330700.2	107.4388802	-0.838641488	0.060400849	-14.7229	4.67E-49	2.47E-48	purple	-0.73516146	1.41E-27		clathrin interactor, putative
Sapur.03G158900.1	56.37478808	-1.662896927	0.113018531	-14.7135	5.28E-49	2.84E-48	purple	-0.68572136	1.83E-23	GO:0046983	transcription factor bHLH122
Sapur.01G027700.1	642.5584969	-0.572192487	0.038905597	-14.7072	5.80E-49	3.12E-48	purple	-0.76180469	4.99E-31	GO:0006396;GO:0005622	cell cycle control protein crooked neck-like protein, putative
Sapur.01G050500.1	626.3758512	-0.704846369	0.05384889	-14.6898	7.50E-49	4.03E-48	purple	-0.76105978	7.8E-31	GO:0003723	CRM family member CFM2 chloroplast RNA splicing factor CRS1
Sapur.01Bc008300.1	1119.985091	-0.850547204	0.058022999	-14.6588	1.18E-48	6.35E-48	purple	-0.77742128	5.05E-33		Ribosomal protein L34e/L30e/S12e/Gad045 family protein
Sapur.03G138800.1	53.79763219	-1.168174409	0.08	-14.6474	1.26E-48	7.00E-48	purple	0.69819348	2.27E-24		
Sapur.01T029100.1	691.8717277	-1.388851895	0.095152747	-14.6406	1.51E-48	8.28E-48	purple	-0.70835284	4.38E-25	GO:0016887;GO:0005524	ATPase;nucleotide binding;ATP binding;nucleoside-triphosphatase;transcription factor binding
Sapur.03G153400.1	430.3638072	-0.823762479	0.05631442	-14.6218	1.86E-48	9.98E-48	purple	-0.75280134	1.3E-30	GO:0005515	Protein of unknown function (DUF231)
Sapur.03G115400.1	97.96231669	-1.211319352	0.082849051	14.62478	1.95E-48	1.04E-47	purple	-0.71773725	3.82E-26	GO:0006355;GO:0003700	integrase-type DNA-binding superfamily protein
Sapur.03G147900.1	1597.646048	-0.587218794	0.056110338	-14.5987	2.29E-48	1.21E-47	purple	-0.78175329	1.32E-33	GO:0005525	Nucleotide GTP-binding protein
Sapur.03G112200.1	830.8623365	-0.973090768	0.066704512	-14.5882	3.34E-48	1.76E-47	purple	-0.73261344	1.26E-27		ARM repeat superfamily protein
Sapur.01G052000.1	441.9996131	-0.857829429	0.05430261	-14.5787	3.48E-48	1.81E-47	purple	-0.79489346	1.4E-35		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.04G106400.1	23.81480621	-1.335070928	0.091570906	-14.5862	3.44E-48	1.83E-47	purple	-0.75671567	2.06E-30		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.08G058000.1	34.33509872	-2.664442298	0.112873088	-14.569	4.42E-48	2.35E-47	purple	-0.62632053	5.16E-18	GO:0046983	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.09G117100.1	3490.131724	0.764826769	0.052622209	14.55082	5.08E-48	2.68E-47	purple	-0.70794722	2.49E-25	GO:0008234;GO:0006508	Cysteine proteinase superfamily protein
Sapur.03G189800.1	33.19624998	-1.646269927	0.113160815	-14.555	5.42E-48	2.86E-47	purple	-0.66199446	2.71E-21		transmembrane protein, putative
Sapur.05Q093700.1	62.38168941	-1.327368168	0.092160746	-14.5445	5.88E-48	3.12E-47	purple	-0.76345007	1.11E-31		Hypothetical protein
Sapur.03G162100.1	696.8838604	-0.467013934	0.032117567	-14.5408	6.06E-48	3.54E-47	purple	-0.76242142	9.32E-32	GO:0016593;GO:0016570;GO:0003468	Pol3 complex component
Sapur.03G097500.1	235.8297041	-0.610460423	0.042015169	-14.5337	6.48E-48	3.42E-47	purple	-0.74384304	2.02E-29	GO:0005515;GO:0006290;GO:0003324;GO:0032300	DNA mismatch repair protein
Sapur.03G046600.1	256.0023488	-0.571866037	0.039359306	-14.5294	7.89E-48	4.17E-47	purple	-0.76003071	1.50E-31	GO:0008654;GO:0004609	phosphatidylserine decarboxylase 1
Sapur.01G040500.1	448.0116187	-0.664611227	0.051984384	-14.5245	8.48E-48	4.48E-47	purple	-0.76387624	2.79E-32	GO:0005515	Ser/Thr-rich trehalose and tetratricopeptide repeat
Sapur.01T067100.1	917.1536305	-0.9449264	0.062303815	-14.5245	8.48E-48	4.48E-47	purple	-0.78526022	4.36E-34	GO:0006334;GO:0005634	NRP2 nucleosome/chromatin assembly factor group protein, putative
Sapur.09G118400.1	1612.645311	-1.040926884	0.078553794	-14.5241	8.52E-48	4.50E-47	purple	-0.76811011	8.11E-32		Histone deacetylase 9
Sapur.01G082600.1	17.62505877	-2.284963277	0.157542216	-14.5016	1.06E-47	5.60E-47	purple	-0.64221011	2.21E-19	GO:0005515;GO:0006468;GO:0005524;GO:0004672	Leucine-rich repeat transmembrane protein kinase family protein
Sapur.01G068800.1	244.7839919	-0.560406732	0.038654934	14.49768	1.25E-47	6.59E-47	purple	-0.78975915	1.01E-34		ubiquitin E2 variant 10-4
Sapur.01W012900.1	75.06818	-0.963318687	0.066593873	-14.4662	1.38E-47	7.0E-47	purple	-0.79028586	8.76E-35		Pentatricopeptide repeat (PPR)-like superfamily protein
Sapur.01G238700.1	280.9914829	-0.436958552	0.030148668	-14.4935	1.33E-47	7.01E-47	purple	-0.74966215	1.28E-29	GO:0005515	Transducin/WD40 repeat-like superfamily protein
Sapur.05G147400.1	76.57588884	-0.825197429	0.056968512	-14.4838	1.51E-47	8.05E-47	purple	-0.74707854	-34.69		Transducin/WD40 repeat-like superfamily protein
Sapur.03Q097000.1	695.5762353	-0.535667533	0.037010183	-14.4708	1.85E-47	9.72E-47	purple	-0.78785629	1.86E-34	GO:0006352;GO:0005669	TAF6L/TAF4B TBP-associated factor 4
Sapur.09G028900.1	2.020814341	-3.591375835	0.248688484	-14.4459	2.16E-47	1.36E-46	purple	-0.72722266	-8.27		
Sapur.03G165900.1	240.080169	-0.589323903	0.040832374	-14.4363	3.06E-47	1.60E-46	purple	-0.80837911	1.68E-37	GO:0005515	Galactose-oxidase/kelch repeat superfamily protein
Sapur.03G045000.1	321.6178879	-0.664617366	0.046150565	-14.4321	3.26E-47	1.70E-46	purple	-0.76682415	1.38E-31		Plant protein of unknown function (DUF946)
Sapur.01G054300.3	6.613474304	-2.92066788	0.133205151	-14.4193	3.91E-47	2.04E-46	purple	-0.73349273	8.86E-28	GO:0042254;GO:0005622;GO:0034429	H/ACA ribonucleoprotein complex, subunit Gar1/Naf1 protein
Sapur.7T087600.1	436.234994	1.341878166	0.086206484	14.40155	5.06E-47	2.64E-46	purple	-0.65898251	6.48E-21		
Sapur.09G075700.1	957.5221016	-0.860507872	0.060412645	-14.384	5.64E-47	2.94E-46	purple	-0.77984148	1.29E-32	GO:0016597;GO:0008152;GO:0055114;GO:0051287;GO:0016616	D-3-phosphoglycerate dehydrogenase
Sapur.03G004300.1	60.39829617	-1.121411954	0.07947277	-14.3868	6.24E-47	3.26E-46	purple	-0.76934932	5.66E-32		Pentatricopeptide repeat (PPR)-like superfamily protein
Sapur.01G151500.2	41.48469653	-1.525408634	0.106318475	-14.3487	1.06E-46	5.54E-46	purple	-0.56085277	2.18E-14		cAMP-regulated phosphoprotein/endosulfine motif protein
Sapur.01G161100.1	317.3198613	-0.940088864	0.06568981	-14.3247	1.53E-46	7.93E-46	purple	-0.80643439	2

Sapur.01BG064600.1	5.69155643	-2.01876335	0.16707872	-13.2798	3.03E-40	1.40E-39	pvuba	-0.63857689	2.31E-19	GO:0006355;GO:0003700	ATHAP2;HAP2C;NF-YA3
Sapur.00BG033600.1	46.37405967	-2.21182315	0.09129085	-13.2682	3.54E-40	1.64E-39	pvuba	-0.75039452	1.16E-29		OTP81
Sapur.01BG177400.1	282.1868879	-0.78520353	0.05920609	-13.2623	3.78E-40	1.75E-39	pvuba	-0.67320351	6.87E-22		
Sapur.00AG128100.1	192.4841137	-0.67251427	0.05072377	-13.2585	4.03E-40	1.86E-39	pvuba	-0.73763346	3.54E-28	GO:0006872	
Sapur.01BG197300.1	56.4161373	-0.07184564	0.00839385	-13.2543	4.29E-40	1.97E-39	pvuba	-0.72377794	1.38E-26		
Sapur.00SG016300.1	153.0737715	-0.81525498	0.06156587	-13.2421	5.01E-40	2.31E-39	pvuba	-0.71464317	5.15E-26		
Sapur.01BG028100.1	124.1387331	-0.73327309	0.05537821	-13.2412	5.07E-40	2.34E-39	pvuba	-0.75457428	9.70E-30	GO:0006355;GO:0005739;GO:0003690	
Sapur.00AG042800.1	39.67085029	-1.01781802	0.08756423	-13.2225	6.51E-40	3.00E-39	pvuba	-0.71862555	3.26E-26		
Sapur.00AG078600.1	84.92639903	0.94030282	0.07112181	13.22185	6.58E-40	3.03E-39	pvuba	0.71225152	1.35E-25		Reticulon family protein
Sapur.00SG013300.1	95.80702765	-0.55260257	0.05193678	-13.2067	8.13E-40	3.08E-39	pvuba	-0.73628813	2.28E-28	GO:0003677	ARID/BRIGHT DNA-binding domain;ELM2 domain protein
Sapur.00G181200.1	334.6098836	-0.59585546	0.04529236	-13.177	1.19E-39	5.46E-39	pvuba	-0.71769021	4.33E-26	GO:0006872;GO:0030001;GO:0000166	P-type ATPase of Arabidopsis 2
Sapur.00G133600.1	268.1708888	0.78757877	0.05949151	13.1742	1.23E-39	5.66E-39	pvuba	0.66631703	1.66E-21		
Sapur.00TG139600.1	1798.02849	0.66002984	0.05010862	13.17243	1.26E-39	5.80E-39	pvuba	0.70287752	1.07E-24	GO:0006413;GO:0003743	Translation initiation factor SUI1 family protein
Sapur.01BG041100.1	23.54484469	-0.42867195	0.06475986	-13.1703	1.45E-39	6.64E-39	pvuba	-0.56697828	9.86E-19	GO:0007165;GO:0005515;GO:0043531	Disease resistance protein (TIR-NBS-LRR class) family
Sapur.00GS183200.1	26.6314439	-0.20870465	0.07671427	-13.1492	1.72E-39	7.87E-39	pvuba	-0.73828781	4.64E-28		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01WG043800.1	381.9323913	-0.14183274	0.01723283	-13.1453	1.81E-39	8.27E-39	pvuba	-0.75246058	8.20E-29		Ribosomal protein S24/S26, mitochondrial
Sapur.00SG146600.1	477.9668607	-0.52430271	0.03989243	-13.1438	1.85E-39	8.43E-39	pvuba	-0.72569376	5.52E-27	GO:0042254	sequence-specific DNA binding transcription factors
Sapur.01BG190600.1	2799.095244	-0.62632920	0.04769183	-13.1421	1.89E-39	8.63E-39	pvuba	-0.74237132	9.41E-29	GO:0051082;GO:0006950;GO:0006457;GO:0005524	AtHsp90.5;CRBB;EMB8395&I
Sapur.01BG051000.1	187.2074474	-0.13425649	0.03931487	-13.1249	2.32E-39	1.66E-38	pvuba	-0.72547329	1.20E-27	GO:0003676	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.01BG021700.1	262.1568335	-0.80131409	0.06108071	-13.1174	2.62E-39	1.19E-38	pvuba	-0.75248319	6.54E-30	GO:0006189	phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative
Sapur.01BG188400.1	518.8891687	-0.71131102	0.05334243	-13.0327	7.98E-39	3.56E-38	pvuba	-0.71987603	2.04E-26	GO:0008270	DHHC zinc finger family protein
Sapur.01AG090700.1	32.54468876	-1.1155997	0.08514783	-13.1019	3.21E-39	1.46E-38	pvuba	-0.68305705	6.56E-23		RAD-like 6
Sapur.01BG112800.1	43.94707293	-0.85406366	0.06264315	-13.0667	4.95E-39	1.57E-38	pvuba	-0.72172668	1.51E-26		Nucleic acid-binding protein
Sapur.01BG052300.1	2209.837432	0.37308235	0.02858124	13.08157	4.20E-39	1.90E-38	pvuba	0.69454276	6.26E-24		Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase
Sapur.00AG142100.1	141.3814425	-0.52835767	0.04042667	-13.0725	4.74E-39	2.14E-38	pvuba	-0.76E-08	2.29E-28	GO:0070461	
Sapur.01GS117800.1	12.80074346	-1.46309474	0.11195016	-13.0691	4.94E-39	2.24E-38	pvuba	-0.70287809	1.06E-24		plectin-related
Sapur.00AG207400.1	31.61779007	-2.42716303	0.18576562	-13.0667	5.10E-39	2.31E-38	pvuba	-0.58162724	7.88E-16		
Sapur.00SG127700.1	27.34691896	-2.45221631	0.15424061	-13.0514	6.24E-39	2.82E-38	pvuba	-0.56694857	7.12E-15	GO:0055114;GO:0020037;GO:0016705;GO:0005506	
Sapur.00AG139800.1	342.9380773	-0.51522661	0.03948734	13.04833	6.50E-39	2.93E-38	pvuba	0.72954312	2.32E-27		calcium dependent protein kinase 17
Sapur.00AG122300.1	17.47948462	-1.03888922	0.12568201	-13.0382	7.42E-39	3.35E-38	pvuba	-0.73628087	4.31E-28		
Sapur.00G183800.1	716.3312764	0.90837425	0.06967743	-13.0374	7.55E-39	3.38E-38	pvuba	-0.72502217	6.91E-27	GO:0005515;GO:0006364	Transducin/WD40 repeat-like superfamily protein
Sapur.00SG184500.1	1022.7036	-0.72113102	0.05533243	-13.0327	7.98E-39	3.56E-38	pvuba	-0.71985703	2.34E-26	GO:0042254;GO:0005634	ribosome biogenesis regulatory protein (RRS1) family protein
Sapur.00BG057000.1	24.71414741	-0.69400718	0.07869878	-13.0285	8.42E-39	3.76E-38	pvuba	-0.71277435	1.09E-25	GO:0007084	Mad1/BUB1 homology region 1
Sapur.00AG102300.1	428.4723274	0.68547285	0.05276514	13.00343	1.17E-38	5.25E-38	pvuba	0.69548306	5.16E-24		NADPH-quinone oxidoreductase
Sapur.15WG137000.1	2150.25788	1.31869652	0.10150121	12.99197	1.36E-38	6.09E-38	pvuba	0.63377812	5.17E-19	GO:0004857	Plant invertase/pectin methylesterase inhibitor superfamily protein
Sapur.00G264400.1	296.5276611	-0.65238541	0.05021111	-12.9992	1.39E-38	6.21E-38	pvuba	-0.71543006	1.78E-26	GO:0046872	CCCH-type zinc finger protein with ARM repeat domain
Sapur.01BG062800.1	951.4102369	0.77276789	0.05940183	12.99014	1.39E-38	6.24E-38	pvuba	0.67651188	6.02E-23		
Sapur.00G139300.1	1066.022882	0.76268476	0.05718076	-12.9871	1.45E-38	6.48E-38	pvuba	-0.72917681	2.55E-27	GO:0006412;GO:0005840;GO:0003735	Ribosomal protein L4/L1 family
Sapur.00SG086000.1	788.3815456	-0.67462693	0.05807889	-12.9842	1.53E-38	6.75E-38	pvuba	-0.70960434	2.37E-25	GO:0003676	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.01G187700.1	853.9098792	-0.31938179	0.02465942	-12.9865	1.58E-38	7.06E-38	pvuba	-0.72642067	1.86E-27	GO:0003676	EMBP/RD DEFECTIVE 140
Sapur.01TG007900.1	184.5652215	-0.95327423	0.07344835	-12.9794	1.60E-38	7.18E-38	pvuba	-0.70812433	3.36E-25	GO:0005515	nucleotide binding protein
Sapur.15WG104000.1	58.36892876	-0.73373793	0.05678796	-12.9211	3.42E-38	1.52E-37	pvuba	-0.71767216	4.46E-26		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.00AG102000.1	31.65105006	-2.62894506	0.20425645	-12.9174	3.59E-38	1.60E-37	pvuba	-0.69569494	4.92E-24		
Sapur.00SG065000.1	55.78310562	-1.43803237	0.11194523	-12.8538	8.19E-38	3.62E-37	pvuba	-0.6796974	1.28E-22		alpha carbonic anhydrase 7
Sapur.00AG121200.1	211.0668569	-0.80805479	0.07080627	-12.8468	8.65E-38	3.82E-37	pvuba	-0.66898867	8.12E-22		Cellulose synthase catalytic subunit
Sapur.00ZG032800.1	5.29281875	-1.90526428	0.14841702	-12.8372	1.01E-37	4.48E-37	pvuba	-0.70381205	8.66E-25		Pentatricopeptide repeat (PPR-like) superfamily protein
Sapur.00AG035000.1	1100.054528	-0.67162281	0.04800871	-12.8368	1.02E-37	4.51E-37	pvuba	-0.71674748	4.80E-26	GO:0005681;GO:0000398	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.00G296400.1	60.15208354	-0.97609153	0.07638486	-12.8366	1.02E-37	4.51E-37	pvuba	-0.68425203	5.16E-23		
Sapur.01ZG009400.1	66.9612392	-0.73608614	0.05798796	-12.8238	1.21E-37	5.32E-37	pvuba	-0.69628292	4.07E-24		
Sapur.01ZG027700.1	145.8509905	-0.69938681	0.03897873	-12.8076	1.46E-37	6.54E-37	pvuba	-0.72472756	5.42E-27	GO:0005515	
Sapur.00AG029700.1	474.3599696	0.59240544	0.04260509	12.80602	1.52E-37	6.68E-37	pvuba	0.74482617	5.52E-29		
Sapur.00SG117600.1	19.31463873	-2.05202457	0.17098805	-12.8013	1.61E-37	7.10E-37	pvuba	-0.71771757	3.84E-26		
Sapur.00SG144800.1	54.68731835	-1.36022841	0.10635476	-12.7969	1.87E-37	8.22E-37	pvuba	0.65280605	1.97E-20	GO:0055114;GO:0016491	AT2G14TAGA20DX;GA20D
Sapur.00G007900.1	359.758206	-0.60284506	0.04714861	-12.7837	2.34E-37	1.02E-36	pvuba	-0.69779178	1.32E-22		CMT3
Sapur.00TG127700.1	436.3483637	-0.77289789	0.06058881	-12.7581	2.81E-37	1.23E-36	pvuba	-0.71384255	1.06E-26		
Sapur.00SG056000.1	1671.777167	0.66184664	0.04673828	12.75667	2.86E-37	1.25E-36	pvuba	0.64734842	6.06E-24		
Sapur.01BG238300.1	43.75102224	-1.53122158	0.12023194	-12.7364	3.71E-37	1.62E-36	pvuba	-0.68483532	1.12E-21		
Sapur.01G089600.1	254.6286692	0.45413202	0.02254119	12.72594	4.24E-37	1.85E-36	pvuba	0.73431623	7.22E-28	GO:0003677	
Sapur.00BG067000.1	230.8326046	-0.66367986	0.07037625	-12.7136	4.97E-37	2.16E-36	pvuba	-0.62470552	5.25E-18		Metallo-hydrolase/oligopeptidase superfamily protein
Sapur.01GG049700.1	376.5702085	0.56700307	0.04457549	12.71213	5.06E-37	2.21E-36	pvuba	0.69389461	7.26E-24		delta(3,5)-delta(2,4)-dienoyl-CoA isomerase 1
Sapur.00AG100200.1	2209.498071	0.56245169	0.04429129	12.70749	5.42E-37	2.36E-36	pvuba	-0.72332186	1.28E-27	GO:0005524;GO:0051082;GO:0006457	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.01GG161600.1	564.0893086	-0.36237584	0.02809166	-12.6796	7.67E-37	3.33E-36	pvuba	-0.72171565	5.51E-26	GO:0003676	RNA-binding (RRM/RBD/RNP motifs) family protein
Sapur.01BG042800.1	648.0388325	-0.65376827	0.05193118	-12.6621	9.47E-37	4.10E-36	pvuba	-0.71450174	7.78E-26		
Sapur.01GG094200.1	1420.631522	-0.93263382	0.07374058	-12.6473	1.16E-36	5.01E-36	pvuba	-0.76338178	3.18E-31	GO:0005524	
Sapur.01BG274400.1	488.2232096	-0.55605162	0.04396618	-12.6466	1.17E-36	5.05E-36	pvuba	-0.58617027	7.31E-16		Barwin-related endoglucanase
Sapur.00SG109000.1	12.7368001	-0.93556096	0.15062041	-12.6456	1.18E-36	5.11E-36	pvuba	-0.69527847	5.27E-24		UDP-Glycosyltransferase superfamily protein
Sapur.00AG153300.1	53.98018893	-1.16346384	0.08782183	-12.6386	1.47E-36	6.34E-36	pvuba	-0.68606472	1.38E-24		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01BG066300.1	127.1250767	-2.52545029	0.20034205	-12.6057	1.98E-36	8.46E-36	pvuba	-0.73661202	4.07E-28	GO:0055114;GO:0020037;GO:0008379;GO:0004601	Peroxidase family protein
Sapur.00AG062900.1	188.4032071	1.39588866	0.10074537	12.60456	1.99E-36	8.57E-36	pvuba	0.72640471	5.05E-22		
Sapur.00WG082600.1	400.2187283	-0.63478819	0.06587956	-12.5851	2.67E-36	1.15E-35	pvuba	-0.68706197	2.58E-23	GO:0006351;GO:0003887;GO:0003677	DNA polymerase V
Sapur.01DG064300.1	36.20960743	-0.94175176	0.07496882	-12.5622	3.41E-36	1.46E-35	pvuba	-0.73094245	1.66E-27		
Sapur.01WG086700.1	116.3660831	-1.14705622	0.09134861	-12.5374	4.36E-36	1.91E-35	pvuba	-0.64379631	9.51E-20		
Sapur.00BG165300.1	932.2229895	-0.27137034	0.02163106	-12.5319	3.88E-36	1.66E-35	pvuba	-0.71362255	1.06E-26		
Sapur.00AG166600.1	24.14791495	-1.00262793	0.08211246	-12.5484	4.66E-36	2.75E-35	pvuba	-0.73431279	7.23E-28		
Sapur.01BG008300.1	627.4944595	-0.95978278	0.07615302	-12.5373	4.66E-36	1.99E-35	pvuba	-0.72445066	7.93E-27	GO:0005524;GO:0006508;GO:0004176;GO:0004252;GO:0016163	
Sapur.00AG127800.1	223.3062944	-0.97209182	0.08019745	-12.5254	5.98E-36	2.97E-35	pvuba	-0.68746586	2.97E-23	GO:0008408;GO:0006139;GO:0003676;GO:0005829;GO:0003887	GO:0003677
Sapur.00BG127800.1	1327.451016	-1.49884464	0.11999993	-12.4987	7.59E-36	3.23E-35	pvuba	-0.59529886	1.99E-16		
Sapur.00TG076000.1	571.6473399	-0.42651268	0.03437921	-12.4422	1.54E-35	6.51E-35	pvuba	-0.71403431	8.89E-26	GO:0005525	GTP-binding protein-related
Sapur.00SG179300.1	26.67617775	-5.60104921	0.08060207	-12.4202	2.06E-35	8.56E-35	pvuba	-0.73183286	4.77E-26		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01DG012100.1	41.07013344	-0.87198765	0.07024128	-12.4142	2.19E-35	9.22E-35	pvuba	-0.71357918	9.90E-26		mitochondrial editing factor 18
Sapur.00BG094300.1	1410.657717	-1.44620183	0.11652899	-12.4127	2.23E-35	9.36E-35	pvuba	-0.59328214	1.16E-16	GO:0006355;GO:0003700;GO:0003677	AP2/EREBP and B3 domain transcription factor RAV1
Sapur.01BG085500.1	175.1652642	-0.83842304	0.06757096	-12.4088	2.34E-35	9.86E-35	pvuba	-0.6578217	8.03E-21	GO:0046983	LRL1-like 1
Sapur.00G265500.1	1631.307504	-0.81385826	0.06561169	-12.4066	2.41E-35	1.01E-34	pvuba	-0.64989664	1.26E-20		alanine glyoxylate aminotransferase
Sapur.00TG054100.1	718.2745026	-0.58369528	0.04713816	-12.3838	3.20E-35	1.34E-34	pvuba	-0.65377525	5.26E-22		ribonuclease II family protein
Sapur.00AG100300.1	682.1989	-1.69689432	0.05647771	-12.3818	3.23E-35	1.35E-34	pvuba	-0.70944665	2.45E-27	GO:0005515	gibberellin protein 1
Sapur.01BG151500.1	576.8875054	-0.59806576	0.04833725	-12.3741	3.61E-35	1.51E-34	pvuba	-0.69981651	1.98E-24	GO:0006188;GO:0004018	L-Aspartase-like family protein
Sapur.00AG094100.1	156.0131239	-0.90020161	0.07283883	-12.3488	5.18E-35	2.17E-34	pvuba	-0.72017045	1.27E-26	GO:0007049;GO:0005634	Pentatricopeptide repeat (PPR) superfamily protein
Sapur.00TG039800.1	10.37500136	-1.38893513	0.11231868	-12.3657	4.03E-35	1.68E-34	pvuba	-0.71288801	1.66E-25		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.01BG094700.1	245.382124	-0.61470527	0.04981675	-12.3393	5.56E-35	2.32E-34	pvuba	-0.70087608	1.62E-24		Pre-rRNA-processing protein TSR2, conserved region
Sapur.01BG088900.1	405.3462858	-0.78839172	0.06393247	-12.3315	6.13E-35	2.56E-34	pvuba	-0.67838033	1.68E-22	GO:0005515;GO:0003676	Arginase/agmatinase family protein
Sapur.00TG115800.1	1967.689518	-0.48772464	0.03957481	-12.3242	6.57E-35	2.80E-34	pvuba	-0.69667459	1.42E-23	GO:0008270;GO:0005622	MER18
Sapur.00AG100400.1	4.56065234	-2.04326494	0.16845645	-12.3205	7.03E-35	2.93E-34	pvuba	-0.65767241	2.61E-21	GO:0006488;GO:0005524;GO:0004672	EDH;TMK1
Sapur.01GG059600.1	35.34629699	-1.05835802	0.09406195	-12.3168	7.35E-35	3.06E-34	pvuba	-0.64575052	6.79E-20		
Sapur.00SG079600.1	1541.190017	-0.67008119	0.05383356	-12.2991	9.16E-35	3.81E-34	pvuba	-0.64989664	1.26E-20		RNA polymerase I specific transcription initiation factor RRN3 protein
Sapur.01DG074100.1	31.19704777	1.57034091	0.12794634	12.27361	1.26E-34	5.20E-34	pvuba	0.59368814	2.51E-16		
Sapur.01WG042700.1	2.53210454	-3.62840117	0.31064809	-12.2563	1.55E-34	6.43E-34	pvuba	-0.54455784	1.78E-13	GO:0016021;GO:0016020;GO:0022857	nodulin MtN21 /EamA-like transporter family protein
Sapur.00AG047000.1	128.3240365	-1.04379826	0.08131651	-12.246	1.76E-34	7.29E-34	pvuba	-0.70371817	8.84E-25		HSP20-like chaperones superfamily protein
Sapur.00SG176000.1	28.88876767	-1.26407829	0.10342994	-12.2245	1.92E-34	9.48E-34	pvuba	-0.71659647	4.97E-26		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.00TG027400.1	756.0114959	-0.44417184	0.03634304	-12.2216	2.38E-34	9.82E-34	pvuba	-0.68812866	2.32E-23		U3 small nucleolar RNA-associated-like protein
Sapur.00GS019400.1	255.1635764	-0.48458509	0.03965155	-12.2211	2.40E-34	9.89E-34	pvuba	-0.70925677	2.62E-25		nucleoporin protein Nup96
Sapur.01TG004200.1	6.11302727	-1.72839313	0.14108153	-12.1981	3.18E-34	1.31E-33	pvuba	-0.61397944	1.47E-19	GO:0006468;GO:0005524;GO:0004672	receptor serine/threonine kinase, putative
Sapur.01GG258900.1	452.5471887	-0.68676493	0.05630527	-12.1955	3.26E-34	1.32E-33	pvuba	-0.67431234	3.66E-22		KDSB
Sapur.00G125100.1	291.9763556	-0.78169153	0.06431564	-12.1881	3.60E-34	1.46E-33	pvuba	-0.68560618	1.87E-23	GO:0008173;GO:0006396;GO:0003723	RNA/RNA methyltransferase family protein
Sapur.00ZG054900.1	857.5118399	-0.62231337	0.0518655	12.18793	3.60E-34	1.48E-33	pvuba	0.69613607	4.48E-24	GO:0008121;GO:0006122	Ubiquinol-cytochrome C reductase hinge protein
Sapur.00GS126700.1	17.38719974	-1.61684329	0.13112658	-12.1878	3.61E-34	1.48E-33	pvuba	-0.69733669	1.49E-24		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.00BG048200.1	244.7541346	-0.45896763	0.07368159	-12.1781	4.07E-34	1.67E-33	pvuba	-0.73026351	2.08E-28		
Sapur.00AG088000.1	831.8083009	-0.59807463	0.04911483	12.17218	4.37E-34	1.79E-33	pvuba	0.68052302	1.79E-23		
Sapur.00SG088000.1	57.65700464	-0.81921289	0.06724027	-12.1635	4.86E-34	1.99E-33	pvuba	-0.70052959	1.76E-24		
Sapur.00AG067000.1	351.3999847	-0.47404847	0.03904767	-12.1402	6.47E-34	2.65E-33	pvuba	-0.71113661	1.72E-25		
Sapur.01BG124000.1	49.94695562	-4.49423775	0.12152074	-12.1353	6.74E-34	3.18E-33	pvuba	-0.67443431	1.58E-22		
Sapur.01GG022200.1	504.18691	-0.35927868	0.02669138	-12.0989	1.07E-33	4.36E-33	pvuba	-0.69018467	1.55E-23	GO:0005634	
Sapur.01BG121800.1	7.39695532	-2.13647829	0.17468162	-12.0867	1.18E-33	4.78E-33	pvuba	-0.60188396	7.98E-17		
Sapur.01GG132700.1	678.1751055	-0.62588395	0.05196177	-12.0848	1.27E-33	5.17E-33	pvuba	-0.70404705	8.22E-25	GO:0006810;GO:0005643	
Sapur.00TG000100.1	1.60729887	-3.17556721	0.26307964	-12.0707	1.51E-33	6.12E-33	pvuba	-0.64004906	2.50E-20	GO:0005515	
Sapur.00AG127800.1	938.8174495	-0.43682951	0.03612571	-12.0865	2.29E-33	9.25E-33	pvuba	-0.69704353	3.70E-24		
Sapur.01BG082600.1	588.5519229	-0.85628201	0.10840226	-12.0256	2.38E-33	1.05E-32	pvuba	-0.70209604	2.56E-24	GO:0016787;GO:0005524;GO:0003677	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.00AG064400.1	59.16418219	-0.92285232	0.01016917	-12.018	2.86E-33	1.15E-32	pvuba	-0.70856719	3.06E-25		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.00SG160400.1	250.7334947	-0.03188362	0.0861635	-12.002	3.47E-33	1.40E-32	pvuba	-0.72637575	1.36E-27	GO:0005515	pentatricopeptide (PPR) repeat-containing protein
Sapur.15WG008400.1	80.6243057	-1.14560519	0.09546057	-11.9999	3.56E-33	1.44E-32	pvuba	-0.66228151	1.68E-21		
Sapur.00TG028500.1	18.34664105	-2.31832204	0.19860487	-11.9988	3.60E-33	1.45E-32	pvuba	-0.6978782	9.32E-28		Protein of unknown function (DUF677)
Sapur.00BG060100.1	810.761541	-0.64197049	0.0860561	-11.9908	3.91E-33	1.57E-32	pvuba	-0.68111233	5.97E-23		
Sapur.00ZG010300.1	25.26050881	-1.48309783	0.12836613	-11.9834	4.24E-33	1.75E-32	pvuba	-0.66695671	1.71E-21	GO:0006508;GO:0004252	Subtilisin-like serine endopeptidase family protein
Sapur.00GS024600.1	1357.325251	-0.78109169	0.06136605	-11.9678	5.24E-33	2.11E-32	pvuba	0.66097956	9.95E-22		1/FE Family of 2-oxoglutarate/Fe(II)-dependent 1 alpha subcomplex subunit 6
Sapur.01GG161700.1	59.76842572	-2.23308071	0.10277569	-11.9606	5.71E-33	2.30E-32	pvuba	-0.73175388	1.36E-27		
Sapur.00AG087200.1	19.55150667	-1.26797865	0.10823995	-11.9569	5.98E-33	2.40E-32	pvuba	-0.68461363	7.92E-23		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.00GS035500.1	15.68403732	-1.43596331	0.12018754	-11.9477	6.68E-33	2.68E-32	pvuba	-0.61706155	7.58E-18	GO:0016747	Esterase/lipase/thioesterase family protein
Sapur.00AG100100.1	1006.017807	-0.66481614	0.07344473	11.94713	6.73E-33	2.70E-32	pvuba	0.69244512	7.72E-24		Ribosomal protein L7Ae family
Sapur.01GG069300.1	147.4625756	-0.48617413	0.04384958	-11.9389	7.42E-33	2.97E-32	pvuba	-0.69591815	4.70E-24		HIT zinc finger protein
Sapur.00AG062400.1	205.6379918	-0.78268896	0.06564934	-11.9233	8.95E-33	3.58E-32	pvuba	-0.71205532	1.69E-25		mitochondrial HSP70 2
Sapur.01BG089300.1	931.9389156	-0.41490428	0.03486613	-11.9003	1.18E-32	4.71E-32	pvuba	-0.68726129	2.74E-23	GO:0004386	RNA helicase, nucleolar protein
Sapur.01DG020100.1	878.9247958	-0.44124726	0.03713426	-11.8827	1.46E-32	5.80E-32	pvuba	-0.69834356	2.81E-24	GO:0005524	TCP-1/cpn60 chaperonin family protein
Sapur.00ZG067300.1	272.8387562	-0.62487777	0.05381266	-11.8778	1.54E-32	6.11E-32	pvuba	-0.70098835	1.61E-24	GO:0070588;GO:0016020;GO:0005524	Preprotein translocase SecA family protein
Sapur.00SG162200.1	291.7506885	1.36183765	0.11480996	11.86173	1.87E-32	7.44E-32	pvuba	0.58469903	8.98E-16	GO:0016788	GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.01GG211900.1	188.8820000	-0.57808728	0.06847761	-11.8525	2.09E-32	8.26E-32	pvuba	-0.62546827	2.00E-18	GO:0055114;GO:0050661;GO:0060006;GO:0004045	glucose-6-phosphate dehydrogenase 6
Sapur.00AG149700.1	373.7746618	-0.51365206	0.04334916	-11.8503	2.15E-32	8.51E-32	pvuba	-0.67680806	2.22E-22	GO:0005515	Leucine-rich repeat (LRR) family protein
Sapur.01BG280000.1	12.34505212	-0.86056304	0.07259422	-11.8356	2.55E-32	1.01E-31	pvuba	-0.68891168	2.45E-24		
Sapur.01DG078800.1	143.024231	-0.38108423	0.03221984	-11.8276	2.81E-32	1.11E-31	pvuba	-0.70619708	5.14E-25		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.00AG130100.1	56.84042605	-0.67730919	0.05498406	-11.8017	3.83E-32	1.51E-31	pvuba	-0.68837318	1.03E-22	GO:0005543	epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related
Sapur.01ZG060600.1	643.4862303	0.46689427	0.03956846	11.7912	4.33E-32	1.71E-31	pvuba	0.68791314	2.46E-23	GO:0016788	SGNH hydrolase-type esterase and lipase family protein
Sapur.00G117500.1	1175.398885	0.71394384	0.06054647	11.79304	4.34E-32	1.71E-31	pvuba	0.63062704	8.68E-19	GO:0055114;GO:0016491;GO:0016651	PKSD reductase 2
Sapur.01DG063000.1	2817.644206	-0.90047483	0.05017885	-11.7794	4.99E-32	1.96E-31	pvuba	-0.69393435	5.68E-24	GO:0055114;GO:0009680;GO:0004455;GO:0016491	ketol-acid reductoisomerase
Sapur.01BG194900.1	116.977989	0.70200194	0.05961856	-11.7753	5.23E-32	2.06E-31	pvuba	-0.67083165	7.14E-22		activator of basal transcription protein, putative
Sapur.01TG058500.1	8.52383916	-1.81408642	0.15458027	-11.7526	6.85E-32	2.69E-31	pvuba	-0.69393513	1.24E-24	GO:0008655	early nodulin-like protein 11
Sapur.00ZG020900.1	42.91634196	-0.07252492	0.08276281	-11.7509	6.99E-32	2.74E-31	pvuba	-0.71797267	3.62E-26		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.01TG039300.1	1384.462169	-0.68268018	0.05831078	-11.7489	7.16E-32	2.80E-31	pvuba	-0.70747207	1.88E-25	GO:0055114;GO:0051082;GO:0006457	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.01DG108800.1	208.3592966	-0.66106029	0.05638812	-11.7275	9.21E-32	3.61E-31	pvuba	-0.68914768	1.67E-23	GO:0006351;GO:0003899;GO:0003677	DNA-directed RNA polymerase
Sapur.01AG078100.1	512.4478323	-0.50432312	0.05270466	-11.7191	1.02E-31	3.98E-31	pvuba	-0.68844003	1.62E-23		NADH-binding Rossmann-fold superfamily protein
Sapur.01AG047000.1	373.9007861	0.59641835	0.05291259	11.71463	1.07E-31	4.19E-31	pvuba	0.65320025	1.81E-20	GO:0006486;GO:0005784	protein transporter Sec61 beta subun

Sapur.002G086800.1	33.26396663	-1.56089317	0.144206337	-10.824	2.65E-27	9.41E-27	gene	-0.613679399	1.50E-17	GO:0006355;GO:0005634	AtSGS630.2	IAA9	auxin-responsive protein (Aux/IAA)
Sapur.010G111100.1	223.9765507	-0.718464754	0.066479952	-10.8054	3.24E-27	1.15E-26	gene	-0.644429896	8.53E-20		AtSGD8800.1		ARM repeat superfamily protein
Sapur.003G145300.1	661.3657758	0.107505164	0.010142862	10.601	3.40E-27	1.21E-26	gene	-0.630282245	4.15E-19	GO:0016787;GO:0005634;GO:0003677	AtSGD2635.1		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.007G039100.1	10.89902422	-1.181430297	0.109450315	-10.7942	3.67E-27	1.30E-26	gene	-0.665395085	5.01E-21		AtSGA7840.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.010G094800.1	982.5413358	-0.430057853	0.039931017	-10.7924	3.76E-27	1.32E-26	gene	-0.650568537	2.93E-20	GLN1	AtSGD1400.1		genomes uncoupled 1
Sapur.011G108200.1	131.5385325	0.372631548	0.034531671	10.79107	3.79E-27	1.34E-26	gene	-0.644887309	7.75E-20		AtSGS1500.1		lectin-domain receptor kinase A6.2, putative
Sapur.005G177300.1	221.9072115	-0.635029533	0.058936405	-10.7884	3.91E-27	1.38E-26	gene	-0.686885433	3.04E-23	GO:0005515	AtSGU3240.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.010G283300.1	127.3220015	-0.595494612	0.055132897	-10.7841	4.08E-27	1.45E-26	gene	-0.639451257	1.99E-19		AtSGD5190.1		Protein of unknown function (DUF3133)
Sapur.001G187900.1	628.2481515	0.677306613	0.062952892	10.76895	4.82E-27	1.70E-26	gene	-0.60757682*	3.25E-17	GO:0022900;GO:0005747;GO:0005739	AtSGJ4450.1		NADH dehydrogenase (ubiquinone)
Sapur.013W022700.1	13.74719835	-1.357348489	0.126139483	-10.7421	6.46E-27	2.27E-26	gene	-0.672541788	1.32E-18		AtSGJ5065.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.002G011000.1	828.5378652	-0.580108769	0.054015719	-10.7413	6.51E-27	2.29E-26	gene	-0.629460883	1.05E-18	CPUORF7	AtSGJ1281.1		conserved peptide upstream open reading frame 7
Sapur.006G217300.1	8.006617274	-1.469869266	0.139443193	-10.7364	6.87E-27	2.42E-26	gene	-0.649311241	3.65E-20		AtSGD3540.1		Pentatricopeptide repeat (PPR-like) superfamily protein
Sapur.007G068200.1	19.7395046	-0.816061325	0.076109087	-10.734	7.05E-27	2.48E-26	gene	-0.679165767	1.42E-22		AtSGD8305.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.004G096800.1	1068.363621	-0.307799681	0.028245436	-10.5138	1.15E-27	2.51E-26	gene	-0.611932182	2.30E-18		AtSGJ1930.2		pectin lyase-like superfamily protein, putative
Sapur.005G015500.1	1827.082965	-0.504876301	0.047061187	-10.7281	7.51E-27	2.64E-26	gene	-0.679662271	1.45E-22	GO:0005515	AtSG11420.1	ATIEF3A-1,ATTIF3A1,EIF3A1	eukaryotic translation initiation factor 3A
Sapur.005G139100.1	14.18868802	-1.322182707	0.125532258	-10.7278	7.54E-27	2.65E-26	gene	-0.643050507	1.02E-20				
Sapur.003G069500.1	568.101824	-0.687754299	0.064139786	-10.7244	7.82E-27	2.74E-26	gene	-0.666225812	1.69E-21		AtSGJ3183.1	AFH14	Formin Homology 14
Sapur.009G033000.1	27.03047617	-0.881866189	0.082271313	-10.719	8.29E-27	2.91E-26	gene	-0.623731041	2.65E-18		AtSGD7270.1		Cell division control, Cdc6
Sapur.006G182200.1	1052.050027	-0.364904717	0.04196828	-10.6488	8.29E-27	2.97E-26	gene	-0.827172197	5.52E-22	CDCF2;LIF1	AtSGB6910.1		Cysteine/tyr-beta-synthase (CBS) family protein
Sapur.014G113600.1	190.8793235	-0.401076919	0.037046651	-10.7055	9.59E-27	3.36E-26	gene	-0.664970035	2.15E-21	GO:0005524;GO:0003676	AtSGD3065.2		P-loop containing nucleoside triphosphate hydrolases superfamily protein
Sapur.010G117100.1	842.4871236	-0.406825219	0.038204495	-10.6719	1.18E-26	3.86E-26	gene	-0.667331554	2.46E-21		AtSGA2620.1	PUR4	purine biosynthesis protein PUR4, putative
Sapur.005G039800.2	21.6482712	-1.203675883	0.112885920	-10.6672	1.45E-26	5.05E-26	gene	-0.655092097	2.10E-20	GO:0006468;GO:0005634;GO:0004672	AtSGK5430.3	ATNEK1,NEK1	N-NAM-related serine/threonine kinase 1
Sapur.002G037900.1	252.1502664	-0.499885146	0.047014176	-10.6317	2.12E-26	7.37E-26	gene	-0.658549423	7.01E-21		AtSGT6280.3		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.005G199500.2	8.392657511	-1.718759691	0.161918249	-10.615	2.54E-26	8.79E-26	gene	-0.561360869	2.05E-14	GO:0006508;GO:0005634;GO:0004222	AtSGA2730.1	FTSH5,VAR1	FtsH extracellular protease family
Sapur.010G027000.1	1937.40388	-0.356611603	0.033626921	-10.6138	2.57E-26	8.90E-26	gene	-0.658337125	2.86E-20		AtSGD7610.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.018G201400.1	82.92509634	-0.679445902	0.064259294	-10.5735	3.95E-26	1.36E-25	gene	-0.634698848	4.43E-19		AtSGT2700.1		ATP binding;nucleic acid binding;helicases
Sapur.002G182800.1	769.3819661	-0.487444831	0.046146753	-10.5629	4.43E-26	1.52E-25	gene	-0.66051864	4.90E-21	GO:0005811;GO:0015085;GO:0016021;GO:0015296;GO:0006812	AtSGD8630.1	ATKEA2,KEA2	Kx-effflux antiporter 2
Sapur.005G176700.1	907.6755062	-0.504242266	0.047863726	-10.53479	5.97E-26	2.05E-25	gene	-0.61621918	6.65E-18	GO:0005737;GO:0000045	AtSGD5630.1	ATGID	Ubiquitin-dependent protein catabolism
Sapur.011G135200.1	42.08739931	-0.776091988	0.073833712	-10.5223	6.82E-26	2.34E-25	gene	-0.670948874	6.98E-22		AtSGD5750.1	CLB19,PDE247	Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.007G005400.1	1.922693913	-2.226407008	0.306762888	-10.5178	7.16E-26	2.45E-25	gene	-0.621618875	3.71E-18	GO:0006355;GO:0005634;GO:0032502;GO:0006351	AtSGA2240.1	AtGRF1,GRF1	growth-regulating factor 1 protein
Sapur.002G154600.1	56.74049641	-0.608565863	0.057909348	-10.5172	7.20E-26	2.47E-25	gene	-0.638535832	2.31E-19	GO:0006468;GO:0004672	AtSGD2970.1	ATWEE1,WEE1	WEE1 kinase homolog
Sapur.017G052200.1	69.7087569	-0.846631621	0.080819375	-10.5127	7.55E-26	2.58E-25	gene	-0.673868459	2.61E-19		AtSGA1310.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.006G040600.1	15.97338895	-1.128263523	0.107334186	-10.517	7.63E-26	2.61E-25	gene	-0.593076207	2.75E-16	GO:0005525	AtSGJ1630.1		elongation factor family protein
Sapur.006G087600.1	425.255575	-0.331017329	0.031777155	-10.4798	1.07E-25	3.66E-25	gene	-0.647172836	1.30E-20	GO:0008270	AtSGC2281.1		Ubiquitin C-terminal hydrolase superfamily protein
Sapur.016G207400.1	11.70964519	-1.299387861	0.124126485	-10.4682	1.21E-25	4.12E-25	gene	-0.66041573	4.79E-21		AtSGJ3980.1		
Sapur.005G177600.1	1937.40388	-0.356611603	0.033626921	-10.6138	2.57E-26	8.90E-26	gene	-0.658337125	2.86E-20		AtSGD4230.1	ELIP2,ELIP1	Chlorophyll A-B binding family protein
Sapur.012G111400.1	88.18135392	-1.638512658	0.157182085	-10.4243	1.92E-25	6.52E-25	gene	-0.533202243	7.48E-13	GO:0055085;GO:0016020;GO:0015297;GO:0015238;GO:0006855	AtSGS6240.1	ATDTX35,DTX35,FIT	detoxifying efflux carrier 35
Sapur.004G082300.1	223.103727	0.719108392	0.069081385	10.40958	2.24E-25	7.60E-25	gene	-0.639085673	2.12E-19	GO:0016853;GO:0005507	AtSGS7580.1	ADC3	allene oxide cyclase 3
Sapur.013G056500.1	837.6607739	0.467406316	0.044946426	10.40309	2.45E-25	8.30E-25	gene	-0.627857571	1.41E-18		AtSGS2575.1		hypothetical protein
Sapur.015G073400.1	1016.061655	0.346070793	0.033232585	10.38236	2.98E-25	1.01E-24	gene	-0.652885094	1.95E-20		AtSGT8870.2	UBC13A,UBC35	ubiquitin-conjugating enzyme 35
Sapur.018G075200.1	980.3870053	-0.272421759	0.079332045	-10.3486	3.16E-25	1.07E-24	gene	-0.607173846	7.80E-17		AtSGT7960.1		
Sapur.006G028700.1	309.6629991	-0.682771257	0.065882342	-10.3629	3.66E-25	1.23E-24	gene	-0.62118846	3.97E-18	GO:0006265;GO:0005524;GO:0003918;GO:0003677	AtSGD4130.1	GYRB2	DNA GYRASE B2
Sapur.T046100.1	31.51202705	-0.916111488	0.088152099	-10.3454	3.98E-25	1.34E-24	gene	-0.598842679	9.11E-12		AtSGP4570.1		Protein of unknown function, DUF538
Sapur.15W0G0018800.1	126.0685748	-0.954911759	0.092334649	-10.3432	4.48E-25	1.51E-24	gene	-0.627463	1.45E-18	GO:0008270;GO:0005634	AtSGB8950.1		C3HC zinc finger-like
Sapur.004G130000.1	49.13175162	-0.684799883	0.066246349	-10.3372	4.78E-25	1.61E-24	gene	-0.612404045	2.96E-21		AtSGT6630.1		Tetratricopeptide repeat (TPR) superfamily protein
Sapur.010G176700.1	9.404885069	-1.189571066	0.115205838	-10.3256	5.40E-25	1.81E-24	gene	-0.589393504	4.29E-16	GO:0006468;GO:0004672	AtSGJ9180.1	ATCBR2,CCR2	CRINKLY4 related 2
Sapur.016G226000.1	1067.048801	-0.347156221	0.034018691	-10.3168	5.92E-25	1.99E-24	gene	-0.658436236	1.97E-18	GO:0005975;GO:0004553	AtSGA7610.2	ATVPS29,MAG1,VPS29	Calcineurin-like metallo-phosphoesterase superfamily protein
Sapur.003G039800.2	17.74657219	0.874407421	0.08452479	10.31029	6.13E-25	2.13E-24	gene	-0.648975028	8.36E-19	GO:0016787;GO:0009058;GO:0005515	AtSGJ7630.1	IAR3,IR3	Trimeric Lipoic acid-like enzyme
Sapur.005G025300.1	12.68242069	-1.326793462	0.129133085	-10.2901	7.81E-25	2.62E-24	gene	-0.603817263	6.63E-17	GO:0007165;GO:0005515	AtSGJ1470.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Sapur.006G049700.1	165.215505	-0.474681884	0.046139519	-10.2775	8.98E-25	2.98E-24	gene	-0.643917787	7.92E-20	GO:0005515;GO:0008977;GO:0006571;GO:0004665	AtSGB3610.1		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.004G272700.1	178.9240444	-0.519122147	0.050516842	-10.2762	9.02E-25	3.02E-24	gene	-0.651683721	2.90E-20		AtSGA2960.1		arogenate dehydrogenase
Sapur.018G075000.1	980.3870053	-0.272421759	0.079332045	-10.3486	3.16E-25	1.07E-24	gene	-0.607173846	7.80E-17		AtSGB2610.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Sapur.003G128700.1	56.04124008	-0.371064497	0.036182771	-10.2553	1.12E-24	3.76E-24	gene	-0.629319555	1.07E-18	GO:0003723;GO:0003676	AtSGB9760.2	PABP,PABP8	polyA(A) binding protein 8
Sapur.003G045200.1	18.04442123	-0.916111488	0.088152099	-10.3454	3.98E-25	1.34E-24	gene	-0.598842679	9.11E-12		AtSGP3530.1		Protein of unknown function, DUF538
Sapur.008G134800.1	13.22192048	-0.257186007	0.12270552	-10.246	1.23E-24	4.11E-24	gene	-0.538369893	3.00E-14		AtSGJ4590.1		Nucleotide-diphosphe-sugar transferase family protein
Sapur.006G138500.1	131.3157775	-0.364688774	0.036181197	-10.2457	1.24E-24	4.12E-24	gene	-0.643728267	9.54E-20	GO:0005515	AtSGT4260.1	ELFE1,VPR	binding
Sapur.002G097400.1	103.7985107	0.572969001	0.055935543	10.24302	1.27E-24	4.24E-24	gene	-0.59007567	4.21E-16		AtSGZ7695.2		glycine-rich protein
Sapur.008G092800.1	125.319239	-0.649062445	0.063488519	-10.2405	1.31E-24	4.35E-24	gene	-0.623151509	2.90E-18		AtSGZ5690.1	CHUP1	Hydroxyproline-rich glycoprotein family protein
Sapur.008G163300.1	717.0738079	-0.554047952	0.065546296	-10.2108	1.43E-24	4.76E-24	gene	-0.62243678	1.25E-18		AtSGA4040.1		Apoptosis inhibitor 5 (API5)
Sapur.016G084200.1	62.96619868	-0.771862472	0.075488331	-10.2317	1.43E-24	4.75E-24	gene	-0.648823949	5.64E-20	GO:0006468;GO:0004672	AtSGB0780.1	ATCRRL,CCR1	CRINKLY4 related 1
Sapur.016G236000.1	2175.214363	-0.343156221	0.034018691	-10.3168	5.92E-25	1.99E-24	gene	-0.658436236	1.97E-18	GO:0005975;GO:0004553	AtSGA7610.2	ATVPS29,MAG1,VPS29	Calcineurin-like metallo-phosphoesterase superfamily protein
Sapur.005G034200.1	512.2862204	-0.362606558	0.035418536	-10.2231	1.56E-24	5.19E-24	gene	-0.648975028	6.26E-20	GO:0016779;GO:0009058;GO:0005515	AtSGB7690.1		Trimeric Lipoic acid-like enzyme
Sapur.004G169025.1	17847.61008	-0.567284864	0.055538302	-10.2157	1.68E-24	5.60E-24	gene	-0.610704448	2.02E-17		AtSGJ8370.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Sapur.015G134800.1	23.45403393	-1.129369839	0.110650572	-10.2083	1.82E-24	6.04E-24	gene	-0.615704564	9.26E-18		AtSGZ7228.1	CPUORF6	conserved peptide upstream open reading frame 6
Sapur.016G187800.1	238.0237344	-0.659281197	0.065118424	-10.2035	1.90E-24	6.31E-24	gene	-0.623864621	1.56E-18		AtSGB4861.1	DVL1	DVL family protein
Sapur.018G061500.1	200.4076142	-1.001457577	0.098615438	-10.2016	1.94E-24	6.43E-24	gene	-0.554518055	4.89E-14				hypothetical protein
Sapur.006G044600.1	18.12768848	-0.818367831	0.079705488	-10.2006	1.97E-24	6.53E-24	gene	-0.654027055	1.61E-20		AtSGJ5030.1		pentatricopeptide (PPR) repeat protein, putative
Sapur.005G019900.1	64.20547168	-0.675727328	0.066352159	-10.184	2.34E-24	7.76E-24	gene	-0.615113591	1.03E-17	GO:0005524;GO:0003676	AtSGD5740.1	RECQ1	RECQ helicase 1E
Sapur.010G081100.1	203.8496084	-0.374315691	0.036754042	-10.1802	2.43E-24	8.03E-24	gene	-0.645513471	1.41E-19	GO:0003127;GO:0008270;GO:0006886;GO:0006886	AtSGA3670.1		Sec23/Sec24 protein transport family protein
Sapur.013G085000.1	12.21123848	-0.984423313	0.191964818	-10.1759	2.54E-24	8.39E-24	gene	-0.513541664	4.06E-12	GO:0016757	AtSGS6020.1	AtGoS2,GoS2	galactinol synthase
Sapur.005G148100.1	96.41575775	-2.56655504	0.252025152	-10.1758	2.54E-24	8.40E-24	gene	-0.445609041	4.93E-09		AtSGT6780.2		pathogenesis-related family protein
Sapur.006G098700.1	4.9531052	-2.567408065	0.252682863	-10.1684	2.72E-24	8.97E-24	gene	-0.588855504	2.30E-14		AtSGB8330.1		hypothetical protein
Sapur.010G179400.1	3010.61301	-0.46490787	0.045882787	10.15021	3.31E-24	1.09E-23	gene	-0.603027164	6.63E-17	GO:0005515	AtSGA2300.1	UBL5	ubiquitin-like protein 5
Sapur.004G130900.1	323.7031122	-0.464882774	0.045831319	10.14135	3.62E-24	1.19E-23	gene	-0.616150053	1.47E-18		AtSGT4915.1	ELF4-L4	ELF4-like 4
Sapur.003G045100.1	27.96832745	-0.788532214	0.077814606	10.1345	3.93E-24	1.29E-23	gene	-0.60924909	2.61E-17		AtSGJ6566.1	HINT4	histidine triad nucleotide-binding 4
Sapur.005G096300.1	285.5241161	-0.457089193	0.045144947	-10.1279	4.16E-24	1.37E-23	gene	-0.578413235	2.62E-15	GO:0043531	AtSGD6650.2	ZAR1	NBS-LRR disease resistance protein, putative
Sapur.011G155700.1	19.68915601	-0.813691279	0.080359977	-10.1256	4.25E-24	1.40E-23	gene	-0.642596549	1.17E-19		AtSGS3850.1		Uncharacterized protein family (UPF0497)
Sapur.010G047000.1	18.19554616	0.956887234	0.094650024	10.11782	4.61E-24	1.51E-23	gene	-0.58810297	8.50E-15				hypothetical protein
Sapur.010G088700.1	1132.918138	-0.345332009	0.034152775	-10.1146	4.76E-24	1.56E-23	gene	-0.642874215	1.11E-19	GO:0006396;GO:0003872	AtSGT4830.1	PFK2	phosphofructokinase 2
Sapur.016G091000.2	16.79549601	0.764325771	0.075567591	10.11453	4.78E-24	1.56E-23	gene	-0.618190808	6.36E-18	GO:0006457;GO:0048513;GO:0042761;GO:0010154	AtSGA5010.1	DE1,PAG1	Peptidyl-prolyl cis-trans isomerase PASTICCINO protein
Sapur.006G190000.1	254.7656287	0.510358168	0.050481584	10.10024	5.03E-24	1.65E-23	gene	-0.593043706	2.82E-16		AtSGD9200.1		Protein of unknown function (DUF1012)
Sapur.002G091800.1	5.857319549	-1.884875486	0.186239949	-10.0999	5.53E-24	1.81E-23	gene	-0.526136348	1.20E-15	GO:0043565;GO:0005515;GO:0003700;GO:0003677	AtSGT7790.1	HAT22	transcription factor
Sapur.006G167200.1	548.1410218	-0.358267373	0.038700726	-10.0868	5.60E-24	1.84E-23	gene	-0.639797222	2.12E-19		AtSGJ9190.1		hypothetical protein
Sapur.012G046600.1	305.9573667	-0.375379466	0.037195214	10.09214	5.98E-24	1.96E-23	gene	-0.613730305	1.27E-17		AtSGD8840.1		hypothetical protein
Sapur.008G102600.1	12.73918854	-0.988252752	0.08811242	-10.062	6.60E-24	1.96E-23	gene	-0.797582824	7.60E-26		AtSGZ3280.1	ELF4-L4	MAK16 protein-related
Sapur.001G147500.1	10.34863652	-1.107842562	0.10909024	-10.0796	6.80E-24	2.22E-23	gene	-0.641265561	1.47E-19		AtSGZ4072.1		Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.15W0G0018900.1	11.05124619	-0.284473202	0.027512749	10.0752	7.11E-24	2.32E-23	gene	-0.578413235	2.62E-15	GO:0043531	AtSGA6650.2	ZAR1	DEAD/H box helicase family protein
Sapur.010G078500.1	1883.820238	-0.485515932	0.048204245	-10.0645	7.93E-24	2.58E-23	gene	-0.640863154	5.17E-19	GO:0055114;GO:0004616;GO:0050661;GO:0006098	AtSGA5670.1		E-phosphoglucomutase dehydrogenase family protein
Sapur.002G141400.1	403.7959541	-0.469445838	0.046622156	-10.0605	8.26E-24	2.69E-23	gene	-0.615228205	1.01E-17	GO:0008556;GO:0008886;GO:0005515	AtSGA6520.1		cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative
Sapur.002G068400.1	402.0768342	-0.365611637	0.036541521	-10.0527	8.61E-24	2.81E-23	gene	-0.611154200	1.07E-17	GO:0008168;GO:0008152	AtSGB0910.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.003G174200.1	297.9024668	0.387788672	0.038656582	10.02775	1.15E-23	3.74E-23	gene	-0.630632421	8.67E-19	GO:0051125;GO:0031032	AtSGZ6980.1		HALS auxin-like complex subunit 2
Sapur.006G020200.1	2224.74746	0.362318637	0.036128164	10.0265	1.17E-23	3.79E-23	gene	-0.603636477	5.87E-17	GO:0022904;GO:0016655;GO:0005743	AtSGZ2640.1		NADH ubiquinone oxidoreductase-related
Sapur.006G065600.1	14.19808333	-1.111173337	0.11108623	-10.01	1.38E-23	4.47E-23	gene	-0.621091804	4.03E-18	GO:0005975;GO:0004553	AtSGB8060.1		D-Glycosyl hydrolases family 17 protein
Sapur.005G060200.1	206.6113982	-0.700207341	0.070350684	-10.0042	1.46E-23	4.72E-23	gene	-0.582213275	2.75E-15	GO:0055114;GO:0005507;GO:0016705;GO:0005506	AtSGD1;CYP701A3,GA3		Cytochrome P450 family
Sapur.012G224700.1	11.92628746	-1.783696666	0.178471852	-9.9958	1.59E-23	5.14E-23	gene	-0.545175144	2.85E-13	GO:0043565;GO:0006355;GO:0003700	AtSGA6180.1	ATWRKY26,WRKY26	WRKY DNA-binding protein 26
Sapur.008G088200.1	944.1088347	-0.484063611	0.048481495	-9.99069	1.67E-23	5.41E-23	gene	-0.626476477	1.14E-19		AtSGA2730.1		splicing factor, 28 kDa-like 1
Sapur.007G018700.1	29.68176763	-1.490894739	0.149999698	9.987318	1.73E-23	5.60E-23	gene	-0.589429023	4.62E-16	GO:0008168	AtSGB4711.1	ATBSMT1,BSMT1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.006G074800.1	26.68152242	-0.808359303	0.081009485	-9.98569	1.76E-23	5.68E-23	gene	-0.635422128	3.98E-19		AtSGA7180.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.008G121400.3	10.6272785	-1.12231588	0.112412714	-9.98389	1.79E-23	5.76E-23	gene	-0.532608834	9.18E-13	GO:0005515	AtSGJ9330.1	ARIA	ARM repeat protein interacting with ABF2
Sapur.008G246700.2	27.34399113	-0.784637754	0.078600859	9.982565	1.82E-23	5.87E-23	gene	-0.607417237	3.33E-17		AtSGJ2560.1	ATTBP2,TRFL9	TRF-like 9
Sapur.003G090600.1	188.2514847	-0.280535154	0.12889228	-9.98156	1.84E-23	5.93E-23	gene	-0.484573448	3.30E-10		AtSGA5150.1	PMI1	phosfoinositol mannose 1
Sapur.010G061600.1	23.91092592	-0.809647474	0.081179309	-9.97357	1.99E-23	6.42E-23	gene	-0.6263158	1.66E-18		AtSGJ4850.1	LOL1,MEF11	Pentatricopeptide repeat (PPR) superfamily protein
Sapur.017G062100.1	7.348402604	-1.725153	0.173767771	-9.93748	2.03E-23	6.55E-23	gene	-0.449093842	3.94E-11	GO:0006508;GO:0004252	AtSGD7060.1		Subtilisin-like serine endopeptidase family protein
Sapur.007G130500.1	20.86915596	-1.111073499	0.111628949	-9.95331	2.44E-23	7.85E-23	gene	-0.628743267	1.18E-18		AtSGZ5970.1		Pentatricopeptide repeat (PPR) superfamily protein
Sapur.012G051100.1	980.7512237	-0.327773681	0.03196608	9.946165	2.62E-23	8.40E-23	gene	-0.614897553	1.24E-17	GO:0016787	AtSGD4180.2	PP2A-2	protein phosphatase 2
Sapur.15W0G0019600.1	251.0193783	-0.355650592	0.03570855	-9.94303	2.71E-23	8.70E-23	gene	-0.61727259	6.84E-18		AtSGJ1380.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Sapur.003G425200.1	18.71486109	-0.543838327	0.05528217	-9.84033	3.98E-23	9.21E-23	gene	-0.519080952	1.01E-12	GO:0046872;GO:0030001	AtSGD6365.1		Heavy metal transport/detoxification superfamily protein
Sapur.003G158800.1	191.7942609	-0.357148264	0.035972452	-9.92808	3.13E-23	1.01E-22	gene	-0.635201494	4.07E-19	GO:0008270;GO:0006355	AtSGT6320.1	FRS4	FARS-related sequence 4
Sapur.012G022300.1	548.8706515	-0.520548909	0.052450224	-9.92463	3.25E-23	1.06E-22	gene	-0.637541817	2.76E-19	GO:0016758;GO:0008152	AtSGT6180.1	UGT88A1	UDP-glucosyl transferase 88A1
Sapur.009G098200.1	820.1910553	-0.532024837	0.052426564	-9.92389	3.28E-23	1.05E-22	gene	-0.633925861	1.64E-19	GO:0005515;GO:0008577	AtSGJ6485.1		nucleic acid binding;DNA binding;DNA binding
Sapur.004G007700.1	329.6318952	0.595881799	0.06007592	9.918813	3.45E-23	1.11E-22	gene	-0.581913387	1.46E-15		AtSGJ1740.1		ankyrin repeat family protein
Sapur.006G060500.1	373.3677316	-0.352008293	0.034670681	-9.9149	3.56E-23	1.15E-22	gene	-0.639682651	5.92E-19		AtSGD7150.1	PMI1	phosfoinositol mannose 1
Sapur.008G159100.1	1084.695821	-0.819839888	0.08237516	9.909207	3.80E-23	1.22E-22	gene	-0.556892265	2.01E-14		AtSGZ5560.1		Putative thiol-disulphide oxidoreductase DCC
Sapur.003G000100.1	11.29073087	-0.979079652	0.098835514	-9.9042	3.98E-23	1.28E-22	gene	-0.622604103	2.51E-18	MEF21	AtSGD5540.1		mitochondrial factor 21
Sapur.001G097800.1	686.7484964	0.731005613	0.073911699	9.903988	4.00E-23	1.28E-22	gene	-0.60832073	2.95E-17		AtSGT6250.1		receptor serine/threonine kinase, putative
Sapur.015G000300.1	23.02027144	-0.807867364	0.08661171	-9.8769	4.59E-23	1.46E-22	gene	-0.633925861	1.31E-18		AtSGD5630.1		Protein of unknown function (DUF1012)
Sapur.010G080900.1	387.2619798	-0.313719149	0.03753146	-9.87804	5.18E-23	1.66E-22	gene	-0.66673296	1.54E-21	GO:0008234;GO:0006508	AtSGS1880.1	ATSEAD,ESD4	Cysteine proteinases superfamily protein
Sapur.005G123900.1	20.45336279	-0.585461428	0.06273555	-9.86785	5.74E-23	1.81E-22	gene	-0.585404258	1.97E-16		AtSGZ3100.1		Protein kinase superfamily protein
Sapur.007G128700.1	287.7774996	-1.660883343	1.69285579	-9.85671	6.41E-23	2.04E-22	gene	-0.539288861	4.75E-13		AtSGS8850.1		Pectin lyase-like superfamily protein
Sapur.006G069000.1	2792.785745	0.515757895	0.052177759	9.842874	7.38E-23	2.34E-22	gene	-0.576296683	8.25E-16	GO:0005525	AtSGB8820.1	ATRAB7B,ATRABG3F,RAB71	RAB GTPase homologs G3F
Sapur.006G234500.1	156.6412852	-0.351880711	0.03578591	-9.82883	8.38E-23	2.66E-22	gene	-0.639393672	2.01E-19	GO:0070461	AtSGZ4530.1		transcriptional regulator of RNA polII, SAGA, subunit
Sapur.15W0G0040800.1	12.54067419	-0.028072973	0.104985999	-9.79248	1.21E-22	3.85E-22	gene	-0.63591455	1.88E-19		AtSGB9320.1		Metal-dependent protein hydrolase
Sapur.010G022300.1	27.95660009	0.767292204	0.075499526	9.76063	1.26E-22	4.02E-22	gene	-0.61361542	9.07E-18		AtSGB6380.1		Meiliixa family protein
Sapur.010G065800.1	139.345479	-1.724863466	1.76237616	-9.76771	1.27E-22	4.03E-22	gene	-0.580408889	7.44E-16	GO:0006508;GO:0004190	AtSGD2220.1		Eukaryotic aspartyl protease family protein
Sapur.003G189100.1	278.6347944	-0.406329435	0.04154811	-9.78758	1.27E-22	4.08E-22	gene	-0.620027535	4.77E-18	GO:0055524;GO:0003676;GO:0004386	AtSGD6190.1		DEAD/H box helicase family protein
Sapur.002G089800.1	9.075983012	-0.952137267	0.107524008	-9.78514	1.30E-22	4.13E-22	gene	-0.588989036	6.60E-16		AtSGD1570.1	RGA,RGA1	GRAS family transcription factor family protein
Sapur.010G100600.1	1344.585124	-0.408489766	0.042034197	9.77869	1.40E-22	4.43E-22	gene	-0.58542755	5.51E-16		AtSGD6130.1	ARF4,ATARF4

Sapur.01G0236100.1	1474.97879	-0.61442087	0.068124737	-0.01906	1.90E-19	5.54E-19	purple	-0.5798724	1.76E-15	GO:0016020;GO:0006075;GO:0003843;GO:0000148	AT4G04970.1	ATG5;01ATG5;1.GSL01.GSL	glucan synthase-like 1	1%2C3-beta-glucan synthase
Sapur.01G0231500.1	652.694423	0.29320154	-0.03251103	-0.01852	1.91E-19	5.56E-19	purple	-0.60091084	8.79E-17		AT1G70100.3		Ribosomal L18p/L5e family protein	NA
Sapur.01G0329500.1	1.52691238	3.39168411	0.15453767	-0.00587	2.14E-19	6.24E-19	purple	-0.55031482	8.27E-14	GO:0006412;GO:0005840;GO:0005622;GO:0003735	AT1G08845.2		1-deoxy-D-xylulose 5-phosphate reductoisomerase	structural constituent of ribosome protein
Sapur.15W0265900.1	3534.95784	3.99668772	0.04460394	-0.98932	2.49E-19	7.25E-19	purple	-0.56461359	1.34E-14	GO:0005515;GO:0070402;GO:0055114;GO:0046872;GO:0000049;GO:0008299	AT5G27790.1	DXR;FOE129	1-deoxy-D-xylulose 5-phosphate reductoisomerase	1-deoxy-D-xylulose 5-phosphate reductoisomerase
Sapur.01G0123700.1	23.4857576	-0.80264124	0.08044428	-0.6845	2.62E-19	7.57E-19	purple	-0.56050008	2.27E-14	GO:0043531	AT4G14470.1		NB-ARC domain-containing disease resistance protein	NA
Sapur.7D48800.1	488.722438	0.34654388	0.03857985	0.982823	2.64E-19	7.68E-19	purple	-0.56119291	2.09E-14		AT5G42960.1			outer envelope pore protein 24A
Sapur.09G0123200.1	531.825746	0.36332628	0.04047592	0.977036	2.78E-19	8.09E-19	purple	-0.5814393	1.21E-14	GO:0015031;GO:0008565	AT2G19790.1		SNARE-like superfamily protein	AP-4 complex subunit sigma-1 protein, putative
Sapur.01G0318300.1	8.83295852	-0.40079454	0.01737232	-0.96062	2.98E-19	8.64E-19	purple	-0.55341149	5.60E-14		AT3G60550.1		TPX2 (targeting protein for Xklp2) protein family	NA
Sapur.01T0268800.0	19.2874123	-0.89402566	0.09978534	0.96429	3.12E-19	9.07E-19	purple	-0.55724395	1.16E-14		AT5G64130.1		cAMP-regulated phosphoprotein/endosulfine motif protein	cAMP-regulated phosphoprotein/endosulfine motif protein
Sapur.09G0277800.1	2823.05872	0.47222404	0.04143156	0.96429	3.22E-19	9.33E-19	purple	-0.5777563	5.60E-14	GO:0003723;GO:0003676	AT4G09760.1	PABB;PABP8	poly(A) binding protein	polyadenylate-binding protein, animal type 1, 2, 3, 4 family protein
Sapur.05G0102400.1	34.0687851	-0.72921646	0.08142399	-0.95377	3.44E-19	9.96E-19	purple	-0.62410564	4.68E-18		AT5G66331.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein
Sapur.09G0266600.1	145.254949	0.72168475	0.09461683	-0.95119	3.50E-19	1.01E-18	purple	-0.55319475	2.77E-14		AT3G12260.1			NA
Sapur.01G0381000.1	309.074786	-0.42888947	0.04703927	-0.93985	3.90E-19	1.13E-18	purple	-0.55737144	3.41E-14	GO:0006508;GO:0004252	AT4G10530.3		Subtilase family protein	subtilisin-like serine protease family protein
Sapur.01T0282000.1	448.266645	0.38917202	0.05206309	-0.93409	4.30E-19	1.13E-18	purple	-0.55819785	1.06E-17	GO:0005125	AT5G08880.1			HAUS augmin-like complex subunit 5
Sapur.01G0254700.1	292.7353297	-0.54003851	0.06045293	-0.93325	4.14E-19	1.20E-18	purple	-0.60782388	1.13E-17		AT3G40550.1	ETG1	E2F target gene 1	mini-chromosome maintenance complex-binding protein
Sapur.01G0251900.1	66.8361482	-0.46236344	0.07014519	-0.92468	4.62E-19	1.34E-18	purple	-0.54439014	1.46E-14	GO:0005515;GO:0006468;GO:0005524;GO:0004672	AT2G38850.1		Leucine-rich repeat receptor-like protein kinase family protein	tyrosine kinase domain protein
Sapur.01T0294300.1	414.807236	-0.33414764	0.03747799	-0.91584	4.84E-19	1.40E-18	purple	-0.59418507	2.34E-16	GO:0003723	AT5G15270.2		RNA-binding KH domain-containing protein	poly C-binding protein
Sapur.01G0132300.1	88.8985241	-0.69133450	0.07760554	-0.91089	5.06E-19	1.46E-18	purple	-0.59686347	1.59E-16	GO:0005525	AT5G07615.1		GTP-binding protein Obg/CgtA	NA
Sapur.09G0183200.1	499.682424	0.36290192	0.08758856	0.90129	5.28E-19	1.52E-18	purple	-0.55622992	3.94E-14		AT5G19600.1		pfkB-like carbohydrate kinase family protein	pfkB family carbohydrate kinase
Sapur.01G0279800.1	18.2037958	0.94867624	0.10651192	0.903479	5.41E-19	1.56E-18	purple	-0.56043871	2.30E-14					NA
Sapur.01J0200300.1	594.409493	0.35208301	0.05674666	0.89203	5.99E-19	1.71E-18	purple	-0.55672428	3.98E-14	GO:0005515;GO:0008017	AT5G25580.1	AT1E81;AT1E81B;FB1B	end binding protein 1B	microtubule-associated protein RP/EB family protein
Sapur.05G0262800.1	1595.96505	-0.27168955	0.03054746	-0.88854	6.19E-19	1.78E-18	purple	-0.62769254	1.46E-18		AT4G39680.1	CXIP4	SAP domain-containing protein	apoptotic chromatin condensation inducer in, putative
Sapur.09G0127200.2	101.754861	-0.64835296	0.07257685	-0.87756	6.83E-19	1.96E-18	purple	-0.49644114	3.79E-11		AT3G49910.1	CXIP4	CAK interacting protein 4	zinc knuckle protein
Sapur.04G0267004.4	6.08400525	-2.15122339	0.13688521	-0.87681	6.88E-19	1.98E-18	purple	-0.54261953	2.12E-13		AT5G69320.2	SFR6	sensitive to freezing 6	mediator of RNA polymerase II transcription subunit 16
Sapur.01G0169800.1	901.802563	0.39917202	0.05184831	0.87179	7.17E-19	2.06E-18	purple	-0.58974254	9.16E-17	GO:0005515	AT1G66160.1		Sterile alpha motif (SAM) domain-containing protein	SAM domain protein, putative
Sapur.01G0266900.1	907.865897	-0.51082105	0.06159988	-0.86856	7.41E-19	2.13E-18	purple	-0.54830627	1.06E-13	GO:0005515;GO:0006468;GO:0004672	AT5G61480.1		Leucine-rich repeat transmembrane protein kinase	NA
Sapur.01G0220400.1	2.9078325	-1.63467075	0.18632084	-0.867	7.51E-19	2.16E-18	purple	-0.57525779	3.28E-15	GO:0006887;GO:0000145	AT5G07390.1	ATEXO70G1;EXO70G1	exocyst subunit exo70 family protein G1	Exo70 exocyst complex subunit
Sapur.06G0201800.1	1834.23836	0.61077015	0.07739429	0.85689	8.29E-19	2.38E-18	purple	-0.55391806	1.24E-14		AT4G14510.1			NA
Sapur.06G0496600.1	1963.84339	-0.21347366	0.02144174	-0.84162	9.43E-19	2.70E-18	purple	-0.55923325	6.28E-14	GO:0003676;GO:0006418;GO:0005524;GO:0004812;GO:0000166	AT5G31180.2		Class II aminoacyl-tRNA and biotin synthetases superfamily protein	aspartyl-tRNA synthetase
Sapur.09G0138200.1	337.870926	0.44106204	0.04887884	0.84125	9.61E-19	2.94E-18	purple	-0.55491761	4.66E-14		AT4G26230.1		hydroxyproline-rich glycoprotein family protein	transmembrane protein, putative
Sapur.01G0319900.1	839.467897	0.34584538	0.03918561	0.829391	1.05E-18	3.01E-18	purple	-0.58327107	1.48E-15	GO:0045454;GO:0015035;GO:0009055	AT5G38270.1	ATGRX2;CXIP2	CAK-interacting protein 2	monothiol glutaredoxin-S16 protein
Sapur.05G0271500.1	335.714529	0.53680423	0.06080862	-0.82926	1.05E-18	3.01E-18	purple	-0.55738875	3.45E-14		AT5G66875.2		Tetratricopeptide repeat (TPR)-like superfamily protein	NA
Sapur.09G0123700.1	732.9148845	0.52097782	0.05907743	0.815904	1.19E-18	3.39E-18	purple	-0.56788422	8.76E-15	GO:0016042;GO:0005509;GO:0004623	AT4G19690.1	PLA2-BETA	phospholipase A2 beta	phospholipase A2
Sapur.09G0260300.1	3271.912827	0.39170302	0.04464452	0.81325	1.24E-18	3.53E-18	purple	-0.55326422	5.90E-14		AT5G20230.1	ACP;ACP1	acyl carrier protein 1	acyl carrier protein
Sapur.05G0291300.1	41.2613632	0.70208201	0.08192687	0.791816	1.47E-18	4.20E-18	purple	-0.58221818	1.27E-15					hypothetical protein
Sapur.7D31400.1	706.873931	-0.35667021	0.04523822	0.77604	1.61E-18	4.70E-18	purple	-0.55730304	3.32E-14		AT5G18310.2			hypothetical protein
Sapur.01G0681000.4	37.1200825	0.55284663	0.06266503	0.775433	1.70E-18	4.85E-18	purple	-0.59543372	1.92E-16		AT3G29130.2			hypothetical protein
Sapur.07G0287700.1	167.378239	0.71370641	0.08190120	0.765081	1.80E-18	5.13E-18	purple	-0.53282145	6.81E-13		AT5G06868.1			DUF740 family protein
Sapur.01J0268600.1	438.944756	0.62868947	0.07170473	0.75849	1.96E-18	5.57E-18	purple	-0.50345068	1.80E-11		AT5G67560.1	NDL1	N-MYC downregulated-like 1	pollen-specific protein SF21
Sapur.15W0265400.1	43.1838867	0.67110475	0.07627886	0.753022	2.08E-18	5.90E-18	purple	-0.53770165	8.32E-13					NA
Sapur.01G0188200.1	1269.88349	-0.59684259	0.08218372	-0.75041	2.13E-18	6.04E-18	purple	-0.56493642	1.68E-16	GO:0005580;GO:0005886	AT5G09540.1	HSC70-5;MTHSC70-2	mitochondrial HSC70 2	heat shock 70 kDa protein
Sapur.02G0151200.1	595.256667	-0.38705884	0.04426154	-0.74502	2.23E-18	6.33E-18	purple	-0.62116146	3.98E-18		AT4G01680.1	HEMG1;PPO1;PPOX	Flavin containing amine oxidoreductase family	protoporphyrinogen IX oxidase
Sapur.01G0307200.1	1351.29861	-0.29192322	0.04088429	-0.74057	2.32E-18	6.58E-18	purple	-0.52232008	1.36E-15		AT1G31020.2	VCS	Transducin/WD40 repeat-like superfamily protein	peptidase 32A, signal peptidase I, WD40-like protein, putative
Sapur.01G0635300.1	257.808767	0.64577602	0.07400231	-0.71969	2.59E-18	6.62E-18	purple	-0.54026792	2.82E-13		AT1MES17;MES17	MES17	methyl esterase 17	alpha/beta fold hydrolase
Sapur.09G0347500.1	185.568852	-0.27529162	0.03151719	-0.7304	2.54E-18	7.20E-18	purple	-0.55723818	1.51E-16				D-fucose/D-arabinose family protein	CgA protein
Sapur.09G0230300.1	1073.87496	-0.32684776	0.03744292	-0.72813	2.59E-18	7.34E-18	purple	-0.55889533	2.81E-14	GO:0003676	AT1G07160.1		CCCH-type zinc fingerfamily protein with RNA-binding domain	zinc finger CCCH domain protein
Sapur.05T0202800.3	4.15344422	2.34168889	1.65598885	-0.70616	3.14E-18	8.89E-18	purple	-0.57861222	2.80E-15		AT1G30800.2		Protein of unknown function, DUF547	terminal complex protein MPI1 leucine-zipper protein
Sapur.01G0266100.1	23.2706166	0.58383161	0.06593879	0.705945	3.21E-18	9.07E-18	purple	-0.51864629	3.45E-13		AT5G45260.1		chaperone protein dnaJ-related	drought-induced protein
Sapur.01J0243000.1	848.315167	-0.24116545	0.02775593	-0.69513	3.46E-18	9.79E-18	purple	-0.53278124	2.86E-16		AT5G09770.1	ATCOCL4;ATMYBCOCL5;COCL5	cell division cycle 5	cell division cycle-like protein
Sapur.01J0283800.1	877.599837	-0.30232197	0.03416824	-0.68786	3.68E-18	1.04E-17	purple	-0.57586001	1.02E-15	GO:0055114;GO:0016491;GO:0050664;GO:0004601	AT5G10610.1	ATRBOHC;RBOHC;RHD2	NADPH/respiratory burst oxidase protein D	respiratory burst oxidase-like protein
Sapur.01T0109900.1	749.17826	-0.59470422	0.06856164	-0.66965	4.33E-18	1.22E-17	purple	-0.61374954	1.27E-17		AT5G09660.1		Tetratricopeptide repeat (TPR)-superfamily protein	PPR containing plant protein
Sapur.5G0601300.1	46.3215267	-0.70164205	0.09976765	0.667891	4.40E-18	1.24E-17	purple	-0.50272756	1.96E-11	GO:0055114;GO:0016491	CCR2;CRTISO	CCR2;CRTISO	carotenoid isomerase	carotenoid isomerase
Sapur.09G0111400.1	274.176243	-0.49538424	0.05722933	-0.65734	4.83E-18	1.36E-17	purple	-0.57310148	4.38E-15					RNA polymerase II-associated protein, putative
Sapur.01B0248800.1	1793.02279	0.54862291	0.06502627	-0.65435	4.94E-18	1.40E-17	purple	-0.53732016	1.26E-13	GO:0003723			KH domain-containing protein	nucleic acid-binding protein, putative
Sapur.03G0100600.2	3.07741581	-0.89133490	0.17095888	-0.65329	5.00E-18	1.41E-17	purple	-0.52028304	2.87E-12	GO:0006396;GO:0005622	GSL01		crooked neck protein, putative / cell cycle protein, putative	cell cycle control protein crooked neck-like protein, putative
Sapur.09G0121400.1	83.6801246	-0.43617708	0.12051443	-0.65258	5.02E-18	1.42E-17	purple	-0.58402426	1.21E-10	GO:0009731	AT5G48240.1		SALIM-like auxin-responsive family protein	SALIM family protein
Sapur.03G0463600.1	123.811957	-0.99692128	0.11568393	-0.64501	5.19E-18	1.46E-17	purple	-0.47607053	2.83E-10		AT4G17050.1		Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region	auxin canalization protein
Sapur.05G0153800.1	773.958802	0.89203947	0.10328196	-0.64123	5.56E-18	1.56E-17	purple	-0.53281543	6.82E-13	GO:0055114;GO:0020037;GO:0006979;GO:0004601	AT5T0169.1		Peroxidase superfamily protein	horseradish peroxidase
Sapur.01G0195800.1	23.0661797	0.77512785	0.10469846	0.626692	6.38E-18	1.79E-17	purple	-0.54180552	6.62E-14					NA
Sapur.05G0037700.1	7.27658886	-0.94188558	0.19025416	-0.61855	6.78E-18	1.90E-17	purple	-0.58932395	7.56E-16		AT5G49142.1		Tetratricopeptide repeat (TPR)-like superfamily protein	PPR containing plant protein, putative
Sapur.01G0291200.1	102.464673	0.59182025	0.09491683	0.61669	6.88E-18	1.93E-17	purple	-0.57449456	3.64E-15		AT5T0181.1			hypothetical protein
Sapur.01C0194600.1	424.478711	0.23601563	0.02743291	0.603086	7.76E-18	2.17E-17	purple	-0.55732046	3.31E-14	GO:0016020;GO:0006897	AT5G58600.1		Adaptin ear-binding coat-associated protein 1 NECAP-1	adaptin ear-binding coat-associated protein 1
Sapur.01G0266105.1	765.064726	0.52360268	0.07364172	0.594179	8.35E-18	2.33E-17	purple	-0.51384205	6.02E-14	GO:0043565;GO:0003700	AT5G35980.1	AtbZIP44;bZIP44	basic leucine zipper 44	bZIP transcription factor
Sapur.15W0067800.1	395.444033	-0.82783827	0.09669634	-0.56122	1.12E-17	3.11E-17	purple	-0.67247813	5.21E-22		AT2G26620.2		Protein of unknown function (duplicated DUF1396)	DNA-binding protein, putative
Sapur.01G0122400.1	124.305033	-0.34167937	0.04107512	-0.56122	1.12E-17	3.11E-17	purple	-0.61456698	1.13E-17		AT5G62480.1	ARA12	Subtilase family protein	NA
Sapur.01G0265500.1	61.1664165	-0.54496205	0.06731271	-0.55334	1.20E-17	3.33E-17	purple	-0.55729098	1.14E-15		AT5G33350.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.01G0125400.1	112.334705	-0.41543189	0.05082826	-0.52617	1.32E-17	3.65E-17	purple	-0.55333402	5.67E-14	GO:0055114;GO:0046616;GO:0051287;GO:0016616;GO:0008152	AT5G54630.2		D-isomer specific 2-hydroxyacid dehydrogenase family protein	D-isomer specific 2-hydroxyacid dehydrogenase family protein, putative
Sapur.01G0117300.1	1486.71059	0.21648111	0.02509744	0.545832	1.28E-17	3.55E-17	purple	-0.56899612	7.56E-15	GO:0005515	AT5G10980.1		Leucine-rich repeat (LRR) family protein	brassinosteroid insensitive 1-associated receptor kinase
Sapur.01G0253000.2	1.10817214	-2.67285451	0.31123584	-0.53625	1.39E-17	3.85E-17	purple	-0.53427883	1.83E-12	GO:0006355;GO:0005634;GO:0005524;GO:0032502;GO:0006351	AT3G46480.1	AtGRF3;GRF3	growth-regulating factor 3	WRC protein
Sapur.05G0560600.1	1381.85674	0.32391327	0.03903608	0.529478	1.47E-17	4.08E-17	purple	-0.51891954	3.66E-12	GO:0033177;GO:0005886;GO:0015078	AT5G19910.1	ATVHA-C2;AVA-2;PE;AVA-P2	ATPase; V0 complex, subunit C protein	vacuolar H+-ATPase 16 kDa proteolipid subunit C
Sapur.05G1698600.1	189.884178	-0.35047252	0.04182968	-0.53269	1.50E-17	4.17E-17	purple	-0.58407034	8.76E-16		AT5G62150.1	ATHMT-2;HMT-2;HMT2	homocysteine methyltransferase 2	NA
Sapur.01G0282100.1	1124.92731	-0.37968459	0.04064237	-0.51876	1.54E-17	4.27E-17	purple	-0.52844331	1.96E-12	GO:0005525	AT5G17220.1	FUG1	Translation factor 2, small GTP-binding protein	translation initiation factor IF-2
Sapur.01G0139700.1	9.15094443	-1.27878691	0.15208199	-0.50833	1.76E-17	4.89E-17	purple	-0.52905679	6.75E-13	GO:0005515;GO:0006468;GO:0055114;GO:0004672	AT2G46130.1		Leucine-rich receptor-like protein kinase family protein	LRR receptor-like Ser/Thr-kinase family protein
Sapur.09G0124100.1	53.7200842	0.82532261	0.09709415	0.50645	1.82E-17	5.05E-17	purple	-0.58075512	7.61E-16	GO:0005515	AT2G35180.1	ARR12;RR12	response regulator 12	type-B response regulator
Sapur.01B0141200.1	106.156303	0.69670949	0.08194198	0.502482	1.86E-17	5.14E-17	purple	-0.59454728	2.22E-16	GO:0005515;GO:0006468;GO:0004672	AT3G24370.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	protein kinase
Sapur.01G0131100.1	43.5375249	0.81018889	0.12146512	-0.4887	2.13E-17	5.88E-17	purple	-0.48287323	5.16E-10	GO:0005515	AT5G39550.1		Calcium-dependent lipid-binding (CaLB domain) family protein	C domain present in soybean protein regulated by cold 2 (SRC2)-like protein, putative
Sapur.01G0172900.1	1425.81281	0.41435289	0.04902391	0.45129	2.88E-17	7.93E-17	purple	-0.53294463	2.13E-12	GO:0006413;GO:0003743;GO:0003723	AT3G04520.1		Nucleic acid-binding, OB-fold-like protein	eukaryotic translation initiation factor 1A
Sapur.01G0207900.1	457.4089136	-0.12988535	0.13371483	-0.45074	2.88E-17	7.97E-17	purple	-0.48032292	1.94E-10	GO:0008199;GO:0008378;GO:0008826	AT5T0181.1;FER1	FER1	ferretin 1	ferritin
Sapur.09G0189100.9	69.566356	-0.46433764	0.05519124	-0.44949	2.95E-17	8.05E-17	purple	-0.60486648	8.86E-17		AT5G49510.1		CDK inhibitor P21 binding protein	p21-carboxy-terminal region-binding protein
Sapur.09G0252500.1	53.1991318	0.58573198	0.06934708	0.446331	3.01E-17	8.27E-17	purple	-0.51304586	6.42E-12		AT5G05710.1		Pleckstrin homology (PH) domain superfamily protein	pleckstrin-like (PH) domain protein
Sapur.01W0201800.1	52.2893591	0.80185476	0.09497663	0.44806	3.12E-17	8.56E-17	purple	-0.50860132	1.14E-11		AT5G05175.1			transmembrane protein, putative
Sapur.02G0164700.1	1566.774303	-0.39197468	0.04648358	-0.43163	3.41E-17	9.36E-17	purple	-0.54562986	1.68E-13		AT3G14080.1	GLN1	genomes uncoupled 1	PPR containing plant protein
Sapur.05T0262200.1	112.129393	-0.37968459	0.04064237	-0.42696	3.48E-17	9.56E-17	purple	-0.55907217	7.15E-14	GO:0006355;GO:0005739;GO:0003690	AT5G29220.1		Mitochondrial transcription termination factor family protein	transcription termination factor family protein
Sapur.09G0154900.1	430.4795048	-0.32983744	0.03915167	-0.42428	3.61E-17	9.96E-17	purple	-0.55143637	2.03E-14	GO:0005515	AT3G20670.1		DNA binding bromodomain-containing protein	bromodomain domain protein
Sapur.01G0184300.1	721.182565	0.50461203	0.06602558	0.39321	4.73E-17	1.29E-16	purple	-0.51958024	4.74E-12	GO:0016020	AT3G07401.1		Transmembrane protein 14C	transmembrane protein 14C
Sapur.01G0275800.2	2.87883019	-1.60797661	0.19856677	-0.38444	5.10E-17	1.39E-16	purple	-0.54357964	1.89E-13	GO:0005515;GO:0006468;GO:0055114;GO:0004672	AT5G27180.1		Leucine-rich receptor-like protein kinase family protein	leucine-rich receptor-like kinase
Sapur.05T0278800.1	419.170374	0.30205993	0.04086002	0.372449	5.62E-17	1.54E-16	purple	-0.54347257	2.52E-13		AT5G05500.1	ATCPSCA;CPSCA	Ribosomal protein L7Ae/L30e/S12e/Gadin family protein	ribosomal protein S12/S23 family protein
Sapur.01G0141300.1	121.729724	-0.34344431	0.04108628	-0.35862	6.35E-17	1.73E-16	purple	-0.56185785	1.92E-14	GO:0016567;GO:0006402;GO:0005515	AT5G07680.1	ATRUBA4;PUB4;SAU11	senescence-associated E3 ubiquitin ligase 1	spotted leaf protein, putative
Sapur.01T0274500.1	1001.54926	-0.32832239	0.03928631	-0.35698	6.43E-17	1.75E-16	purple	-0.58393772	7.57E-15	GO:0016887;GO:0005524;GO:0019538	AT5G45910.1	APG6;CLP4-P;CLP6B	casein lytic proteinase B3	chaperone protein ClpB
Sapur.01T0269500.1	399.297647	-0.46283715	0.05542786	0.351852	6.77E-17	1.84E-16	purple	-0.54773001	1.20E-13	GO:0007049;GO:0005634;GO:0048481	AT5G02390.1	KCS2;KRP2	KPI-related protein 2	cyclin-dependent kinase inhibitor protein
Sapur.09G0176800.1	175.8316117	0.34152197	0.04085051	0.351185	6.76E-17	1.84E-16	purple	-0.51738369	3.97E-12		AT5G58090.1		Disease resistance-responsive (dirigent-like protein) family protein	AT hook motif protein, putative
Sapur.09G0264000.1	1914.397524	-0.41384527	0.05181001	-0.33524	7.73E-17	2.10E-16	purple	-0.54947204	2.07E-13	GO:0005525	AT1G62620.2;TOC120	ATTOC120;TOC120	translocon complex protein 120	import component Toc86/159, G and M domain protein
Sapur.07G0220000.1	2.20351098	-1.65700153	0.19894453	-0.33022	8.07E-17	2.19E-16	purple	-0.56351236	1.55E-14		AT5G63810.1			nucleolar RNA-associated protein, putative
Sapur.05G0207200.1	399.068029	-0.34189387	0.04107512	-0.3126	8.51E-17	2.31E-16	purple	-0.55907217	2.72E-14	GO:0005515	AT5G25610.2	PSD	ARM repeat superfamily protein	vesicle-7 protein
Sapur.01G0196300.1	1026.655637	-0.36762041	0.04418581	-0.31012	8.79E-17	2.38E-16	purple	-0.57561945	1.11E-15	GO:0005515;GO:0031369;GO:0006413;GO:0005852;GO:0003743	AT4G16510.2	ATEIF3C-1;ATTIF3C1;EIF3C-1	eukaryotic translation initiation factor 3C	eukaryotic translation initiation factor 3 subunit C
Sapur.01G0883000.1	4.42888704	-1.68098832	0.20206827	-0.31073	8.82E-17	2.39E-16	purple	-0.48752183	8.46E-11	GO:0005680	AT5G24530.1	APR8;PRR5	pseudo-response regulator 5	PRR response regulator-like protein
Sapur.03G0137900.1	70.2195086	-0.96679229	0.16373024	-0.30776	9.75E-17	2.64E-16	purple	-0.43623398	1.12E-08	GO:0007165	AT5G25130.1	CIPK25;SOS9;2.35	CBL-interacting protein kinase 25	CBL-interacting kinase
Sapur.09G0201100.1	17.7454874	-0.76008427	0.09631088	-0.29671	1.01E-16	2.86E-16	purple	-0.51425518	4.51E-12	GO:0005515	AT1G17280.1	ATRIP;ATRAD25;RAD25	Rav-related protein RIP1-binding family protein	rab1 small GTP-binding protein, putative
Sapur.03G0142600.1	656.4583869	0.52976545	0.09543378	0.286229	1.17E-16	3.16E-16	purple	-0.52875626	2.08E-12	GO:0016021;GO:0008233;GO:0006465;GO:0005787	AT4G40042.1		Microsomal signal peptidase 12 kDa subunit (SPC12)	signal peptidase complex subunit 3
Sapur.09G0252500.1	186.3873588	0.45302212	0.05476305	0.281165	1.23E-16	3.39E-16	purple	-0.52792364	1.20E-12	GO:0003676	AT1G21190.1		RNA-binding (RNA/RNB/RNP motifs) family protein	RNA recognition motif 1 in RNA-binding protein 28 (RBM28)-like protein
Sapur.09G0253800.1	588.735927	-0.24383786	0.02949675	-0.2798	1.23E-16	3.33E-16	purple	-0.55134125	2.75E-14	GO:0005515	AT5G24810.1		2PW1 zinc finger domain protein	2PW1 zinc finger protein
Sapur.7D12000.1	615.369873	0.50197829	0.06072078	-0.26704	1.37E-16	3.70E-16	purple	-0.54650983	1.31E-13	GO:0006355;GO:0005634;GO:0003677;GO:0009725	AT4T4;RTA8		auxin response factor 8	auxin response factor
Sapur.05G0261800.1	13.2293016	-0.91456684	0.2318716	-0.25685	1.56E-16	4.08E-16	purple	-0.5581362	1.96E-14		AT5T5752.1	GASA1	GAST1 protein family	gibberellin-regulated protein
Sapur.15W0121400.1	32.8737877	0.63186488	0.07675107	0.246872	1.58E-16	4.27E-16	purple	-0.52176914	2.43E-12					NA
Sapur.01G0296100.1	406.700381	-0.34449259	0.04175268	-0.24103	1.59E-16	4.28E-16	purple	-0.51750268	4.96E-14	GO:0005515;GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005875	AT1G12430.1	ARK1;PAK	armadillo repeat kinesin 1	armadillo repeat kinesin-like protein
Sapur.01G0071300.1	36.4316546	-0.61940559	0.05123265	-0.23424	1.81E-16	4.86E-16	purple	-0.53794823	2.81E-12					NA
Sapur.09G0281000.1	231.4314868	-0.61984756	0.06195166	-0.22347	1.88E-16	5.04E-16	purple	-0.54883365	1.68E-13	GO:0008033;GO:0006540	AT5G59880.2		Polyserine/histidinyl phosphatase-like	RNase P subunit p30
Sapur.03G0140300.1	153.658786	0.41018374	0.04987583	0.222169	2.00E-16	5.36E-16	purple	-0.52570019	1.55E-12	GO:0080270;GO:0005515	AT2G37580.1		RING/U-box superfamily protein	RING-H2 finger protein ATL2L, putative
Sapur.09G0217500.1	677.2571308	-0.46067793	0.05613789	-0.20614	2.28E-16	6.12E-16	purple	-0.54698822	1.31E-14	GO:0005515	AT5G04580.1	DME	HINV-GPD base excision DNA repair family protein	DNA glycosylase
Sapur.03G0183800.1	141.41699	-0.56435667	0.07247827	-0.20004	2.40E-16	6.42E-16	purple	-0.52826118	1.26E-12		AT1G69190.1			DUF4228 domain protein
Sapur.15W0094600.1	46.7958896	-0.72681291	0.08696624	-0.19487	2.51E-16	6.71E-16	purple	-0.53134272	6.36E-12		AT3G10570.1	RGA;RGA1	GRAS family transcription factor family protein	DELLA domain GRAS family transcription factor GAI/RGA1
Sapur.01G0265500.1	90.4247976	-0.64238422	0.07743175	-0.1762	2.58E-16	8.46E-16	purple	-0.55904767	1.83E-15		AT2G42440.2		DNA/RNA helicase family protein containing protein	NA
Sapur.01G0291000.1	793.1372482	0.38509008	0.04714001	0.188178	2.65E-16	7.09E-16	purple	-0.55766401	2.51E-15	GO:0006404;GO:0000145	AT5G56480.1	SEC15A	exocyst complex component sec15A	NA
Sapur.09G0207200.1	1.86687551	-1.18053	0.28364124	-0.18053	2.83E-16	7.51E-16	purple	-0.78422559	5.93E-24	GO:0016851;GO:0051595;GO:0019979	AT5G05220.1	ALB-1-U;ALB1;CHLD;PDE166	ALBINA 1	magnesium-chelatase subunit D
Sapur.01G0142600.1	264.165347	-0.49463338	0.06107625	0.177651	2.89E-16	7.70E-16	purple	-0.52407792	1.87E-12		AT5G59300.1	ATUBC7;UBC7	ubiquitin carrier protein 7	ubiquitin-conjugating enzyme E2
Sapur.01G0177700.1	188.5669994	-0.42387268	0.05244665	0.176053	2.92E-16	7.80E-16	purple	-0.52420732	1.38E-12		AT5G49651.2		Transducin/WD40 repeat-like superfam

Sapur.006G147200.1	854.8315839	2.07861740E-01	0.08446111	7.071926	1.53E-12	3.63E-12	purple	0.475833968	3.01E-10	GO:0005515			Ubiquitin-like superfamily protein
Sapur.009G109400.1	407.9979133	0.219298656	0.03106589	-7.05899	1.68E-12	3.98E-12	purple	-0.492488852	5.70E-11	GO:0006413;GO:0003743			translation initiation factor 3 (IF-3) family protein
Sapur.006G330700.1	415.4465647	0.456856116	0.06493122	-7.0643	1.71E-12	4.05E-12	purple	-0.49898116	1.38E-09	GO:0055114;GO:0050660;GO:0016491			FAD-binding Berberine family protein
Sapur.002G131500.1	139.4837082	0.334631781	0.047741004	-7.00894	2.40E-12	5.67E-12	purple	-0.506945528	2.48E-11				
Sapur.007G047700.1	288.7095683	-0.712583131	0.101943236	-6.99015	2.75E-12	6.47E-12	purple	-0.533615281	6.88E-10	GO:0008408;GO:0006260;GO:0003887;GO:0003677;GO:0000166	ICL12		DNA-directed DNA polymerases
Sapur.017G141100.1	791.0415882	-0.271058132	0.038792819	-6.98733	2.83E-12	6.60E-12	purple	-0.51231035	7.11E-12	GO:0055511;GO:0006468;GO:0004672			Leucine-rich repeat protein kinase family protein
Sapur.013G139100.1	24.17459927	0.888394016	0.127146828	-6.98716	2.83E-12	6.61E-12	purple	-0.454887063	2.56E-09				conserved peptide upstream open reading frame 44
Sapur.006G090300.1	2109.641884	0.257318307	0.037050402	6.954608	3.54E-12	8.26E-12	purple	0.462683077	9.61E-10				ubiquitin-conjugating enzyme E2
Sapur.010G113400.2	1.02882481	-0.950232823	0.280879359	-6.94364	3.82E-12	8.95E-12	purple	-0.806273234	3.47E-37				polydeoxyribotin factor 1 complex subunit F(F1, putative
Sapur.005G165700.1	826.8267772	-0.341913932	0.051398061	-6.65908	1.57E-12	1.46E-11	purple	-0.515779774	5.16E-11	GO:0005525			Translation-elongation factor EFG/EF2 protein
Sapur.006G192600.1	1865.925953	0.245105909	0.034976647	-6.8918	5.51E-12	1.28E-11	purple	-0.514894162	5.24E-12				
Sapur.009G151800.1	178.6151463	0.2661933312	0.048182807	6.89195	5.52E-12	1.28E-11	purple	-0.505179108	1.51E-11				transmembrane protein
Sapur.014G053300.1	50.98613346	-3.328763688	0.193515657	-6.86644	6.58E-12	1.53E-11	purple	-0.491939426	6.43E-11	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP704A2		cytochrome P450, family 704, subfamily A, polypeptide 2
Sapur.008G252900.2	122.7493271	0.369018	0.053779986	6.82973	8.46E-12	1.96E-11	purple	-0.450947022	2.26E-11				Trypsin family protease
Sapur.15WG008900.1	420.7613691	-0.217164717	0.031660343	-6.8592	6.92E-12	1.61E-11	purple	-0.485454949	1.05E-10	GO:0003723			RNA-binding KH domain-containing protein
Sapur.010G138800.1	734.7536085	-0.2855	0.038898362	-6.85628	7.06E-12	1.64E-11	purple	-0.498645282	3.20E-10	GO:0005515	ATRAD21.1;SYN4		sister chromatid cohesion 1 protein 4
Sapur.15WG021800.1	592.8787512	-0.2815356	0.041169977	-6.83808	8.03E-12	1.85E-11	purple	-0.485523203	1.16E-10	GO:0030688;GO:0003664			nucleolar protein;NopS12 protein
Sapur.001G060900.1	1327.583043	0.343308017	0.050203114	6.821098	9.03E-12	2.09E-11	purple	0.435365647	2.11E-08				Protein of unknown function, DUF538
Sapur.002G052500.1	12.04857594	-3.116139761	0.28829291	-6.80658	9.99E-12	2.31E-11	purple	-0.469594881	7.20E-10	GO:0055114;GO:0020037;GO:0016705;GO:0005506	CYP72A1		cytochrome P450 family 72A, subfamily A, polypeptide 1
Sapur.013G047900.1	153.004828	0.343852088	0.050258149	6.801121	1.04E-11	2.39E-11	purple	-0.454826319	2.26E-09	GO:0046961;GO:0033178;GO:0015991;GO:0016747	emb2448.TUF-TUFF.VHA-E1		vacuolar ATP synthase subunit E1
Sapur.T006060.1	103.7291124	-0.514202663	0.075740024	-6.79808	1.11E-11	2.60E-11	purple	-0.488543878	7.41E-10				NB-ARC domain-containing disease resistance protein
Sapur.016G229300.1	1215.24429	-0.269814049	0.046749789	-6.77867	1.21E-11	2.79E-11	purple	-0.49098007	6.65E-11	GO:0005634;GO:0003676	DDB1A		damaged DNA binding protein 1A
Sapur.009G099900.1	420.5057429	-0.431212898	0.066066444	-6.76794	1.31E-11	3.06E-11	purple	-0.457248312	1.76E-10	GO:0009116	AGE2;ATAGE2;ATPURF2;CIA		GLN phosphoribosylpyrophosphate amidotransferase 2
Sapur.016G125400.1	737.2227788	0.309074023	0.045696562	-6.76356	1.35E-11	3.09E-11	purple	-0.545107786	1.56E-13	GO:0055515;GO:0006508;GO:0004222	ARASP		ARABIDOPSIS SERIN PROTEASE
Sapur.006G204600.2	51.50146778	0.918080877	0.134836526	6.82973	1.45E-11	3.32E-11	purple	-0.475024242	2.26E-11				Heavy metal-associated domain protein
Sapur.010G031700.1	54.69650024	-0.423498542	0.062784994	-6.75255	1.45E-11	3.33E-11	purple	-0.501265133	2.28E-11	GO:0055085;GO:0016021			Major facilitator superfamily protein
Sapur.002G125200.1	3.715096167	-1.257709845	0.186425612	-6.7443	1.54E-11	3.52E-11	purple	-0.435278999	1.22E-08		UBD31		UDP-glucan-containing protein 31
Sapur.005G285400.2	2.340455127	-1.224806857	0.181246378	-6.71953	1.58E-11	3.64E-11	purple	-0.51851676	1.49E-12				AT hook DNA-binding protein, putative
Sapur.001G087700.1	881.2774222	-0.092063693	0.028502997	-6.7767	1.63E-11	3.68E-11	purple	-0.48375726	1.88E-10	GO:0016787	TOPP3		type one serine/threonine protein phosphatase 3
Sapur.010G268700.1	4.907949372	-1.157895574	0.17288179	-6.69737	2.12E-11	4.80E-11	purple	-0.44438826	1.58E-08				
Sapur.013G019900.1	518.5024579	-0.305265572	0.045603862	-6.69572	2.15E-11	4.89E-11	purple	-0.506047823	1.27E-11				Tudor/PWWP/MBT superfamily protein
Sapur.002G031000.1	73.32623882	-0.758152276	0.113769186	-6.6628	2.98E-11	6.66E-11	purple	-0.461220117	1.31E-09				conserved peptide upstream open reading frame 7
Sapur.013G068900.1	440.5326159	-0.198693026	0.029848658	-6.6567	2.80E-11	6.35E-11	purple	-0.452469934	2.70E-09	GO:0046872			Zinc finger C-x8-C-x5-C-x3-H type family protein
Sapur.008G118600.1	84.54869497	-0.557132608	0.08377622	-6.64896	2.95E-11	6.69E-11	purple	-0.52289751	6.52E-12				COP1 interacting protein 4 family protein
Sapur.018G098800.1	285.2793418	0.256503346	0.038617471	-6.64216	3.09E-11	7.00E-11	purple	-0.48780174	1.02E-10	GO:0005515			Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.013G127900.2	1.705173381	-1.485416326	0.225148216	-6.59926	4.03E-11	9.13E-11	purple	-0.538790605	2.52E-13	GO:0006470;GO:0004722			protein phosphatase 2C protein, putative
Sapur.016G270800.1	100.1822227	-0.753087671	0.113798402	-6.61731	3.66E-11	8.26E-11	purple	-0.508842646	1.00E-11	GO:0004674;GO:0048544;GO:0006468;GO:0004672			S-locus lectin protein kinase family protein
Sapur.018G299900.1	305.8219602	-0.350982231	0.053055121	-6.61543	3.79E-11	8.37E-11	purple	-0.454882615	2.26E-09	GO:0005085;GO:0016021	PHT4;5		phosphate transporter 4;5
Sapur.003G056000.1	327.2515662	-0.357645173	0.054054628	6.602981	4.03E-11	9.06E-11	purple	-0.446247554	4.68E-09				hypothetical protein
Sapur.15WG015300.3	9.622000139	-0.736858228	0.11668882	-6.59979	4.12E-11	9.28E-11	purple	-0.489616664	7.99E-11	GO:0005085;GO:0016020;GO:0008081;GO:0005216			cyclic nucleotide gated channel 1
Sapur.014G060900.1	371.1084469	-0.21313895	0.03205659	-6.6523	4.32E-11	9.75E-11	purple	-0.502134125	1.86E-11	GO:0004683;GO:0005516	CDPK1;2;CAM1;2;CAM3;CDPK		calcium-dependent protein kinase 1
Sapur.010G029900.2	15.95820018	0.791884019	0.120253137	6.585105	4.55E-11	1.02E-10	purple	-0.574863869	3.64E-15	GO:0046983	BPE;BPLip;BPLdp;ZCW32		BPC PETAL P
Sapur.008G124300.1	356.4562767	-0.308316209	0.047000127	-6.56365	4.73E-11	1.06E-10	purple	-0.483334963	1.46E-10	GO:0016021			transmembrane 70 protein family
Sapur.004G131200.1	244.5454686	-0.369875649	0.053402478	-6.55167	5.68E-11	1.28E-10	purple	-0.489504603	7.68E-11	GO:0009116	AGE2;ATAGE2;ATPURF2;CIA		GLN phosphoribosylpyrophosphate amidotransferase 2
Sapur.006G146700.1	641.9788861	-0.257608819	0.03932906	-6.55041	5.74E-11	1.29E-10	purple	-0.468182268	4.28E-10	GO:0016020;GO:0015079	ATK3;ATKUP;KUP3		K+ uptake permease 3
Sapur.013G083300.1	490.211662	0.276407042	0.042268593	6.540957	6.11E-11	1.37E-10	purple	-0.457210651	1.75E-09				
Sapur.009G144400.1	1.637539176	-0.249692	0.031898612	-6.53842	6.21E-11	1.39E-10	purple	-0.456218199	5.08E-09	GO:0005681;GO:0000398			CwfJ5/Cwc15 cell cycle control family protein
Sapur.016G056400.1	93.98548559	-0.584651017	0.090295113	-6.47489	9.48E-11	2.11E-10	purple	-0.473631997	9.32E-10	GO:0006508;GO:0004252			subtilisin serine protease, putative
Sapur.15WG149000.1	215.7675932	-0.329482813	0.050897229	-6.47349	9.58E-11	2.13E-10	purple	-0.464814775	8.64E-10	GO:0003170;GO:0009058			1-aminocyclopropane-1-carboxylate synthase 12
Sapur.016G285300.1	600.3954638	-0.243150974	0.037398338	-6.45849	1.06E-10	2.35E-10	purple	-0.492216087	5.08E-11	GO:0005515	CHC1		SWI/SNF/NuRD chromatin remodeling complex subunit
Sapur.016G044100.1	58.78242379	-0.530267233	0.081645184	-6.45497	1.08E-10	2.40E-10	purple	-0.487662216	9.50E-11	GO:0005515			C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
Sapur.004G060800.1	55.73664029	-0.525238148	0.08142379	-6.45008	1.11E-10	2.47E-10	purple	-0.448092923	3.91E-09	GO:0016868	OSU1;QUA2;TSD2		S-adenosyl-L-methionine-dependent methyltransferase, putative
Sapur.001G065500.2	56.5027922	0.755108805	0.114205724	6.43855	1.21E-10	2.67E-10	purple	-0.448502813	4.00E-09	GO:0008152;GO:0003824	AAE18		acyl-activating enzyme 18
Sapur.013G035900.1	995.0322777	-0.341509	0.052856657	-6.45016	1.62E-10	3.57E-10	purple	-0.423721267	5.38E-10				Aldehyde dehydrogenase protein / MA3 domain-containing protein
Sapur.001G105900.1	124.2882929	-0.575833743	0.093319671	-6.37551	1.82E-10	4.01E-10	purple	-0.438226125	9.46E-09				conserved peptide upstream open reading frame 47
Sapur.001G069700.1	23.20053619	-0.848148024	0.131414514	-6.37076	1.88E-10	4.14E-10	purple	-0.462833352	1.96E-09				AT-TCP20;ATTCP20;PCF1;TC	TCDNA5E7 BINDING PROTEIN 5
Sapur.001G184500.1	287.5.85847	-0.280551812	0.044006658	-6.3674	1.92E-10	4.23E-10	purple	-0.481287381	1.76E-10	GO:0006418;GO:0000166;GO:0005524;GO:0004812			ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases
Sapur.014G079400.1	491.9677012	-0.264186014	0.041662287	-6.34098	2.28E-10	5.00E-10	purple	-0.468995529	7.94E-10	GO:0008336;GO:0008386;GO:0005515			cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative
Sapur.004G131100.1	2322.442077	-0.180180671	0.071808709	-6.28184	3.38E-10	7.43E-10	purple	-0.422779082	1.47E-08	GO:0007264;GO:0005525	ARAC3;ATROPH;RAC3;RHO3		RAC like 3
Sapur.003G016800.1	4117.293158	-0.379862588	0.060467086	-6.28214	3.34E-10	7.27E-10	purple	-0.4484253	3.87E-09	GO:0005515;GO:0003723;GO:0016023;GO:0000398;GO:0017070;GO:0005681	EMB3143;MBI177;EMB3143_SU		Pre-mRNA-processing-splicing factor
Sapur.019G144400.1	1.996544480	-1.2	0.319185175	-6.24992	4.13E-10	8.96E-10	purple	-0.498543877	1.17E-11				Leucine-rich repeat family protein
Sapur.009G156900.1	63.61382233	-0.461485743	0.07081569	-6.23395	4.51E-10	9.85E-10	purple	-0.447283129	4.30E-09				Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.004G056200.1	440.0581217	-0.251180223	0.034394346	-6.15664	7.31E-10	1.57E-09	purple	-0.442160466	6.72E-09		ATTIC40;PDE120;TIC40		Hydroxyproline-rich glycoprotein family protein
Sapur.004G064300.1	219.3304998	-0.306266955	0.050184286	-6.10285	1.04E-09	2.22E-09	purple	-0.442539868	6.48E-09	GO:0003723			RNA-binding KH domain-containing protein
Sapur.013G011600.1	1148.27696	-0.249105	0.041000261	-6.08995	1.14E-09	2.42E-09	purple	-0.420280201	1.67E-08		AHP2;-B15.2;P2-B15		phosphotransfer protein 2
Sapur.005G060600.1	234.4900683	0.316681074	0.052091209	6.079357	1.21E-09	2.57E-09	purple	-0.42905322	2.06E-08				transmembrane protein, putative
Sapur.008G145300.1	150.9368687	0.353811665	0.058279668	6.07197	1.22E-09	3.00E-09	purple	-0.448283651	4.69E-09	GO:0005515			Sterile alpha motif (SAM) domain-containing protein
Sapur.016G185000.2	0.85315489	-1.714274754	0.281177033	-6.05372	1.42E-09	3.00E-09	purple	-0.651619702	2.43E-20	GO:0010468;GO:0005777			Putative endonuclease or glycosyl hydrolase
Sapur.013G121300.1	196.0139824	-0.299272103	0.049511462	-6.05359	1.42E-09	3.00E-09	purple	-0.435238872	1.22E-08				myosin heavy chain-related
Sapur.007G068800.4	17.23665444	-0.572501989	0.095075472	-6.01655	1.78E-09	3.76E-09	purple	-0.507042776	1.28E-11				transducin family protein / WD-40 repeat family protein
Sapur.010G131800.1	112.0546426	-0.534410537	0.088946367	-6.00533	1.91E-09	4.03E-09	purple	-0.446152049	4.76E-09				pre-mRNA-processing protein 40C
Sapur.016G031500.1	105.3518004	-0.341587827	0.052566657	-6.00116	1.94E-09	4.10E-09	purple	-0.437209361	1.01E-08	GO:0003333			Tryptophan/tyrosine permease
Sapur.001G185600.1	267.1665469	-0.229372058	0.038298701	-5.98903	2.11E-09	4.46E-09	purple	-0.463161693	1.01E-09	GO:0006468;GO:0004672			BAK1-interacting receptor-like kinase 1
Sapur.001G060700.1	147.4648831	-0.181303707	0.030283833	-5.98626	2.44E-09	5.13E-09	purple	-0.451422148	2.66E-09	GO:0004386			RNA helicase family protein
Sapur.016G229200.1	343.2604212	-0.195179838	0.032765763	-5.95678	2.57E-09	5.40E-09	purple	-0.441100958	7.38E-09		ATCPSF30;CPSF30		cleavage and polyadenylation specificity factor 30
Sapur.016G229100.1	1230.832041	-0.244916847	0.041118174	-5.94286	2.80E-09	5.87E-09	purple	-0.428854549	2.48E-08	GO:0005515	EMB2753		tetratricopeptide repeat (TPR)-containing protein
Sapur.006G141200.1	339.8163952	-0.49182333	0.082845785	-5.93658	2.91E-09	6.10E-09	purple	-0.451257588	2.32E-09	GO:0019538			Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein
Sapur.006G088800.1	17.90506837	-0.734974989	0.123755132	-5.93485	2.94E-09	6.16E-09	purple	-0.445487025	5.02E-09	GO:0008017;GO:0007018;GO:0005524;GO:0003777;GO:0005871			ATP binding microtubule motor family protein
Sapur.006G182000.1	1307.461972	-0.554564493	0.093561406	-5.93123	3.05E-09	6.29E-09	purple	-0.458381096	1.98E-09	GO:0005506;GO:0004252	SLP2		subtilisin-like serine protease 2
Sapur.010G051100.1	1174.718786	-0.307112847	0.051879731	-5.92028	3.21E-09	6.72E-09	purple	-0.412291884	8.11E-08		ATHO2;THO2		THO complex subunit
Sapur.006G112100.1	151.9621583	-0.804867369	0.136356427	-5.89309	3.74E-09	7.81E-09	purple	-0.422348662	3.66E-08				ARM repeat superfamily protein
Sapur.004G060900.1	0.651026113	-1.962645053	0.329774473	-5.89025	3.86E-09	8.04E-09	purple	-0.831817759	6.91E-38				HSP20-like chaperones superfamily protein
Sapur.001G174200.1	1451.573981	-0.210869159	0.036928448	-5.87421	4.29E-09	8.84E-09	purple	-0.435501681	1.20E-08				Protein of unknown function (DUF3411)
Sapur.018G023600.1	902.3250818	-0.30866691	0.052521609	-5.87319	4.27E-09	8.90E-09	purple	-0.443052508	6.20E-09	GO:0005515	EBF1;EBF2		EIN3-binding F box protein 1
Sapur.002G036000.1	2.204824967	1.125680205	0.192157966	5.85766	4.68E-09	9.75E-09	purple	-0.559664685	2.51E-14		GAMMA CA1		gamma carbonic anhydrase, putative
Sapur.015G055600.1	335.0337224	-0.276061644	0.047331984	-5.83207	5.47E-09	1.13E-08	purple	-0.454351849	2.27E-09				F-box family protein
Sapur.015G020300.1	50.09338804	-0.447164914	0.076750739	-5.83749	5.37E-09	1.24E-08	purple	-0.428854549	2.48E-08				ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases
Sapur.006G073800.1	43.78704023	-0.562060357	0.097000014	-5.79444	6.86E-09	1.41E-08	purple	-0.442318684	6.13E-09				conserved peptide upstream open reading frame 47
Sapur.001G115300.1	96.90791162	-0.485615985	0.083978885	-5.78942	7.06E-09	1.46E-08	purple	-0.447248512	4.30E-09	GO:0006915;GO:0006281;GO:0000724	SMC5		structural maintenance of chromosomes 5
Sapur.010G061600.1	253.1437234	-0.465605701	0.033931814	-5.78603	7.18E-09	1.48E-08	purple	-0.408819	1.24E-07				S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.004G028500.1	1651.120954	-0.242261977	0.041907769	-5.78036	7.45E-09	1.54E-08	purple	-0.429637312	1.96E-08	GO:0006351;GO:0008409;GO:0003677;GO:0032549	EMB1988;RRP82;RP82		DNA-directed RNA polymerase family protein
Sapur.T006100.4	4.585816153	-0.705377003	0.121577889	-5.80147	7.77E-09	4.00E-08	purple	-0.503742749	3.61E-14				Protein of unknown function, DUF241
Sapur.003G196800.1	1181.051132	-0.364995528	0.06337101	-5.75966	8.43E-09	1.73E-08	purple	-0.437796046	9.82E-09	GO:0005524	HSP60;HSP60-3B		heat shock protein 60
Sapur.015G163000.1	388.8510532	-0.216173132	0.03758175	-5.75209	8.81E-09	1.81E-08	purple	-0.435501681	1.20E-08				S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Sapur.018G092600.1	400.8613657	-0.40612822	0.070745021	-5.73673	9.65E-09	1.98E-08	purple	-0.428587139	1.50E-08		UBP23		ubiquitin-specific protease 23
Sapur.001G178300.1	631.8316959	-0.175871551	0.03063846	-5.7005	9.99E-09	2.05E-08	purple	-0.420773061	1.78E-08	GO:0005515	ATMRS1;MRE70;MRS1		Transducin/WD40 repeat-like superfamily protein
Sapur.015G169500.1	110.4576667	-0.463796059	0.079732241	-5.69457	1.24E-08	2.52E-08	purple	-0.434317782	1.32E-08				
Sapur.005G171100.1	267.6802579	-0.368384104	0.064716164	5.692934	1.25E-08	2.55E-08	purple	-0.388841273	4.82E-07	GO:0007186;GO:0005634;GO:0004871	AGG3;ATAGG3;GG1		Gγ protein
Sapur.013G117200.1	123.0255791	-0.291563789	0.051296858	-5.68407	1.32E-08	2.68E-08	purple	-0.428627212	4.14E-08				Gγ subunit 3
Sapur.001G295400.1	722.3479865	-0.251128865	0.04504244	-5.57608	2.48E-08	4.96E-08	purple	-0.41806178	5.09E-08	GO:0003677			Tetratricopeptide repeat (TPR)-like superfamily protein
Sapur.005G091000.1	6.712905	-0.823065517	0.147632969	-5.57494	2.48E-08	4.99E-08	purple	-0.404043445	4.67E-07		ENBD7;MAPK9KK4;YDA		AKR2/BRIGHT DNA-binding domain-containing protein
Sapur.006G063000.1	750.8452202	-0.281051965	0.050451585	-5.57076	2.54E-08	5.11E-08	purple	-0.427652277	2.91E-08	GO:0006468;GO:0006672			Protein kinase superfamily protein
Sapur.001G024200.1	781.6943864	-0.153836761	0.027661348	-5.5422	2.96E-08	5.95E-08	purple	-0.414845125	5.56E-08	GO:0016787;GO:0005524;GO:0003677			DEAD/H(x) box helicase family protein
Sapur.013G026100.1	668.7310856	-0.19889767	0.036037822	-5.52163	3.36E-08	6.73E-08	purple	-0.437226412	1.03E-08				phosphoinositide binding
Sapur.015G039200.1	459.0413953	-0.252881932	0.045611175	-5.53808	3.14E-08	7.06E-08	purple	-0.450750663	2.53E-09	GO:0016020;GO:0008378;GO:0006486;GO:0030246			Galactosyltransferase family protein
Sapur.013G174100.1	16.128.9219	-0.234656623	0.043114245	-5.44717	5.12E-08	1.02E-07	purple	-0.416639368	5.71E-08	GO:0005525			GTP binding Elongation factor Tu family protein
Sapur.015G118800.1	941.0070284	-0.202228738	0.036475546	-5.54183	3.29E-08	7.09E-08	purple	-0.423708561	2.44E-08	GO:0005525			GTP binding Elongation factor Tu family protein
Sapur.010G041500.1	138.4026615	-0.438453937	0.081302181	-5.38892	7.09E-08	1.40E-07	purple	-0.417359756	5.36E-08	GO:0004648;GO:0005524;GO:0004674;GO:0004672	AGC (cAMP-dependent, cGMP-dependent and protein kinase C)-kinase family protein		AGC (cAMP-dependent, cGMP-dependent and protein kinase C)-kinase family protein
Sapur.005G041300.1	891.6421537	-0.252136573	0.047328842	-5.31666	1.08E-07	2.07E-07	purple	-0.402865829	1.71E-07	GO:0003723	FLK		RNA-binding KH domain-containing protein
Sapur.010G134400.1	128.7618418	-0.603808588	0.075888944	-5.61081	1.75E-07	2.10E-07	purple	-0.402472476	1.75E-07		ENBD217		Pentatricopeptide (PPR)-containing protein
Sapur.016G294100.2	0.953918286	-3.348004302	0.255498751	-5.27597	1.32E-07	2.58E-07	purple	-0.80715911	2.62E-37	GO:0010200;GO:0006810;GO:0005215	NIPS-1;NLM6;NLM8		NODULE-like intrinsic protein 5;1
Sapur.008G129600.1	35.10164812	-0.482564767	0.087880241	-5.26379	1.47E-07	2.86E-07	purple	-0.418911766	5.58E-08				
Sapur.15G204500.1	17.7677992	-0.422761737	0.080391348	-5.22573	1.73E-07	3.38E-07	purple	-0.411105845	8.87E-08				Pentatricopeptide repeat (PPR) superfamily protein
Sapur.006G189300.1	5.582615161	-0.904936366	0.17367202	-5.20869	1.94E-07	3.79E-07	purple	-0.367545452	2.56E-06				Protein of unknown function (DUF231)
Sapur.007G087500.1	0.971859179	-3.384051517	0.267176549	-5.18318	2.18E-07	4.23E-07	purple	-0.911483653	1.17E-41	GO:0006351;GO:0003714			Protein of unknown function (DUF2550/UPF0682)
Sapur.002G049600.1	106.5244313	-0.519587557	0.101208149	-5.13398	2.87E-07	5.56E-07	purple	-0.404688098	1.88E-07	GO:0008312;GO:0003824			Acid phosphatase/vanadate-dependent phosphohydrolases-like domain
Sapur.012G138600.1	167.5663016	-0.291443943	0.057006752	-5.08567	3.66E-07	7.01E-07	purple	-0.381447044	8.65E-07				Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Sapur.003G030500.1	0.60313651	-1.811867459	0.359015794	-5.03442	4.79E-07	9.15E-07	purple	-0.752583008	1.36E-22				DUA/CDE4 bin bin like family protein
Sapur.015G029200.2	0.931010527	-1.482719604	0.294808135	-5.02773	4.96E-07	9.43E-07	purple	-0.725182651	6.67E-27	GO:0015126;GO:0003824;GO:0008173;GO:0006364;GO:0005737			Radical SAM superfamily protein
Sapur.003G017000.3	24.26559608	-0.818007088	0.164386414	-4.97631	6.48E-07	1.23E-06	purple	-0.533763232	5.12E-13	GO:0005992;GO:0008824	ATTPS;TPS5		trehalose phosphatase/synthase 5
Sapur.013G082700.2	4.488807456	-0.893549346	0.180186259	-4.96068	7.08E-07	1.34E-06	purple	-0.75456524	3.71E-30				alpha/beta-hydrolases superfamily protein
Sapur.016G200400.2	0.785657837	-1.417874807	0.286400967	-4.95055	7.40E-07	1.40E-06	purple	-0.786978267	2.51E-34	GO:0006396;GO:0003723;GO:0000175;GO:0006402;GO:0004654			polyribonucleotide nucleotidyltransferase, putative
Sapur.001G147500.1	6.606139493	-0.966174907	0.197121159	-4.94507	7.91E-07	1.46E-06	purple	-0.505692628	1.48E-11	GO:0016787;GO:0016740	SPLH		lipase superfamily with adhesome and alpha/beta hydrolases-like domain
Sapur.008G029600.1	433.4637621	-0.28392023	0.057664487	-4.92366	8.49E-07	1.60E-06	purple	-0.367678115	2.17E-05	GO:0005509			mitochondrial substrate carrier family protein
Sapur.008G000500.1	68.82511988	-0.382252442	0.077767821	-4.90458	9.34E-07	1.76E-06	purple	-0.39134411	4.02E-07				Pentatricopeptide (PPR)-containing protein
Sapur.016G219000.1	882.6180039	0.16983217	0.034587304	4.785716	1.70E-06	3.16E-06	purple	-0.37354298	1.13E-06	GO:0055114;GO:0016491	ATMDAR6;MDAR4		monodehydroascorbate reductase 4
Sapur.006G041700.1	1715.405628	-0.181751165	0.04076767	-4.46076	1.37E-06	2.56E-06	purple	-0.357984646	2.97E-06	GO:0008152;GO:0003824			dehydratase family protein
Sapur.011G117400.1	485.0650562	-0.151836135	0.027898426	-4.63343	3.63E-06	6.62E-06	purple	-0.337960722	1.50E-05				LA RNA-binding protein
Sapur.006G093500.2	24.29912023	0.301680160	0.065432715	4.610235	4.02E-06	7.32E-06	purple	0.87837833	3.79E-51				MYO5 family protein
Sapur.015G176800.1	1153.6.2026	-0.242521864	0.052806428	-4.59387	4.37E-06	7.96E-06	purple	-0.367692237	2.18E-06	GO:0005525			GTP binding Elongation factor Tu family protein
Sapur.014G032700.1	52.79411961	0.348372242	0.077625	4.467302	6.88E-06	1.24E-05	purple	0.807151796	2.66E-37	GO:0019325;GO:0006139;GO:0005524	PYR6		6-oxo/-oxo/-oxo/-oxo nucleotide triphosphate hydrolases superfamily protein
Sapur.018G151200.1	15.74171521	0.364882311	0.081218805	4.49254	7.04E-06	1.26E-05	purple	0.653872239	1.61E-20				adenylate kinase
Sapur.003G167700.2	1.481040592	-1.048837875	0.235185567	-4.45943	8.22E-06	1.47E-05	purple	-0.475619281	3.08E-10				hypothetical protein
Sapur.015G179800.1	7.456861594	-0.552021553	0.126773763	-4.35546	1.34E-05	2.39E-05	purple	0.616154895	8.77E-18	GO:0034061;GO:0005634;GO:0003677	CLPP5;NCLYP1;NCLYP5		nuclear encoded CLP protease 5
Sapur.006G040100.1	196.4995981	-0.2202059	0.051143659	-4.30561	1.67E-05	2.93E-05	purple	0.807151796	2.66E-37	GO:0019325;GO:0006139;GO:0005524	ATTMG2-LT;MG2-1		translocase of

Sapur.002G178500.1	1.316188591	-0.353488129	0.243991941	-1.44877	0.14740191	0.187708717	royalblue	-0.075764977	0.345628408		AT2G05710.1	ACO3	aconitase 3	NA
Sapur.017G074600.2	0.218968643	0.674045448	0.581280686	1.159587	0.246217052	0.302435667	royalblue	0.198235063	0.012818251		AT5G15460.2	MUB2	membrane-anchored ubiquitin-fold protein 2	membrane-anchored ubiquitin-fold protein
Sapur.004G076300.1	0.340143225	0.552276525	0.504389455	1.094941	0.273542632	0.333301982	royalblue	0.138512756	0.083623089		AT1G21280.1			NA
Sapur.011G108800.2	0.546007701	0.445707374	0.408462672	1.091183	0.275192527	0.33520118	royalblue	0.102786845	0.200186843	GO:0016020,GO:0006810,GO:0005215	AT4G10380.1	NIP5;1,NLM6,NLM8	NOD26-like intrinsic protein 5;1	nodulin-like intrinsic protein NIP1-1
Sapur.013G092300.1	0.175052366	0.728270086	0.777398858	0.936804	0.348859568	0.416345446	royalblue	0.202583444	0.010942821	GO:0048544,GO:0006468,GO:0005524,GO:0004672	AT5G60900.1	RLK1	receptor-like protein kinase 1	LRR receptor-like Serine/Threonine-kinase
Sapur.017G124100.1	0.966578169	-0.223981797	0.282183134	-0.79375	0.427343184	0.499750671	royalblue	0.011957648	0.881840148					NA
Sapur.001G001500.1	0.403392823	-0.360666164	0.456972486	-0.78925	0.429965099	0.502355012	royalblue	0.008591896	0.914949371					NA
Sapur.15WG045700.1	0.312120236	0.391271072	0.527050662	0.742378	0.457858052	0.531676048	royalblue	0.099211624	0.216370618		AT3G18360.1		VQ motif-containing protein	NA
Sapur.005G161300.2	0.162001448	0.505646084	0.718091913	0.704152	0.481337922	0.555896726	royalblue	0.122240064	0.127221828		AT1G53580.1	ETHE1,GLX2-3,GLY3	glyoxalase II 3	hydroxyacylglutathione hydrolase
Sapur.018G044600.1	0.156041553	0.57821527	0.859475006	0.672754	0.501103791	0.575928929	royalblue	0.170146974	0.033133761					NA
Sapur.006G221100.1	0.13315428	0.632613275	0.944938659	0.669475	0.503192209	0.578068048	royalblue	0.210477573	0.008147162	GO:0003824,GO:0006470,GO:0004722	AT4G31750.1	WIN2	HOPW1-1-interacting 2	protein phosphatase 2C
Sapur.012G049300.2	0.226355104	0.325957417	0.534718118	0.609587	0.542135172	0.617656862	royalblue	0.096464234	0.229425687		AT5G07980.1		dentin sialophosphoprotein-related	hypothetical protein
Sapur.008G115800.2	0.161704882	0.405385271	0.712108636	0.569274	0.569169885	0.644594054	royalblue	0.125189494	0.118232084		AT2G02148.1			NA
Sapur.002G134700.2	0.550328683	0.190006592	0.34919339	0.54413	0.586352032	0.661087681	royalblue	0.07046041	0.380539949	GO:0008234,GO:0006508	AT1G02305.1		Cysteine proteinases superfamily protein	cathepsin B-like cysteine protease
Sapur.004G001200.1	0.214757005	0.292397872	0.583548754	0.501068	0.616322947	0.689916238	royalblue	0.0489285	0.542830798	GO:0055114,GO:0009916	AT4G22260.1	IM,IM1	Alternative oxidase family protein	ubiquinol oxidase
Sapur.017G046300.1	0.439548932	0.194506259	0.388435157	0.500743	0.616551872	0.690125783	royalblue	0.070115546	0.382881527	GO:0030246,GO:0005975,GO:0004553	AT2G32810.1	BGAL9	beta galactosidase 9	NA
Sapur.017G012300.1	0.197973638	0.294670043	0.594803796	0.495407	0.620312761	0.693678126	royalblue	0.076227661	0.342682275		AT5G05800.1			NA
Sapur.001G030300.4	0.198979826	0.279168152	0.574597548	0.48585	0.627073604	0.700007843	royalblue	0.074751265	0.352138904	GO:0008612	AT5G05920.1	DHS,EDA22	deoxyhypusine synthase	deoxyhypusine synthase
Sapur.016G064600.1	0.447960376	0.186817518	0.394794847	0.473202	0.63606942	0.70875817	royalblue	0.06127405	0.445855265	GO:0006355,GO:0003677	AT2G35940.1	BLH1,EDA29	BEL1-like homeodomain 1	BEL1-related homeotic protein, putative
Sapur.009G124300.2	7.508109251	-0.048353479	0.104250158	-0.46382	0.642775539	0.715363018	royalblue	-0.014169877	0.860185463		AT3G20770.1	AtEIN3,EIN3	Ethylene insensitive 3 family protein	transcription factor EIL1
Sapur.010G195800.1	0.226264352	-0.245429038	0.565312115	-0.43415	0.664181081	0.735818486	royalblue	-0.046616184	0.562085366					NA
Sapur.001G090300.1	0.169920953	0.332513723	0.77404115	0.429581	0.66750013	0.738679001	royalblue	0.147642192	0.064994735	GO:0006355,GO:0003700	AT5G52020.1		Integrase-type DNA-binding superfamily protein	AP2/ERF domain transcription factor
Sapur.008G158000.1	0.203996736	-0.249701197	0.602398676	-0.41451	0.678499525	0.748622007	royalblue	-0.079111177	0.324681272		ATCG00860.1		Chloroplast Ycf2;ATPase, AAA type, core	NA
Sapur.010G137500.1	0.1648405	0.280634747	0.803366093	0.349324	0.726846372	0.793102072	royalblue	0.121299395	0.130197073	GO:0006355,GO:0003677	AT1G79580.1	ANAC033,SMB	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	NAC domain transcription factor superfamily protein, putative
Sapur.005G009400.1	0.100846056	0.436923767	1.281630971	0.340912	0.733169602	0.798447528	royalblue	0.141166847	0.077812328	GO:0005515	AT1G07390.3	AtRLP1,RLP1	receptor like protein 1	Serine/Threonine kinase, plant-type protein%2C putative
Sapur.004G053900.1	0.274185424	-0.182757212	0.548525424	-0.33318	0.738999087	0.80355248	royalblue	0.001306541	0.987042846		AT5G04010.1		F-box family protein	NA
Sapur.004G084000.2	0.191797298	0.204074435	0.629277998	0.324299	0.745711424	0.809520453	royalblue	0.06144887	0.444556094					NA
Sapur.T021500.1	0.094761504	0.413819878	1.279529104	0.323416	0.746380395	0.810166892	royalblue	0.157585922	0.048712348	GO:0005681,GO:0000398,GO:0000387	AT1G54385.2		ARM repeat superfamily protein	NA
Sapur.013G025100.2	0.202330295	0.196560163	0.608370824	0.323093	0.74662505	0.810405858	royalblue	0.06840912	0.394596062		AT2G24960.2			Myb/SANT-like DNA-binding domain protein
Sapur.T040000.1	0.207786719	0.179220543	0.570958894	0.313894	0.753601584	0.81650458	royalblue	0.042852286	0.594108509					NA
Sapur.T160500.1	0.084533321	0.378785251	1.747887377	0.21671	0.828434097	0.878980518	royalblue	0.157739633	0.04849011		AT5G24280.1	GMI1	gamma-irradiation and mitomycin c induced 1	NA
Sapur.15WG001300.1	0.100963841	0.23260737	1.132921717	0.205316	0.837324958	0.885857772	royalblue	0.067520285	0.400781983		AT4G03220.1		Protein with RNI-like/FBD-like domains	F-box/LRR protein
Sapur.010G090400.4	0.099674353	0.227194602	1.128533744	0.201318	0.84044962	0.888403771	royalblue	0.0894282	0.265360222		AT1G68185.1		Ubiquitin-like superfamily protein	ubiquitin-like Rad60 SUMO-like protein
Sapur.005G097500.1	0.082395112	0.267530172	1.486464922	0.179977	0.857170268	0.902321826	royalblue	0.113397525	0.157338968		AT2G18290.1	APC10	anaphase promoting complex 10	anaphase-promoting complex subunit 10
Sapur.T128600.1	0.081420307	0.305171109	1.753147605	0.17407	0.861810134	0.905735887	royalblue	0.130265974	0.103923849	GO:0003677				NA
Sapur.T128400.1	0.086534792	0.26761507	1.603698797	0.166874	0.867469467	0.909981866	royalblue	0.119584455	0.135758491	GO:0003677				NA
Sapur.009G047300.3	0.108526872	0.200239403	1.283757419	0.155979	0.876049449	0.915810853	royalblue	0.063181813	0.431794011	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	AT3G08040.2	ATFRD3,FRD3,MAN1	MATE efflux family protein	MATE efflux family protein
Sapur.011G077000.6	0.074241749	0.269197719	1.937512483	0.13894	0.88949767	0.925803126	royalblue	0.117909399	0.141364197	GO:0005096	AT5G55060.1			Rab3 GTPase-activating protein catalytic subunit
Sapur.018G000800.1	0.161089202	0.081408343	0.624695193	0.130317	0.896315708	0.930206336	royalblue	0.033976573	0.672700064	GO:0006468,GO:0004672	AT4G31170.3		Protein kinase superfamily protein	Serine/Threonine/tyrosine kinase, putative
Sapur.016G244100.3	0.061103451	0.271087403	2.453610535	0.110485	0.912024667	0.942457784	royalblue	0.118044302	0.140906313	GO:0016020,GO:0008236,GO:0006508	AT1G53530.1		Peptidase S24/S26A/S26B/S26C family protein	inner membrane protease subunit 1
Sapur.005G014800.3	0.075269742	0.197936437	2.138231872	0.09257	0.926245062	0.951563309	royalblue	0.114512508	0.153270612		AT5G26940.1		Polynucleotidyl transferase, ribonuclease H-like superfamily protein	DNA polymerase III subunit epsilon
Sapur.007G052700.3	0.109996535	0.117416211	1.272217434	0.092293	0.926465595	0.951742175	royalblue	0.072457575	0.367151507	GO:0008270,GO:0006281,GO:0004518	AT4G36050.2		endonuclease/exonuclease/phosphatase family protein	NA
Sapur.003G169800.3	0.19048909	0.054903757	0.657354478	0.083522	0.933436247	0.956574036	royalblue	0.015934558	0.842985203		AT5G56310.1		Pentatricopeptide repeat (PPR) superfamily protein	PPR containing plant protein
Sapur.018G075500.1	0.077387257	0.085325011	1.614347676	0.052854	0.957848098	0.972192598	royalblue	0.052103049	0.516937902	GO:0016021,GO:0016020,GO:0022857	AT4G30420.1		nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4
Sapur.016G245400.1	19.29473761	0.008653292	0.176437603	0.049044	0.960883841	0.974317008	royalblue	0.063970039	0.426059491	GO:0055114,GO:0016491	AT1G17020.1	ATSRG1,SRG1	senescence-related gene 1	leucoanthocyanidin dioxygenase, putative
Sapur.017G009100.1	0.21885079	-0.025641393	0.573178162	-0.04474	0.964318163	0.976213122	royalblue	0.002775746	0.97247674	GO:0006355,GO:0006351,GO:0003677	AT5G44180.1		Homeodomain-like transcriptional regulator	homeobox protein, putative
Sapur.014G100900.1	3.801559519	0.004853545	0.159291016	0.03047	0.975692482	0.983917502	royalblue	-0.029024431	0.718215349	GO:0005515,GO:0007165,GO:0000155	AT2G40940.1	ERS,ERS1	ethylene response sensor 1	ethylene receptor
Sapur.008G152000.2	0.073100472	0.04984763	1.939498797	0.025701	0.979495591	0.986715314	royalblue	0.050177997	0.532563493		AT1G10670.1	ACLA-1	ATP-citrate lyase A-1	ATP-citrate synthase
Sapur.016G097100.1	0.07280611	-0.023304189	1.76580478	-0.0132	0.989470233	0.993224028	royalblue	0.021088091	0.793205291	GO:0006412,GO:0005840,GO:0003735	AT2G09990.1		Ribosomal protein S5 domain 2-like superfamily protein	NA
Sapur.001G076000.2	0.088123914	0.010293147	1.481117675	0.00695	0.994455081	0.996843814	royalblue	0.038261121	0.634249847		AT2G19170.1	SLP3	subtilisin-like serine protease 3	peptidase inhibitor I9
Sapur.014G007200.3	0.054288048	0.016239374	2.835683974	0.005727	0.995430706	0.997120491	royalblue	0.040372264	0.615649672	GO:0005515	AT1G27460.1	NPGR1	no pollen germination related 1	TPR protein 7A
Sapur.016G044700.2	0.123945365	0.00460682	1.055261144	0.004366	0.996516787	0.997546632	royalblue	0.03543209	0.659536309		AT2G42280.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH130, putative
Sapur.004G003800.2	0.047014872	0.134525488	1.552107299	0.086673	0.930931596	NA	royalblue	0.026403044	0.742728138		AT1G11950.1		Transcription factor jumonji (jmjC) domain-containing protein	lysine-specific demethylase 3A-B, putative
Sapur.001G061900.1	0.049178229	0.235520464	2.904820075	0.081079	0.935378974	NA	royalblue	0.098893115	0.21785638					NA
Sapur.018G041100.4	0.009541113	0.164281247	2.904822183	0.056555	0.954899948	NA	royalblue	0.018328643	0.819769721	GO:0015986,GO:0015078,GO:0000276	AT4G26210.1		Mitochondrial ATP synthase subunit G protein	hydrogen-transporting ATP synthase, rotational mechanism protein%2C putative
Sapur.017G046100.1	0.042451336	0.085367418	1.694675112	0.050374	0.959824424	NA	royalblue	-0.084336363	0.293644849	GO:0000049,GO:0006418,GO:0005524,GO:0004812,GO:0000166	AT4G13780.1		methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative	methionyl-tRNA synthetase
Sapur.006G067100.1	0.023450332	0.124943025	2.759576496	0.045276	0.96388719	NA	royalblue	0.275581364	0.000477046	GO:0006796,GO:0005737,GO:0004427,GO:0000287	AT3G53620.1	AtPPa4,PPa4	pyrophosphorylase 4	inorganic pyrophosphatase
Sapur.008G072800.2	0.037786219	0.12866172	2.904823276	0.044292	0.964671295	NA	royalblue	0.078548531	0.32814497	GO:0016757	AT2G03360.2		Glycosyltransferase family 61 protein	glycosyltransferase, putative
Sapur.016G293200.2	0.008528418	0.128661719	2.904823276	0.044292	0.964671295	NA	royalblue	0.063972488	0.426041743		AT4G38120.1		ARM repeat superfamily protein	HEAT repeat protein
Sapur.019G065000.1	0.023703606	-0.056846222	2.904824395	-0.01957	0.984386723	NA	royalblue	-0.024837001	0.7574984	GO:0006415,GO:0003747	AT1G33330.1		Class I peptide chain release factor	peptide chain release factor, putative
Sapur.016G198900.1	0.026279802	0.051847333	2.719189318	0.019067	0.984787495	NA	royalblue	-0.03792739	0.637211625	GO:0016747	AT5G41130.1		Esterase/lipase/thioesterase family protein	esterase/lipase/thioesterase family protein
Sapur.001G052100.2	0.011879286	0.018098013	2.904824395	0.00623	0.995028949	NA	royalblue	0.163998267	0.040131895	GO:0005737,GO:0005515,GO:0005096	AT5G13300.1	AGD3,SFC,VAN3	ARF GTPase-activating protein	ADP-ribosylation factor GTPase-activating protein AGD3
Sapur.016G309100.4	0.402431943	1.605781797	0.358488647	4.47931	7.49E-06	1.34E-05	saddlebrown	0.092546891	0.248984844	GO:0005515	AT3G13340.1		Transducin/WD40 repeat-like superfamily protein	transducin/WD40 domain protein
Sapur.016G156500.1	0.562089711	2.696248757	0.654969075	4.116605	3.84E-05	6.62E-05	saddlebrown	0.167827705	0.035641279	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G12740.1	CYP87A2	cytochrome P450, family 87, subfamily A, polypeptide 2	cytochrome P450 family protein
Sapur.002G115600.1	1.365219715	-1.731647488	0.485997745	-3.56308	0.000366533	0.000593901	saddlebrown	-0.230804465	0.003634772		AT1G02050.1	LAP6	Chalcone and stilbene synthase family protein	chalcone synthase family protein, putative
Sapur.008G112400.1	0.776646682	1.47838206	0.556464301	2.656742	0.007889981	0.011564513	saddlebrown	0.127130118	0.112591644	GO:0050662,GO:0003824	AT4G35420.1	DRL1	dihydroflavonol 4-reductase-like1	NA
Sapur.016G236100.1	0.309651258	1.889847474	1.009966804	1.871198	0.061317695	0.082062941	saddlebrown	0.137904772	0.085001998	GO:0016887,GO:0005524,GO:0016020	AT3G13220.1	ABCG26,WBC27	ABC-2 type transporter family protein	ABC transporter family protein
Sapur.014G042800.1	0.648598103	0.254222435	0.359453769	0.707247	0.47941328	0.553867361	saddlebrown	0.081361168	0.311066615		AT1G02050.1	LAP6	Chalcone and stilbene synthase family protein	chalcone synthase family protein, putative
Sapur.014G112800.1	0.157924963	1.245073703	2.093931335	0.594611	0.552103813	0.627414841	saddlebrown	0.112195301	0.161815884		AT3G63095.1		Tetratricopeptide repeat (TPR)-like superfamily protein	AAA ATPase von willebrand factor type A, putative
Sapur.019G087700.1	0.103195931	0.739207227	1.761929788	0.419544	0.67481854	0.745082571	saddlebrown	0.135985599	0.089474483		AT1G06280.1	LBD2	LOB domain-containing protein 2	LOB domain protein, putative
Sapur.018G024100.1	0.914322901	0.180660064	0.452107353	0.399596	0.689454471	0.759088455	saddlebrown	0.012347811	0.878014154		AT5G16080.1	AtCXE17,CXE17	carboxyesterase 17	arylacetamide deacetylase
Sapur.016G290700.1	0.065152793	0.519217501	1.416863743	0.366455	0.714025218	0.781399379	saddlebrown	0.179794595	0.024245833	GO:0008270,GO:0005515	AT3G61460.1	BRH1	brassinosteroid-responsive RING-H2	anaphase-promoting complex subunit 11 RING-H2 finger protein
Sapur.003G043600.1	0.460749054	-0.128721624	0.564970347	-0.22784	0.819772308	0.871861512	saddlebrown	-0.077712548	0.333335029		AT4G20050.1	QRT3	Pectin lyase-like superfamily protein	polygalacturonase QRT3
Sapur.003G160200.1	0.054351158	0.451887339	2.00408006	0.225484	0.821603023	0.873359208	saddlebrown	0.178453293	0.025343541	GO:0005975,GO:0004553	AT2G44480.1	BGLU17	beta glucosidase 17	beta-glucosidase
Sapur.016G212700.1	0.026537451	0.284497142	2.904818685	0.09794	0.921980156	NA	saddlebrown	0.083637137	0.297679831					hypothetical protein
Sapur.001G155700.2	0.021486296	0.249206619	2.904819682	0.085791	0.931632771	NA	saddlebrown	0.082400948	0.304902803		AT1G80420.2	ATXRCC1	BRCT domain-containing DNA repair protein	DNA repair protein XRCC1
Sapur.003G024900.7	0.015766363	0.199900829	2.904821116	0.068817	0.945135353	NA	saddlebrown	0.078548531	0.32814497	GO:0006468,GO:0004672	AT3G13690.1		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	tyrosine kinase domain protein
Sapur.018G110300.1	0.011569783	0.192740588	2.904821328	0.066352	0.947097616	NA	saddlebrown	0.129453725	0.106116917		AT1G58190.1	AtRLP9,RLP9	receptor like protein 9	NA
Sapur.007G118500.2	0.032835534	0.122981296	2.095262828	0.058695	0.953195101	NA	saddlebrown	0.01182794	0.883112686		AT2G43465.1		RNA-binding ASCH domain protein	NA
Sapur.016G076700.6	0.011224492	0.164281247	2.904822183	0.056555	0.954899948	NA	saddlebrown	0.111242591	0.165430748	GO:0008270,GO:0003676	AT2G37340.2	ATRSZ33,RSZ33	arginine/serine-rich zinc knuckle-containing protein 33	splicing factor, putative
Sapur.013G110000.1	0.009440835	0.164281247	2.904822183	0.056555	0.954899948	NA	saddlebrown	0.110989064	0.166402765		AT2G31085.1	CLE6	CLAVATA3/ESR-RELATED 6	CLAVATA 3/ESR (CLE)-related protein, putative
Sapur.006G100100.1	0.008697586	0.164281247	2.904822183	0.056555	0.954899948	NA	saddlebrown	0.109821986	0.170932221	GO:0008270,GO:0005515	AT5G22920.1		CHY-type/CTCHY-type/RING-type Zinc finger protein	RING finger and CHY zinc finger protein
Sapur.007G035200.1	0.008697586	0.164281247	2.904822183	0.056555	0.954899948	NA	saddlebrown	0.109821986	0.170932221		AT2G23570.1	ATMES19,MES19	methyl esterase 19	NA
Sapur.002G100300.2	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497	GO:0043565,GO:0006355,GO:0003700	AT4G24240.1	ATWRKY7,WRKY7	WRKY DNA-binding protein 7	WRKY transcription factor
Sapur.005G044600.2	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497		AT2G38820.2		Protein of unknown function (DUF506)	DUF506 family protein
Sapur.006G062100.1	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497					NA
Sapur.007G105500.2	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497		AT1G11480.1		eukaryotic translation initiation factor-related	translation initiation factor-like protein, putative
Sapur.008G129400.2	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497		AT3G55760.2			hypothetical protein
Sapur.013G081100.4	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497	GO:0016888	AT5G17570.1		TatD related DNase	TatD-related deoxyribonuclease
Sapur.018G053100.1	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497		AT2G03500.1		Homeodomain-like superfamily protein	Myb-like DNA-binding domain protein
Sapur.15WG012800.9	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497	GO:0006468,GO:0005524,GO:0004672	AT5G53450.2	ORG1	OBP3-responsive gene 1	kinase domain protein
Sapur.T049000.1	0.005120144	0.128661719	2.904823276	0.044292	0.964671295	NA	saddlebrown	0.078548531	0.32814497		AT1G76065.1		LYR family of Fe/S cluster biogenesis protein	LYR family of Fe/S cluster biogenesis protein
Sapur.016G269600.1	0.014258251	0.126809129	2.904822183	0.043655	0.965179652	NA	saddlebrown	0.033788245	0.674410698					NA
Sapur.014G059500.3	0.009769127	0.091189602	2.904823276	0.031392	0.97495654	NA	saddlebrown	0.003727888	0.963041493	GO:0008168	AT4G00750.1		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	dehydration-responsive family protein
Sapur.018G062200.1	0.010952336	0.091189602	2.904823276	0.031392	0.97495654	NA	saddlebrown	-0.008602215	0.914847614		AT5G37000.1		Exostosin family protein	exostosin family protein
Sapur.001G137700.1	1956.136677	6.004392215	0.14766777	40.66149	0	0	salmon	0.667450092	1.35E-21		AT4G20050.1	QRT3	Pectin lyase-like superfamily protein	polygalacturonase QRT3
Sapur.002G189100.1	779.136931	8.381005713	0.20271923	41.34292	0	0	salmon	0.646796394	5.66E-20	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	AT4G13090.1	XTH2	xyloglucan endotransglucosylase/hydrolase 2	xyloglucan endotransglucosylase/hydrolase, putative
Sapur.003G077700.1	251.8606972	5.098330328	0.112688218	45.2428	0	0	salmon	0.794729651	1.97E-35	GO:0005992,GO:0003824	AT4G22590.1		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	trehalose-phosphate phosphatase
Sapur.005G035900.1	1512.809975	7.602566109	0.191381226	39.72472	0	0	salmon	0.569979726	6.63E-15	GO:0016747	AT1G54570.1		Esterase/lipase/thioesterase family protein	esterase/lipase/thioesterase family protein
Sapur.005G190400.1	928.5413493	12.829797	0.319693576	40.13154	0	0	salmon	0.653151371	1.85E-20					NA
Sapur.006G098700.1	178.0401681	6.855645103	0.162347785	42.22814	0	0	salmon	0.751995608	7.45E-30	GO:0042545,GO:0030599,GO:0005618	AT2G36710.1		Pectin lyase-like superfamily protein	pectinesterase
Sapur.008G070000.1	1187.422078	2.584497101	0.0643429	40.16756	0	0	salmon	0.882029651	1.61E-52		AT1G18720.1		Protein of unknown function (DUF962)	NA
Sapur.009G017800.1	1737.243088	4.825018461	0.10618296	45.44061	0	0	salmon	0.764946593	2.03E-31		AT2G44260.1		Plant protein of unknown function (DUF946)	vacuolar protein sorting-associated protein, putative
Sapur.011G044800.1	4336.101777	14.04314988	0.328890038	42.69862	0	0	salmon	0.591496313	3.44E-16	GO:0008234,GO:0006508	AT5G45890.1	SAG12	senescence-associated gene 12	cysteine protease
Sapur.011G052500.1	801.9753546	12.80577481	0.335748241	38.141	0	0	salmon	0.618885588	5.70E-18	GO:0016788	AT1G29660.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-lipase, putative
Sapur.013G105200.1	909.6816227	8.151678142	0.170284373	47.87097	0	0	salmon	0.652154578	2.21E-20		AT4G09600.1	GASA3	GAST1 protein homolog 3	gibberellin-regulated protein
Sapur.013G112900.1	6357.431599	9.306982636	0.196417994	47.38355	0	0	salmon	0.552790978	6.07E-14	GO:0008234,GO:0006508	AT1G06260.1		Cysteine proteinases superfamily protein	cysteine protease, putative
Sapur.014G076500.1	7480.543184	13.68460254	0.336404962	40.67896	0	0	salmon	0.6037601	5.76E-17		AT5G59310.1	LTP4	lipid transfer protein 4	protease inhibitor/seed storage/LTP family protein
Sapur.014G125000.1	287.9533181	6.361252983	0.151054557	42.11229	0	0	salmon	0.695957683	4.65E-24	GO:0008270	AT5G41060.1		DHHC-type zinc finger family protein	NA
Sapur.016G050400.1	226.1816289	7.666759962	0.166848838	45.95033	0	0	salmon	0.826764173	1.45E-40	GO:0043565,GO:0006355,GO:0005634,GO:0003700	AT2G41690.1	AT-HSFB3,HSFB3	heat shock transcription factor B3	heat stress transcription factor
Sapur.016G256100.1	2311.617632	14.3705187	0.348462138	41.23983	0	0	salmon	0.572088073	5.01E-15	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT4G39490.1	CYP96A10	cytochrome P450, family 96, subfamily A, polypeptide 10	cytochrome P450 family protein
Sapur.016G261900.1	419.2893932	12.13270558	0.310456788	39.08017	0	0	salmon	0.665789915	1.85E-21					NA
Sapur.15WG015900.1	461.4733053	7.384031007	0.160907617	45.88988	0	0	salmon	0.7046265	7.25E-25	GO:0006355,GO:0003677	AT5G61430.1	ANAC100,ATNAC5,NAC100	NAC domain containing protein 100	NAC transcription factor
Sapur.010G129900.1	818.1383386	6.606379864	0.176243948	37.48429	1.66E-307	9.72E-306	salmon	0.64146249	1.42E-19	GO:0033897,GO:0003723	AT1G26820.1	RNS3	ribonuclease 3	ribonuclease T2
Sapur.005G042200.1	403.9779677	4.596695746	0.122805313	37.43076	1.24E-306	7.17E-305	salmon	0.71513917	6.94E-26	GO:0046872	AT2G30580.1	DRIP2	DREB2A-interacting protein 2	zinc finger, C3HC4 type (RING finger) protein, putative
Sapur.001G174800.1	855.52989	10.55454259	0.288774124	36.54947	1.82E-292	9.86E-291	salmon	0.551658678	6.99E-14	GO:0016747,GO:0008610,GO:0016020,GO:0006633	AT1G71160.1	KCS7	3-ketoacyl-CoA synthase 7	NA
Sapur.007G001800.1	460.6964497	6.157447681	0.169876095	36.2467	1.12E-287	5.89E-286	salmon	0.70398074	8.35E-25	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT5G36110.1	CYP716A1	cytochrome P450, family 716, subfamily A, polypeptide 1	cytochrome P450 family 716 protein
Sapur.008G069900.1	166.3320589	7.393957824	0.207325487	35.66353	1.45E-278	7.20E-277	salmon	0.618018928	6.53E-18		AT1G14160.1		Uncharacterised protein family (UPF0497)	casparian strip membrane protein
Sapur.T047300.1	292.114968	7.191639771	0.201711358	35.65312	2.11E-278	1.04E-276	salmon	0.644052401	9.10E-20	GO:0055085,GO:0016021,GO:0016020,GO:0006810,GO:0005215	AT1G32450.1	NRT1.5	nitrate transporter 1.5	peptide transporter, putative
Sapur.009G102400.2	119.4690417	2.952496087	0.086594504	34.09565	8.56E-255	3.60E-253	salmon	0.790091253	9.16E-35	GO:0009116,GO:0003824	AT4G38800.1	ATMTAN1.ATMTN1.MTAN1	methylthioadenosine nucleosidase 1	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
Sapur.010G123200.1	168.3530224	8.246847759	0.245318061	33.61696	9.48E-248	3.82E-246	salmon	0.629096277	1.11E-18	GO:0005975,GO:0004553	AT1G26560.1	BGLU40	beta glucosidase 40	beta-glucosidase
Sapur.016G261700.1	125.5741401	10.05623559	0.30283017	33.20751	8.39E-242	3.28E-240	salmon	0.629299127	1.08E-18	GO:0016887,GO:0005524,GO:0016020	AT4G27420.1		ABC-2 type transporter family protein	NA
Sapur.009G108600.1	268.6761253	7.272361312	0.222855511	32.63263	1.41E-233	5.26E-232	salmon	0.561949928	1.90E-14	GO:0046983	AT2G16910.1	AMS	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	BHLH transcription factor
Sapur.018G075700.1	272.5117844	6.51582203	0.201014521	32.41468	1.70E-230	6.20E-229	salmon	0.722843965	1.16E-26	GO:0003333	AT3G28960.1		Transmembrane amino acid transporter family protein	amino acid transporter
Sapur.011G011800.1	427.125295	11.14472241	0.34518683	32.28606	1.10E-228	3.93E-227	salmon	0.52623735	1.46E-12		AT4G33355.2		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	NA
Sapur.010G123300.1	208.903514	5.030382631	0.155827707	32.2817	1.26E-228	4.52E-227	salmon	0.702291854	1.20E-24	GO:0005975,GO:0004553	AT1G26560.1	BGLU40	beta glucosidase 40	beta-glucosidase
Sapur.016G023600.1	10043.71128	4.356784113	0.139550762	31.22007	5.69E-214	1.83E-212	salmon	0.643792045	9.52E-20	GO:0046556,GO:0046373	AT3G10740.1	ARAF,ARAF1,ASD1,ATASD1	alpha-L-arabinofuranosidase 1	alpha-L-arabinofuranosidase
Sapur.010G164900.1	1012.208326	7.636477162	0.246640919	30.96192	1.76E-210	5.55E-209	salmon	0.632435932	6.44E-19	GO:0016021,GO:0016020,GO:0022857	AT2G39510.1		nodulin MtN21 /EamA-like transporter family protein	auxin-induced protein 5NG4
Sapur.15WG023000.1	136.5532004	8.977880715	0.294351281	30.50057	2.56E-204	7.76E-203	salmon	0.605825944	4.23E-17	GO:0055085,GO:0016021	AT1G73220.1	1-Oct,AtOCT1	organic cation/carnitine transporter1	organic cation/carnitine transporter
Sapur.002G175400.1	71.07540093	6.165987108	0.202672993	30.42333	2.70E-203	8.13E-202	salmon	0.688815848	2.05E-23	GO:0016020,GO:0008375	AT1G11940.1		Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	NA
Sapur.013G059200.1	113.2075528	9.943528991	0.329881525	30.14273	1.34E-199	3.94E-198	salmon	0.590203987	4.14E-16		AT3G03760.1	LBD20	LOB domain-containing protein 20	NA
Sapur.009G065500.1	211.8724938	5.447264698	0.183196785	29.7345	2.75E-194	7.84E-193	salmon	0.651633289	2.42E-20	GO:0048046,GO:0016762,GO:0006073,GO:0005618,GO:0005975,GO:0004553	AT2G14620.1	XTH10	xyloglucan endotransglucosylase/hydrolase 10	xyloglucan endotransglycosylase hydrolase
Sapur.T006200.1	70.81706427	9.454359638	0.319837891	29.55985	4.91E-192	1.38E-190	salmon	0.634373698	4.68E-19		AT3G03760.1	LBD20	LOB domain-containing protein 20	NA
Sapur.006G165200.1	107.180402	3.350608695	0.114514484	29.25926	3.42E-188	9.38E-187	salmon	0.740684977	1.45E-28	GO:0046983	AT2G31210.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor bHLH91
Sapur.001G105400.1	70.26110243	6.906023474	0.247942529	27.85332	9.82E-171	2.28E-169	salmon	0.626548742	1.68E-18	GO:0006468,GO:0004672	AT1G61590.1		Protein kinase superfamily protein	tyrosine kinase domain protein
Sapur.002G139300.1	215.1099199	2.332037989	0.08419176	27.69912	7.15E-169	1.63E-167	salmon	0.80399425	8.10E-37		AT2G46735.1			hypothetical protein
Sapur.009G068900.1	99.1827838	4.23016214	0.155712725	27.16645	1.62E-162	3.49E-161	salmon	0.577703475	2.35E-15	GO:0016798,GO:0005975,GO:0004553	AT4G33840.1		Glycosyl hydrolase family 10 protein	endo-1%2C4-beta-xylanase
Sapur.002G018600.1	859.5766847	2.024356809	0.0753161	26.87814	3.96E-159	8.27E-158	salmon	0.811758047	4.88E-38	GO:0006355,GO:0005634,GO:0003677,GO:0009725	AT1G19850.1	ARF5,IAA24,MP	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related	NA
Sapur.002G030400.1	118.4146476	10.23369796	0.381209042	26.84537	9.55E-159	1.99E-157	salmon	0.531069305	8.36E-13	GO:0016765	AT2G17570.1		Undecaprenyl pyrophosphate synthetase family protein	NA
Sapur.010G063400.1	81.53696914	9.281613802	0.354464566	26.18488	3.95E-151	7.79E-150	salmon	0.504483595	1.62E-11	GO:0016758,GO:0008152	AT3G02100.1		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase
Sapur.003G048600.1	1156.222319	1.613164191	0.061726256	26.13417	1.49E-150	2.92E-149	salmon	0.801328885	2.06E-36	GO:0098599	AT3G60340.2		alpha/beta-Hydrolases superfamily protein	palmitoyl-protein thioesterase
Sapur.019G095400.1	59.29094227	4.667210582	0.179355815	26.02208	2.79E-149	5.40E-148	salmon	0.644706316	8.13E-20		AT1G03700.1		Uncharacterised protein family (UPF0497)	CASP-like protein POPTRDRAFT-670582 protein
Sapur.001G066600.1	54.8591558	5.021031404	0.197850175	25.37795	4.42E-142	8.07E-141	salmon	0.64398271	9.21E-20	GO:0009733	AT1G56150.1		SAUR-like auxin-responsive protein family	auxin-responsive family protein
Sapur.009G069000.1	37.51106941	4.926341885	0.194442661	25.3357	1.29E-141	2.35E-140	salmon	0.652265126	2.17E-20	GO:0016798,GO:0005975,GO:0004553	AT4G33840.1		Glycosyl hydrolase family 10 protein	glycosyl hydrolase family 10 protein
Sapur.006G037100.1	78.31610504	4.989674696	0.200017607	24.94618	2.35E-137	4.10E-136	salmon	0.570712677	6.02E-15		AT2G41660.1	MIZ1	Protein of unknown function, DUF617	MIZU-kussei protein, putative
Sapur.009G008900.1	50.37144827	5.120733655	0.211382655	24.22495	1.21E-129	1.98E-128	salmon	0.569610767	6.97E-15		AT5G60520.1		Late embryogenesis abundant (LEA) protein-related	structural constituent of cell wall protein, putative
Sapur.001G094500.1	71.62083047	4.656304546	0.192243927	24.22081	1.34E-129	2.18E-128	salmon	0.608918349	2.65E-17	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	AT4G22790.1		MATE efflux family protein	MATE efflux family protein
Sapur.012G069700.1	21.35000375	7.459397149	0.30875526	24.15958	5.92E-129	9.55E-128	salmon	0.615336666	9.92E-18	GO:0016788	AT3G48460.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.005G102000.1	4643.541931	2.503686519	0.104118546	24.0465	9.08E-128	1.44E-126	salmon	0.675192836	3.09E-22		AT2G23790.1		Protein of unknown function (DUF607)	coiled-coil protein
Sapur.011G066400.1	62.03031718	3.936504334	0.163752296	24.03938	1.08E-127	1.71E-126	salmon	0.690234963	1.53E-23					hypothetical protein
Sapur.005G019800.1	74.40596095	2.518594459	0.105688413	23.83037	1.62E-125	2.51E-124	salmon	0.730684363	1.77E-27					transmembrane protein, putative
Sapur.013G090300.2	38.12451839	2.068161202	0.08682734	23.81924	2.11E-125	3.27E-124	salmon	0.795874881	1.34E-35	GO:0005515	AT3G56230.1		BTB/POZ domain-containing protein	BTB/POZ domain protein
Sapur.004G014100.1	249.0458099	9.647783203	0.405193906	23.81029	2.61E-125	4.04E-124	salmon	0.328626051	2.64E-05		AT3G63095.1		Tetratricopeptide repeat (TPR)-like superfamily protein	transmembrane protein, putative
Sapur.005G197300.1	16.36322944	4.923504542	0.208542706	23.60909	3.11E-123	4.68E-122	salmon	0.748063253	2.13E-29	GO:0003824	AT5G11880.1		Pyridoxal-dependent decarboxylase family protein	ornithine decarboxylase
Sapur.006G065400.1	92.64290691	4.816959988	0.207877805	23.17207	8.71E-119	1.26E-117	salmon	0.526053499	1.49E-12	GO:0016747,GO:0008610,GO:0016020,GO:0006633	AT3G52160.1	KCS15	3-ketoacyl-CoA synthase 15	NA
Sapur.006G192400.1	47.28102335	3.643448443	0.157281468	23.16515	1.02E-118	1.48E-117	salmon	0.655660495	1.18E-20					NA
Sapur.002G146500.1	542.4664587	3.685122021	0.162585123	22.6658	9.75E-114	1.31E-112	salmon	0.58991167	4.31E-16	GO:0080123,GO:0009864,GO:0009694,GO:0009611	AT2G46370.4	FIN219,JAR1	Auxin-responsive GH3 family protein	indole-3-acetic acid-amido synthetase GH3.5 protein, putative
Sapur.004G048400.1	246.6887497	3.013317421	0.137244236	21.95588	7.61E-107	9.44E-106	salmon	0.631361359	7.69E-19	GO:0055085,GO:0016021,GO:0016020,GO:0006810,GO:0005215	AT5G14940.1		Major facilitator superfamily protein	peptide transporter family protein
Sapur.016G133300.1	15.03251533	5.658998903	0.259535401	21.80434	2.11E-105	2.58E-104	salmon	0.743798506	6.51E-29		AT4G31380.1	FLP1	FPF1-like protein 1	flowering-promoting factor-like protein
Sapur.002G055500.1	624.9553196	1.668864972	0.076557983	21.79871	2.39E-105	2.91E-104	salmon	0.807409025	2.39E-37	GO:0006355,GO:0003677	AT1G21340.1		Dof-type zinc finger DNA-binding family protein	F-box protein
Sapur.003G081500.1	103.8617819	2.547240686	0.11863052	21.47205	2.84E-102	3.33E-101	salmon	0.706484192	4.83E-25	GO:0055085,GO:0016020,GO:0015297,GO:0015238,GO:0006855	AT4G22790.1		MATE efflux family protein	MATE efflux family protein
Sapur.016G025000.1	19.27777276	3.519398938	0.16446516	21.39905	1.36E-101	1.58E-100	salmon	0.690818405	1.36E-23					NA
Sapur.009G021000.1	17.30017942	7.575458101	0.356805333	21.23135	4.90E-100	5.58E-99	salmon	0.549302234	9.37E-14		AT2G28780.1			P-hydroxybenzoic acid efflux pump subunit aaeB, putative
Sapur.006G138700.1	196.9701751	3.821373057	0.181487107	21.05589	2.02E-98	2.25E-97	salmon	0.634731078	4.41E-19	GO:0008152,GO:0003824	AT3G21240.1	4CL2,AT4CL2	4-coumarate:CoA ligase 2	4-coumarate:CoA ligase
Sapur.002G020700.1	17.74029636	7.230435117	0.344978106	20.95911	1.55E-97	1.71E-96	salmon	0.600974269	8.71E-17					hypothetical protein
Sapur.002G145200.1	24.16063207	7.561676189	0.361347179	20.92635	3.08E-97	3.39E-96	salmon	0.410665021	9.19E-08	GO:0005515	AT3G59510.1		Leucine-rich repeat (LRR) family protein	receptor kinase, putative
Sapur.002G124700.1	129.4248563	2.289217382	0.109482713	20.9094	4.40E-97	4.83E-96	salmon	0.690663587	1.40E-23		AT3G52790.1		peptidoglycan-binding LysM domain-containing protein	NA
Sapur.003G077600.1	11.26827289	4.81892682	0.231854344	20.78429	6.01E-96	6.49E-95	salmon	0.707598197	3.77E-25		AT4G12432.1	CPuORF26	conserved peptide upstream open reading frame 26	NA
Sapur.014G110900.1	132.056565	3.279871872	0.157880522	20.77439	7.38E-96	7.97E-95	salmon	0.574661029	3.55E-15		AT2G48030.1		DNAse I-like superfamily protein	endonuclease/exonuclease/phosphatase family protein
Sapur.003G023800.1	143.4407835	1.458078084	0.070436962	20.70047	3.43E-95	3.68E-94	salmon	0.750159394	1.22E-29	GO:0005515	AT2G19520.1	ACG1.ATMSI4.FVE.MSI4.NF	Transducin family protein / WD-40 repeat family protein	nucleosome/chromatin assembly factor group protein
Sapur.005G194900.1	113.2750689	4.033034608	0.19536805	20.64327	1.12E-94	1.20E-93	salmon	0.503941914	1.72E-11	GO:0006508,GO:0004252	AT1G20160.1	ATSBT5.2	Subtilisin-like serine endopeptidase family protein	subtilisin-like serine protease
Sapur.15WG097500.1	149.5528124	3.037411303	0.148576383	20.44343	6.87E-93	7.18E-92	salmon	0.583666166	1.04E-15		AT5G62960.1			transmembrane protein, putative
Sapur.002G143800.1	33.13374178	4.800040535	0.237636579	20.19908	9.97E-91	1.01E-89	salmon	0.521913311	2.39E-12	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G01280.1	CYP703,CYP703A2	cytochrome P450, family 703, subfamily A, polypeptide 2	flavonoid 3'-hydroxylase
Sapur.019G057400.1	545.8123949	1.670648959	0.08284537	20.16587	1.95E-90	1.97E-89	salmon	0.71233194	1.31E-25		AT5G17210.1		Protein of unknown function (DUF1218)	transmembrane protein, putative
Sapur.003G077500.1	10.72574453	4.712345886	0.234632675	20.08393	1.02E-89	1.01E-88	salmon	0.71134154	1.64E-25					NA
Sapur.011G088300.1	16.10319312	5.015822654	0.252445872	19.8689	7.56E-88	7.33E-87	salmon	0.624314472	2.41E-18	GO:0016887,GO:0005524,GO:0016020	AT4G27420.1		ABC-2 type transporter family protein	white-brown-complex ABC transporter family protein
Sapur.016G279500.1	16.09351945	3.394489012	0.172659032	19.66007	4.74E-86	4.51E-85	salmon	0.624409614	2.37E-18					NA
Sapur.008G089500.1	21.16879826	6.325942449	0.322189095	19.63425	7.88E-86	7.47E-85	salmon	0.49275096	5.54E-11		AT2G03830.1	RGF8		NA
Sapur.006G167800.1	10.82604824	5.332757464	0.271828462	19.6181	1.08E-85	1.02E-84	salmon	0.639945025	1.84E-19		AT5G06300.1		Putative lysine decarboxylase family protein	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG7
Sapur.009G028500.1	226.2820816	1.242392682	0.063499522	19.56539	3.05E-85	2.86E-84	salmon	0.759751481	8.85E-31		AT5G59070.1		UDP-Glycosyltransferase superfamily protein	glycosyltransferase family 4 protein
Sapur.003G025500.1	63.41504566	3.213759934	0.164277433	19.563	3.20E-85	3.00E-84	salmon	0.621465591	3.80E-18					NA
Sapur.009G057300.1	1077.908338	2.091202987	0.106976343	19.54828	4.27E-85	3.99E-84	salmon	0.633155686	5.72E-19	GO:0071805,GO:0016020,GO:0015079	AT2G30070.1	ATKT1.ATKT1P.ATKUP1.KT1	potassium transporter 1	potassium transporter
Sapur.002G054300.1	12.81985237	7.108095135	0.364159178	19.5192	7.54E-85	7.04E-84	salmon	0.457891533	1.64E-09		AT3G43660.1		Vacuolar iron transporter (VIT) family protein	vacuolar iron transporter-like protein
Sapur.016G036800.1	76.15544693	5.157263093	0.264690607	19.48412	1.50E-84	1.39E-83	salmon	0.417996518	5.12E-08					NA
Sapur.013G137600.1	10.47898289	6.851967059	0.354716378	19.31675	3.88E-83	3.54E-82	salmon	0.458557464	1.55E-09		AT3G51680.1		NAD(P)-binding Rossmann-fold superfamily protein	short-chain dehydrogenase reductase
Sapur.010G067500.1	20.13567108	4.545837302	0.236037215	19.25899	1.19E-82	1.07E-81	salmon	0.600435686	9.42E-17		AT4G11080.1		HMG (high mobility group) box protein	NA
Sapur.T114300.1	16.11367625	4.149292864	0.215752978	19.23168	2.01E-82	1.81E-81	salmon	0.627195318	1.52E-18	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.011G035200.1	68.40388063	6.162656852	0.32154859	19.16555	7.18E-82	6.43E-81	salmon	0.323465599	3.59E-05					hypothetical protein
Sapur.002G026200.1	36.57376745	4.812099501	0.252232377	19.07804	3.84E-81	3.40E-80	salmon	0.573133235	4.36E-15		AT5G42785.1			NA
Sapur.011G052600.1	12.19251967	6.994011739	0.366916101	19.06161	5.26E-81	4.65E-80	salmon	0.516117195	4.57E-12	GO:0016788	AT1G71250.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL-lipase, putative
Sapur.019G109800.1	104.2882664	7.593163076	0.39839026	19.05961	5.47E-81	4.83E-80	salmon	0.484004262	1.35E-10		AT2G30300.1		Major facilitator superfamily protein	nodulin-like protein
Sapur.013G113500.1	11.49737361	6.790507373	0.363235236	18.69452	5.49E-78	4.63E-77	salmon	0.473637674	3.73E-10	GO:0008061,GO:0016998,GO:0006032,GO:0004568	AT3G54420.1	ATCHITIV,ATEP3,CHIV,EP3	homolog of carrot EP3-3 chitinase	class IV endochitinase
Sapur.006G229100.1	34.15714424	3.266504463	0.176538798	18.50304	1.95E-76	1.62E-75	salmon	0.619314151	5.33E-18		AT4G31330.1		Protein of unknown function, DUF599	plant/F12B17-70 protein
Sapur.010G130000.1	25.64726226	5.099993375	0.276153511	18.46796	3.74E-76	3.08E-75	salmon	0.458430804	1.56E-09	GO:0033897,GO:0003723	AT2G02990.1	ATRNS1,RNS1	ribonuclease 1	ribonuclease T2
Sapur.017G038400.1	340.9812711	1.790293563	0.097274964	18.40446	1.21E-75	9.89E-75	salmon	0.628338147	1.26E-18	GO:0004386	AT5G10370.1		helicase domain-containing protein / IBR domain-containing protein / zinc finger protein-related	ATP-dependent RNA helicase, putative
Sapur.011G088500.1	154.2221585	2.18814685	0.119081438	18.37521	2.07E-75	1.69E-74	salmon	0.632958446	5.91E-19	GO:0006355,GO:0003677	AT3G15510.1	ANAC056.ATNAC2.NAC2.NA	NAC domain containing protein 2	NAC transcription factor
Sapur.003G000400.1	576.4717408	3.416159943	0.18611189	18.35541	2.99E-75	2.42E-74	salmon	0.505781782	1.41E-11	GO:0016020,GO:0006810,GO:0005215	AT1G59740.1		Major facilitator superfamily protein	peptide transporter
Sapur.018G119300.1	40.28214082	3.000143604	0.16361586	18.33651	4.23E-75	3.42E-74	salmon	0.628051109	1.32E-18		AT5G08370.1	AGAL2,AtAGAL2	alpha-galactosidase 2	NA
Sapur.007G004400.1	15.90690968	5.397334388	0.29665373	18.19406	5.75E-74	4.58E-73	salmon	0.577758094	2.33E-15		AT1G58420.1		Uncharacterised conserved protein UCP031279	NA
Sapur.008G167900.1	13.52183845	6.49513069	0.358190272	18.13319	1.74E-73	1.38E-72	salmon	0.503033266	1.89E-11	GO:0016020,GO:0006810,GO:0005215	AT3G06100.1	NIP7;1,NLM6,NLM8	NOD26-like intrinsic protein 7;1	aquaporin NIP7, putative
Sapur.018G026900.1	20.8286689	7.652388144	0.423166678	18.08363	4.29E-73	3.38E-72	salmon	0.321438701	4.04E-05	GO:0016747	AT4G29250.1		HXXXD-type acyl-transferase family protein	transferase-like protein, putative
Sapur.013G033200.1	134.4143529	1.652494999	0.091739346	18.01294	1.54E-72	1.21E-71	salmon	0.677162016	2.10E-22					hypothetical protein
Sapur.010G100400.1	8.867761843	6.073004388	0.33718089	18.01112	1.59E-72	1.25E-71	salmon	0.521333044	2.55E-12		AT1G18470.2		Transmembrane Fragile-X-F-associated protein	NA
Sapur.013G050900.1	107.6236739	1.599127038	0.088821724	18.00378	1.82E-72	1.42E-71	salmon	0.737168868	3.54E-28	GO:0006355,GO:0003677	AT5G18270.2	ANAC087	Arabidopsis NAC domain containing protein 87	NAC transcription factor
Sapur.15ZG039100.1	343.148422	2.950086201	0.166162732	17.7542	1.60E-70	1.21E-69	salmon	0.769194758	5.92E-32		AT2G22660.2		Protein of unknown function (duplicated DUF1399)	DNA-binding protein, putative
Sapur.019G005800.1	9.811368728	5.327831663	0.301003448	17.70023	4.18E-70	3.15E-69	salmon	0.576610834	2.73E-15	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	TIR-NBS-LRR disease resistance-like protein
Sapur.016G067100.1	5.320518039	5.848268884	0.335826001	17.41458	6.40E-68	4.66E-67	salmon	0.58974099	4.42E-16		AT5G06300.1		Putative lysine decarboxylase family protein	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG7
Sapur.008G117600.1	163.1357699	2.817257273	0.161833364	17.40838	7.13E-68	5.18E-67	salmon	0.558602116	2.91E-14		AT5G55340.1		MBOAT (membrane bound O-acyl transferase) family protein	long-chain-alcohol O-fatty-acyltransferase, putative
Sapur.008G068200.1	49.43152392	4.458082696	0.260114778	17.13891	7.61E-66	5.37E-65	salmon	0.479466353	2.11E-10		AT5G15240.1		Transmembrane amino acid transporter family protein	amino acid transporter
Sapur.005G030000.2	21.18633323	6.73796052	0.396123167	17.00976	6.95E-65	4.84E-64	salmon	0.386668605	5.67E-07	GO:0016788	AT1G54790.1		GDSL-like Lipase/Acylhydrolase superfamily protein	GDSL esterase/lipase
Sapur.012G052700.1	18.31232142	3.336115526	0.197802928	16.86586	8.02E-64	5.50E-63	salmon	0.632939595	5.93E-19		AT3G28470.1	ATMYB35,TDF1	Duplicated homeodomain-like superfamily protein	Myb-like DNA-binding domain protein
Sapur.001G082500.1	130.7872197	2.865962569	0.171534189	16.70782	1.15E-62	7.73E-62	salmon	0.495741799	4.07E-11	GO:0008270,GO:0005515	AT3G61460.1	BRH1	brassinosteroid-responsive RING-H2	RING zinc finger protein, putative
Sapur.016G200800.1	19.76111706	3.370129301	0.203798065	16.53661	2.00E-61	1.32E-60	salmon	0.471788792	4.45E-10		AT5G17490.1	RGL3	RGA-like protein 3	GRAS family transcription factor
Sapur.016G024800.1	102.3921455	1.826289395	0.110782484	16.48536	4.67E-61	3.07E-60	salmon	0.612423713	1.56E-17	GO:0046556,GO:0046373	AT3G10740.1	ARAF,ARAF1,ASD1,ATASD1	alpha-L-arabinofuranosidase 1	NA
Sapur.019G007000.1	15.63044472	4.478416231	0.272334727	16.44453	9.18E-61	6.00E-60	salmon	0.457286897	1.74E-09	GO:0007165,GO:0005515	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.T116800.1	18.33593557	4.783945143	0.292082891	16.37872	2.71E-60	1.76E-59	salmon	0.515132981	5.10E-12	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.017G017700.1	27.20159841	3.463125134	0.21193078	16.34083	5.06E-60	3.26E-59	salmon	0.532639708	6.96E-13	GO:0005515	AT3G59510.1		Leucine-rich repeat (LRR) family protein	receptor kinase, putative
Sapur.005G142700.1	16.55461049	3.536891123	0.218025385	16.22238	3.50E-59	2.23E-58	salmon	0.445636	4.96E-09		AT1G21660.1		Chaperone DnaJ-domain superfamily protein	NA
Sapur.008G070100.1	24.44971826	2.656518108	0.163899863	16.20818	4.41E-59	2.81E-58	salmon	0.526843457	1.36E-12	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G69500.1	CYP704B1	cytochrome P450, family 704, subfamily B, polypeptide 1	cytochrome P450 family protein
Sapur.017G028100.1	76.59902573	3.408130516	0.211184678	16.13815	1.38E-58	8.69E-58	salmon	0.593831612	2.46E-16	GO:0005515	AT2G32360.1		Ubiquitin-like superfamily protein	nuclear pore localization protein NPL4
Sapur.007G061600.1	21.88042714	3.040320261	0.19306033	15.74803	7.09E-56	4.28E-55	salmon	0.50819082	1.09E-11		AT1G13220.1	LINC2	nuclear matrix constituent protein-related	nuclear matrix constituent protein, putative
Sapur.005G019700.1	268.7039522	1.908536151	0.121378802	15.7238	1.04E-55	6.26E-55	salmon	0.616124856	8.78E-18	GO:0005524,GO:0003676	AT5G27680.1	RECQSIM	RECQ helicase SIM	ATP-dependent DNA helicase RecQ
Sapur.T116900.1	31.73331095	4.995210921	0.320287506	15.59602	7.75E-55	4.60E-54	salmon	0.445016679	5.24E-09	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.016G156400.1	16.25857743	5.39870096	0.348292537	15.50048	3.44E-54	2.03E-53	salmon	0.434867483	1.26E-08	GO:0055114,GO:0020037,GO:0016705,GO:0005506	AT1G12740.1	CYP87A2	cytochrome P450, family 87, subfamily A, polypeptide 2	cytochrome P450 family protein
Sapur.002G162700.1	191.4519231	4.039400684	0.2608803	15.48373	4.47E-54	2.63E-53	salmon	0.322090196	3.89E-05					NA
Sapur.016G118100.1	237.0906435	3.611736096	0.233338316	15.47854	4.84E-54	2.84E-53	salmon	0.413467801	7.36E-08		AT1G20030.2		Pathogenesis-related thaumatin superfamily protein	allergen Pru du protein, putative
Sapur.019G003200.1	18.30700041	4.455637049	0.288741593	15.43123	1.01E-53	5.89E-53	salmon	0.447034925	4.38E-09	GO:0007165,GO:0005515,GO:0043531	AT5G36930.1		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.019G020900.1	6.678270321	2.49397707	0.161737102	15.41994	1.20E-53	7.01E-53	salmon	0.744774454	5.05E-29		AT3G18770.1		Autophagy-related protein 13	autophagy-like protein
Sapur.15WG091900.1	102.682243	1.024679326	0.06746155	15.18909	4.18E-52	2.37E-51	salmon	0.708808256	2.89E-25	GO:0008270,GO:0005515	AT5G40250.1		RING/U-box superfamily protein	RING finger protein
Sapur.15WG087800.1	7.776642285	3.430311878	0.229729469	14.93196	2.04E-50	1.13E-49	salmon	0.608531441	2.82E-17		AT3G28470.1	ATMYB35,TDF1	Duplicated homeodomain-like superfamily protein	NA
Sapur.T116100.1	18.25719595	3.184378118	0.213769429	14.89632	3.48E-50	1.91E-49	salmon	0.5619338	1.90E-14	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.006G137600.1	21.85656153	2.334615885	0.156855338	14.88388	4.19E-50	2.30E-49	salmon	0.671163697	6.70E-22	GO:0006355,GO:0005634	AT5G57420.1	IAA33	indole-3-acetic acid inducible 33	indole-3-acetic acid inducible protein
Sapur.003G158200.1	187.8128712	1.237684118	0.083730583	14.78174	1.92E-49	1.04E-48	salmon	0.715769078	6.01E-26		AT5G12950.1		Putative glycosyl hydrolase of unknown function (DUF1680)	DUF1680 domain protein
Sapur.T193300.1	13.86466253	4.845986404	0.330273295	14.67266	9.65E-49	5.18E-48	salmon	0.462696927	1.05E-09	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.001G049600.1	190.1839187	2.79082726	0.190519204	14.64854	1.38E-48	7.38E-48	salmon	0.678802256	1.53E-22		AT5G13170.1	SAG29	senescence-associated gene 29	bidirectional sugar transporter
Sapur.019G006900.1	16.49115011	4.699318221	0.322736665	14.56084	4.98E-48	2.65E-47	salmon	0.455965166	1.96E-09	GO:0007165,GO:0005515,GO:0043531	AT5G36930.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.005G078900.1	129.7248911	2.636583613	0.181629196	14.5163	9.55E-48	5.04E-47	salmon	0.432186635	1.58E-08		AT3G51430.1	SSL5,YLS2	Calcium-dependent phosphotriesterase superfamily protein	adipocyte plasma membrane-associated protein, putative

Sapur.013G054200.1	56.40068289	1.437172729	0.09984928	14.39347	5.69E-47	2.96E-46	salmon	0.653176001	1.84E-20	GO:0055114;GO:0016491;GO:0006520	AGI51870.1	GDH1	glutamate dehydrogenase 1
Sapur.019G092900.1	4.859936399	4.304679734	0.29946635	14.3745	7.48E-47	3.89E-46	salmon	0.579597467	1.82E-15	GO:0007165;GO:0005515;GO:0043531	AGI53690.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.005G123400.1	379.7713028	0.779402132	0.054385811	14.33088	1.40E-46	7.26E-46	salmon	0.688153877	2.27E-22	GO:0008328;GO:0004190	AGI53100.1		Eukaryotic aspartyl protease family protein
Sapur.006G080300.1	1020.730725	2.095808473	0.146319485	14.27473	3.11E-46	1.62E-45	salmon	0.503415017	1.82E-11	GO:0016746;GO:0008152	AGI38130.1	ATGPAT6,GPAT6	glycerol-3-phosphate acyltransferase 6
Sapur.015G011700.1	13.30138093	0.191262693	0.013163837	14.23364	5.67E-46	2.80E-45	salmon	0.555281815	4.38E-14	RPM1 interacting protein 4	AGI52670.1	RIN4	RPM1 interacting protein 4
Sapur.013G033300.1	613.175344	1.302496465	0.091549969	14.22717	6.21E-46	3.18E-45	salmon	0.424265119	2.65E-08	GO:0016747	AGI55457.6		Esterase/lipase/thioesterase family protein
Sapur.004G165200.1	435.3361601	1.368024682	0.0849924	13.7424	5.68E-43	2.75E-42	salmon	0.676274686	2.27E-22	GO:0055515;GO:0003676	AGI52788.1	AGDS	Arginosuccinate synthase family protein
Sapur.T114800.1	4.332702203	4.74824777	0.349316828	13.5932	4.38E-42	2.10E-41	salmon	0.480089896	1.99E-10	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.T117600.1	5.463786175	2.667977982	0.207533948	12.85514	8.05E-38	3.56E-37	salmon	0.575343023	6.16E-15	GO:0007165;GO:0005515	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.012G022000.1	2.820225515	4.830882224	0.376188224	12.83469	2.34E-38	4.08E-37	salmon	0.439478336	1.84E-10	GO:0007165;GO:0005515;GO:0043531	AGI56930.1		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.017G014000.2	9.462882513	2.960092936	0.152860082	12.8222	1.23E-37	5.43E-37	salmon	0.620629125	4.47E-18	GO:0008270	AGI50127.5		RING/FYVE/PHD zinc finger superfamily protein
Sapur.013G034900.1	3.985279251	2.149121246	0.138268556	12.37859	3.41E-35	1.46E-34	salmon	0.484812661	1.24E-10	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.015G031300.1	375.4827671	1.035025854	0.084272319	12.29247	9.94E-35	4.12E-34	salmon	0.497895927	3.25E-11		AGI51090.1		alpha/beta-Hydrolases superfamily protein
Sapur.010G027400.1	5.541376918	2.187656483	0.15147369	12.07573	1.07E-33	3.85E-33	salmon	0.447056535	6.13E-09	GO:0016747;GO:0016020;GO:0006633	AGI54760.1	KCS20	3-ketoacyl-CoA synthase 20
Sapur.T103100.1	3.055164279	4.593232095	0.318081882	12.05944	1.73E-33	7.02E-33	salmon	0.464868817	8.60E-10	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.T118000.1	2.414849803	4.116882353	0.343486283	11.98519	4.25E-33	1.71E-32	salmon	0.475352269	1.55E-10	GO:0007165;GO:0005515	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.009G028600.1	53.52297597	1.149899911	0.096475944	11.91489	9.90E-33	3.96E-32	salmon	0.572644133	4.65E-15		AGI55950.1	MEE60	maternal effect embryo arrest 60
Sapur.T103700.1	6.303445812	4.176391535	0.352430351	11.85027	2.15E-32	8.51E-32	salmon	0.41875589	4.83E-08	GO:0007165;GO:0005515	AGI56850.1		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.T193400.1	4.119143169	4.745842391	0.342188507	11.8212	3.03E-32	1.20E-31	salmon	0.460189845	1.26E-09	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.I59W127400.1	35.26890949	1.40009473	0.109327431	11.81115	3.42E-32	1.35E-31	salmon	0.602450469	7.00E-17	GO:0055114;GO:0016491;GO:0050664;GO:0004601	AGI51060.1	ATRBOHC,RBOHC,RHD2	NADPH/respiratory burst oxidase protein D
Sapur.005G029900.1	10.77628931	1.564131439	0.109051813	11.75681	4.44E-32	1.76E-31	salmon	0.444042674	3.11E-08	GO:0016887;GO:0070518;GO:0055114;GO:0003777;GO:0005871	AGI24480.2		ATP binding microtubule motor family protein
Sapur.005G029000.1	3.136.437091	1.696310017	0.145038225	11.69699	1.32E-31	5.15E-31	salmon	0.459294229	2.81E-11		AGI24238.1		serine hydrolase
Sapur.005G020400.1	2.715079563	1.782081647	0.152636906	11.62221	3.18E-31	1.23E-30	salmon	0.522242135	1.86E-11				NA
Sapur.006G149300.1	7.025189551	1.574083214	0.136430009	11.53766	8.52E-31	3.26E-30	salmon	0.642620044	6.22E-20				NA
Sapur.006G124600.1	408.5193681	0.815801793	0.07303386	11.48371	1.56E-30	6.06E-30	salmon	0.448203101	3.85E-09		AGI54830.1		NADP-binding Rossmann-fold superfamily protein
Sapur.002G143400.1	989.9039173	0.518017693	0.045570722	11.36734	6.08E-30	2.28E-29	salmon	0.647397556	5.10E-20	GO:0046983	AGI51260.3		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Sapur.010G066600.1	406.5754027	1.148121313	0.10120202	11.34283	8.05E-30	3.01E-29	salmon	0.519242942	5.15E-12	GO:0016872	AGI53520.1		Chalcone-flavanone isomerase family protein
Sapur.T117080.1	1.626016224	3.806238	0.339911927	11.05094	2.17E-28	7.80E-28	salmon	0.484083082	1.34E-10	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.017G088400.1	9923.902992	0.580541595	0.052533407	11.0509	2.17E-28	7.80E-28	salmon	0.636536869	1.24E-19	GO:0008295;GO:0050307;GO:0004014	AGI52470.4	SAMDC	S-adenosylmethionine decarboxylase proenzyme
Sapur.005G088500.1	18.21766082	0.884164	0.136407191	11.04608	2.21E-28	8.05E-28	salmon	0.468816879	7.81E-10				NA
Sapur.002G041200.1	185.0149397	1.423131788	0.132186913	10.83431	2.37E-27	8.42E-27	salmon	0.47829841	2.37E-10	GO:0006629	AGI52200.1	PLA IIIB,PLP8	PATATIN-like protein 8
Sapur.006G171300.1	748.7830921	0.875785359	0.080836232	10.83038	2.47E-27	8.76E-27	salmon	0.584749755	9.92E-16	GO:0016791;GO:0008152	AGI57732.1		Hydrolase phosphatase-related protein
Sapur.004G096100.1	6.796610978	0.881869273	0.078243301	10.87644	2.55E-27	9.07E-27	salmon	0.430904657	1.86E-08	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AGI58450.1	CYP735A1	cytochrome P450,family 735,subfamily A, polypeptide 1
Sapur.T116100.1	3.965005249	1.983231124	0.184617811	10.73881	6.68E-27	2.26E-26	salmon	0.618182299	1.71E-17	GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.008G089400.2	15.00518521	1.350847777	0.126783854	10.65455	1.66E-26	5.78E-26	salmon	0.502262632	2.05E-11		AGI50830.1		18S pre-ribosomal assembly protein gar2-related
Sapur.006G171200.1	1.554810301	2.528665184	0.239347187	10.61237	2.13E-26	7.32E-26	salmon	0.512722773	1.32E-12	GO:0008270			transmembrane proteins, putative
Sapur.007G116200.1	7.861246029	2.916758827	0.274639381	10.62025	2.40E-26	8.31E-26	salmon	0.35123846	6.03E-06		AGI59530.2	LAP3	Calcium-dependent phosphotriesterase superfamily protein
Sapur.005G142300.1	3.274038875	4.236112746	0.398445104	10.60499	2.82E-26	9.77E-26	salmon	0.382192837	7.94E-07	GO:0016020;GO:0006810;GO:0005215	AGI51660.1	ATNRAMP6,NRAMP6	NRAMP metal ion transporter 6
Sapur.016G042400.1	46.13531342	1.267664868	0.120316961	10.53308	4.59E-26	1.68E-25	salmon	0.518854938	3.37E-12		AGI58790.1		
Sapur.I59W150400.1	3.251268828	4.17887529	0.396270719	10.52898	6.35E-26	2.18E-25	salmon	0.42037347	9.40E-08		AGI52390.1		PAR1 protein
Sapur.005G074000.1	21.25435608	1.293155837	0.122763108	10.53085	6.92E-26	2.37E-25	salmon	0.548968208	8.71E-14	GO:0004648;GO:0004672	AGI57861.1		ACT-like protein tyrosine kinase family protein
Sapur.001G105500.1	80.40203089	1.74638808	0.166168426	10.49777	8.84E-26	3.03E-25	salmon	0.466406026	7.40E-10		AGI51460.1		
Sapur.006G031200.1	32.2873688	1.660231205	0.158257222	10.48825	1.94E-25	6.66E-25	salmon	0.460060855	1.35E-09		AGI50150.1		Plant protein of unknown function (DUF247)
Sapur.019G067600.2	8.116614994	2.600329389	0.249802866	10.40873	2.26E-25	7.67E-25	salmon	0.407412843	1.19E-07	GO:0016020;GO:0008378;GO:0006486	AGI53430.1		Galactosyltransferase family protein
Sapur.001G177600.2	81.4844114	1.027732202	0.103521519	10.40762	2.26E-25	7.76E-25	salmon	0.474092319	1.60E-10				
Sapur.T193000.1	4.820261706	3.749320836	0.360440839	10.40304	2.43E-25	8.22E-25	salmon	0.457667075	1.68E-09	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.006G149400.1	3.315564285	3.856482949	0.339477239	10.34719	4.31E-25	1.45E-24	salmon	0.501813676	2.15E-11				
Sapur.019G067200.1	3.978009477	5.613375401	0.541937463	10.23414264	1.61E-24	5.79E-25	salmon	0.473395957	1.14E-10	GO:0007165;GO:0005515;GO:0043531	AGI56930.1		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.I59W121900.1	134.7115147	0.596282604	0.058501155	10.19266	2.14E-24	7.08E-24	salmon	0.594977785	2.24E-16		AGI24910.1		Protein of unknown function (DUF579)
Sapur.014G076400.2	1.006803943	3.267664223	0.32763074	9.97488	6.34E-24	2.27E-23	salmon	0.460786357	1.26E-09	GO:0055085;GO:0016020;GO:0008811;GO:0005216	AGI53461.2	ACBK1,ATCNGC10,CNGC10	cyclic nucleotide-gated ion channel protein, putative
Sapur.016G256200.1	31.45689212	1.601488091	0.159350345	10.04998	9.19E-24	2.99E-23	salmon	0.422066403	5.08E-08		AGI53163.1		hypothetical protein
Sapur.T114900.1	2.482160786	3.146420564	0.314004154	10.01072	1.17E-23	4.40E-23	salmon	0.47927033	1.20E-10	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.T031100.1	52.93969078	1.533616143	0.152908565	9.963163	2.21E-23	7.12E-23	salmon	0.438158526	9.52E-09		AGI53500.1		NA
Sapur.016G024700.1	58.02182639	1.677284973	0.167455287	9.966039	2.12E-23	6.67E-23	salmon	0.438328721	5.64E-10		AGI53700.1		ATP binding;nucleic acid binding;helicases
Sapur.019G091900.1	39.26949022	1.670397821	0.173337898	9.626553	5.60E-22	1.75E-21	salmon	0.47361851	3.73E-10		AGI53100.1		
Sapur.T117200.1	1.463946685	5.241813552	0.545009	9.615091	1.81E-21	5.54E-21	salmon	0.443898296	1.62E-09	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.016G015700.1	2.30851775	1.892132091	0.409067176	9.514653	1.82E-21	5.61E-21	salmon	0.397231529	2.59E-07		AGI52232.1		cysteine-rich TM module stress tolerance protein
Sapur.T193200.1	2.516301152	3.327023611	0.349552151	9.507081	1.96E-21	6.03E-21	salmon	0.469875579	5.78E-10	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.010G066500.1	421.3420229	0.661282622	0.070065373	9.45572	2.18E-21	6.72E-21	salmon	0.559864036	2.48E-14	GO:0004648;GO:0004679	AGI52750.1		Protein tyrosine kinase family protein
Sapur.016G247200.1	156.4356681	0.969663822	0.102115167	9.495757	2.19E-21	6.72E-21	salmon	0.441328881	7.23E-09	GO:0004674;GO:0048544;GO:0006488;GO:0004672	AGI52760.1		S-locus lectin protein kinase family protein
Sapur.015G087200.1	1.690315168	2.748177203	0.291468691	9.427857	3.16E-21	9.68E-21	salmon	0.419848026	8.88E-09	GO:0055114;GO:0020037;GO:0016705;GO:0005506	AGI57241.5	CYP72A15	cytochrome P450, family 72, subfamily A, polypeptide 15
Sapur.013G021300.1	151.3700159	0.866756115	0.09369095	9.29297	2.72E-20	8.34E-20	salmon	0.527122773	1.32E-12	GO:0008270	AGI51730.1		CW-type Zinc Finger
Sapur.T140100.1	4.757029144	5.608369688	0.17467558	9.287913	3.13E-20	9.61E-20	salmon	0.508787832	3.76E-16	GO:0005524	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.010G076300.1	32.4649924	1.402746306	0.152608937	9.186351	4.06E-20	1.21E-19	salmon	0.41372013	5.49E-08	GO:0055114;GO:0016491	AGI52100.1	ATGA2OX8,GA2OX8	gibberellin 2-oxidase 8
Sapur.006G081000.1	92.53617999	1.025616	0.113046262	9.105604	4.58E-20	2.51E-19	salmon	0.500787836	3.20E-12	GO:0005975;GO:0004553	AGI50485.1		glycoside hydrolase family 3 protein
Sapur.016G199700.1	329.5623133	0.81636504	0.091273722	8.944141	3.75E-19	1.09E-18	salmon	0.493891593	4.93E-11	GO:0006355;GO:0003677	AGI53180.1	ANAC083,NAC083,VNI2	NAC transcription factor
Sapur.T115900.1	21.76887223	1.055633846	0.115300273	8.984356	3.97E-19	1.17E-18	salmon	0.426651091	2.52E-08	GO:0005515	AGI51910.1	AIH1,CIM1,SAJ1,AIH1	COPII signalosome complex subunit 5
Sapur.016G128400.1	14.8941486	1.875436165	0.211642868	8.861325	7.91E-19	2.27E-18	salmon	0.490607279	6.91E-11	GO:0046872;GO:0030001	AGI52605.2		Heavy metal transport/detoxification superfamily protein
Sapur.013G033100.1	181.934674	0.887562854	0.102475451	8.661393	4.68E-18	1.31E-17	salmon	0.492787641	5.12E-11				hypothetical protein
Sapur.005G170800.1	244.3636581	0.965660591	0.040219542	8.617441	6.85E-18	1.92E-17	salmon	0.527470331	1.91E-12		AGI52970.1		Protein of unknown function (DUF506)
Sapur.018G077200.1	310.7173393	0.436000503	0.051851382	8.426593	3.56E-17	9.77E-17	salmon	0.521307976	2.56E-12	GO:0055115;GO:0006468;GO:0005524;GO:0004672	AGI23950.1		Leucine-rich repeat protein kinase family protein
Sapur.003G130500.1	2.445738847	2.791327377	0.332452647	8.396165	4.61E-17	1.26E-16	salmon	0.369601589	1.34E-07	GO:0008017;GO:0009506;GO:0005634	AGI27920.1	MAPRS-B	microtubule-associated protein MAPRS-1a
Sapur.008G089400.1	9.948301013	0.96461468	0.115465546	8.360723	5.78E-17	1.57E-16	salmon	0.47361851	7.78E-10		AGI50830.4		18S pre-ribosomal assembly protein gar2-related
Sapur.T117300.1	1.463946685	5.241813552	0.630666959	8.260026	1.13E-16	2.96E-16	salmon	0.414688371	5.68E-08	GO:0016021	AGI57520.1		Auxin-responsive family protein
Sapur.004G039600.1	40.25083309	0.97378828	0.117496794	8.287767	1.15E-16	3.12E-16	salmon	0.477663803	2.52E-10	GO:0016021;GO:0006810;GO:0055137	AGI56120.1	ATENT1,ENT1,FUR1	Major facilitator superfamily protein
Sapur.013G037200.1	27.30788124	0.804756471	0.112474226	8.188449	2.65E-16	7.07E-16	salmon	0.476617172	7.96E-10	GO:0055085;GO:0016020;GO:0015297;GO:0015138;GO:0006855	AGI57835.1		MATE efflux family protein
Sapur.010G051100.1	4004.77626	0.191352279	0.112016627	8.153686	3.51E-16	9.39E-16	salmon	0.442639378	6.45E-09		AGI52950.1		Putative glycosyl hydrolase of unknown function (DUF1680)
Sapur.010G080900.1	816.185587	0.392516984	0.04931967	8.009762	1.15E-15	3.01E-15	salmon	0.469478815	3.40E-11	GO:0005515	AGI50190.1		Oxticoagulase(Hoa)/Beng(p family protein
Sapur.003G007500.1	7.353512896	2.021281793	0.252508047	7.966183	1.64E-15	4.27E-15	salmon	0.555020943	1.52E-11		AGI57220.1	ARF22	auxin response factor 22
Sapur.017G111400.1	344.1080335	0.488245498	0.06178223	7.87046	3.53E-15	9.15E-15	salmon	0.50673086	1.26E-11	GO:0006468;GO:0005524;GO:0004672	AGI56150.1	TMK1	transmembrane kinase 1
Sapur.T025600.1	16.03175853	1.681383507	0.21677582	7.76544	8.73E-15	2.26E-14	salmon	0.304827759	0.000003057		AGI62080.1	AHL1,ATAHL1	AT-hook motif nuclear localized protein 1
Sapur.016G084300.1	7.9565283	1.170135856	0.151419291	7.72816	1.09E-14	2.78E-14	salmon	0.47031599	5.13E-10				NA
Sapur.005G057100.1	28.47957938	0.670817463	0.087186758	7.694029	1.41E-14	3.62E-14	salmon	0.35352211	4.43E-06		AGI63955.1		alpha/beta-Hydrolases superfamily protein
Sapur.017G051200.1	48.19858956	1.12325572	0.147970785	7.587533	3.26E-14	8.19E-14	salmon	0.508588228	1.04E-11	GO:0016491;GO:0008152	AGI51980.4		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.004G087300.1	640.1747372	0.641434469	0.058870684	7.498378	6.46E-14	1.61E-13	salmon	0.445291717	1.08E-09	GO:0016021;GO:0042552;GO:0006508	AGI18620.1	ATRBI,12,RBL12	rhomboid-related intramembrane serine protease family protein, putative
Sapur.009G047500.1	21.62168134	1.06084568	0.142691138	7.434546	1.05E-13	2.59E-13	salmon	0.423549603	3.27E-08		AGI50500.1	AMMRBD1,MYB68	myb domain protein 68
Sapur.013G022100.1	4.567319246	2.545684263	0.338288885	7.413389	1.21E-13	2.03E-13	salmon	0.454847154	4.68E-09	GO:0005663;GO:0003824	AGI47050.1		NAD(P)-binding Rossmann-fold superfamily protein
Sapur.004G020800.1	1522.714919	0.762207167	0.102932292	7.404865	1.33E-13	3.23E-13	salmon	0.4118759	8.35E-08	GO:0005085;GO:0016021	AGI51240.1	ATSTP1,STP1	sugar transporter 1
Sapur.006G170000.2	3.851379804	1.435204126	0.195108053	7.354237	1.89E-13	4.64E-13	salmon	0.468806952	6.36E-10	GO:0003677	AGI62552.2		AP2/B3-like transcriptional factor family protein
Sapur.I59W102100.1	0.686614934	3.067838806	0.380741181	7.318829	2.23E-13	5.48E-13	salmon	0.481835135	1.67E-10	GO:0055085;GO:0015297;GO:0016021	AGI57220.1	1-OctOL,AOCT1	organic cation/carnitine transporter 1
Sapur.T116500.1	2.709344008	1.640322572	0.226619954	7.14277	9.51E-13	2.19E-12	salmon	0.418523819	4.90E-08	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.005G082800.1	1079.125455	0.437988284	0.039125623	7.139169	1.05E-12	2.41E-12	salmon	0.410297562	9.46E-08	GO:0055114;GO:0016491	AGI56500.1		2-oxoglutarate(2oxo) and Fe(II)-dependent oxygenase superfamily protein
Sapur.005G019600.1	40.17906795	2.298272203	0.331206712	6.940488	3.91E-12	8.15E-12	salmon	0.343875573	1.04E-05		AGI55470.1		Actin-binding RhoJ/Rac/Rho family protein
Sapur.005G030000.1	56.42215005	1.604358023	0.231486427	6.711337	1.91E-11	3.98E-11	salmon	0.38667587	5.61E-07	GO:0016788	AGI56150.1		GDSL-like Lipase/Acylhydrolase superfamily protein
Sapur.004G090600.1	105.7682537	0.898869819	0.133281449	6.691628	2.21E-11	5.03E-11	salmon	0.35423804	4.67E-06		AGI19190.1		alpha/beta-Hydrolases superfamily protein
Sapur.004G080400.1	10.65741996	2.254967429	0.34019474	6.624368	3.39E-11	7.67E-11	salmon	0.425672093	2.72E-08	GO:0003677			
Sapur.012G012500.1	21.49773832	1.111818869	0.172405074	6.448876	1.13E-10	2.50E-10	salmon	0.357595621	4.17E-06	GO:0004648;GO:0004672	AGI23190.1	AT-RLK3,CRK11	cysteine-rich RLK (RECEPTOR-like protein kinase) 11
Sapur.006S054000.6	7.233067027	1.060855629	0.164888851	6.447037	1.14E-10	2.53E-10	salmon	0.367984017	2.45E-07	GO:0055114;GO:0016491;GO:0006520	AGI51730.1	GDH1	glutamate dehydrogenase 1
Sapur.012G015500.1	0.851112345	2.759171823	0.434288614	6.354559	2.08E-10	4.59E-10	salmon	0.35104785	6.55E-06	GO:0005515	AGI51400.1		ARM repeat superfamily protein
Sapur.003G031900.1	2184.82187	0.312815501	0.05147831	6.07666	1.23E-09	2.61E-09	salmon	0.412309913	7.69E-08	GO:0005515;GO:0003824;GO:0005471	AGI82300.1	ATNTT1,NTT1	nucleotide transporter 1
Sapur.I59W126200.1	46.15541779	0.573109942	0.098477766	5.799374	6.68E-09	1.38E-08	salmon	0.316849709	4.46E-06				NA
Sapur.T116000.1	0.452249887	2.369950033	0.45675419	5.460761	6.70E-07	1.27E-06	salmon	0.401707317	1.84E-07	GO:0007165;GO:0005515	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.004G088300.1	7.664415674	1.523183394	0.354405828	4.331117	1.54E-05	2.75E-05	salmon	0.669078029	4.61E-24		AGI56740.1		PLC-like phosphodiesterase superfamily protein
Sapur.T114700.1	12.61562881	1.002183868	0.230408404	4.192386	2.76E-05	4.79E-05	salmon	0.325660707	3.16E-05	GO:0007165;GO:0005515;GO:0043531	AGI56930.2		Disease resistance protein (TIR-NBS-LRR class) family
Sapur.005G196500.1	299.5786269	0.102207723	0.075114999	3.844763	0.000120659	0.000201866	salmon	0.224837012	0.00072138		AGI22600.1		Pentatricopeptide repeat (PPR)-containing protein
Sapur.008G092300.1	1368.587536	0.174392624	0.056958935	3.061725	0.002200652	0.00337966	salmon	0.200607028	0.011762003		AGI57260.1	LINC1	little nuclei 1
Sapur.005G020100.1	978.2142766	0.102372582	0.038547074	2.656011	0.017362051	0.027833339	salmon	0.167638041	0.430098926		AGI57573.1		Sec14p-like phosphatidylinositol transfer family protein
Sapur.013G105300.2	2.326997859	0.022227664	0.207950805	0.106889	0.914879691	0.944519961	salmon	0.137387038	1.62E-06	GO:0006355;GO:0005739;GO:0003690	AGI66230.1		Mitochondrial transcription termination factor family protein
Sapur.016G278800.1	0.033351202	0.233595159	2.333869965	0.100089	0.920270116	NA	salmon	0.572155584	6.97E-15		AGI38620.2	HSRG,MUR1A,UXE1	NAD(P)-binding Rossmann-fold superfamily protein
Sapur.005G088400.1	0.021621139	0.089326305	2.786460079	0.031057	0.974639279	NA	salmon	0.38619665	0.000167	GO:0016787	AGI17800.1	ARA4,CATGP2,ATRACL,ATR	Arabidopsis RAC like 1
Sapur.010G021800.1	2324.215399	12.81579287	0.276660109	45.82622	0	0	salmon	0.642739897	1.13E-19	GO:0020246;GO:0005975;GO:0004553	AGI20710.1	BGAL7	beta-galactosidase 7
Sapur.005G064900.1	199.9787861	11.76464465	0.219460703	46.23768	0	0	salmon	0.882014778	1.08E-52		AGI61630.1		
Sapur.010G090200.1	565.8771134	10.73461760	0.234802743	43.17131	0	0	salmon	0.615867118	2.78E-30	GO:0005885;GO:0016021	AGI51260.1	ATSTP9,STP9	sugar transporter 1
Sapur.T118300.1	1026.446884	12.63766861	0.27211925	46.41856	0	0	salmon	0.39419665	1.02E-07	GO:0003824	AGI56050.1	AHDC5,T-ZN2DL7	early nodulin-like protein 7
Sapur.003G064200.1	103.0428632	4.59852613	0.103913332	44.2631	0	0	salmon	0.854653693	2.29E-46	GO:0009341;GO:0005975;GO:0004553;GO:0030246;GO:0004553	AGI77410.1	BGAL16	beta-galactosidase 16
Sapur.005G086600.1	387.4131215	9.785014005	0.144026763	39.98327	0	0	salmon	0.764962172	4.88E-29	GO:0005773	AGI56420.1	HCHOD,MLO1,WLI15	Homodomain-like superfamily protein
Sapur.001G195000.1	972.7626066	9.102458580	0.076034459	45.26223	0	0	salmon	0.892005552	5.62E-57	GO:0008168;GO:0008152	AGI76140.1		S-adenosylmethionine-dependent methyltransferases superfamily protein
Sapur.006G153000.1	638.5453868	11.90763161	0.2606927	45.9487	0	0	salmon	0.825303025	1.58E-49	GO:0006508;GO:0004175	AGI54680.1		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Sapur.005G148600.1	474.6602259	10.19358268	0.060585055	44.99449	0	0	salmon	0.897586919	7.00E-57	GO:0046355;GO:0003677	AGI21340.1		Dof-type zinc finger DNA-binding family protein
Sapur.006G091500.1	270.1057364	8.361482474	0.217828813	42.51515	0	0	salmon	0.773101118	1.86E-32		AGI44050.1		PQ-loop protein family protein / transmembrane family protein
Sapur.009G140200.1	551.8258507	9.755357176	0.2087194	46.64493	0	0	salmon	0.8	1.01E-60	GO:0016021	AGI57910.1	TET15	tetraspanin 15
Sapur.007G069800.1	351.7042492	7.202875083	0.150897514	64.95413	0	0	salmon	0.891977977	3.88E-55	GO:0016597;GO:0008152	AGI56890.1	ACR1	ACT domain repeat 1
Sapur.007G080800.1	160.9749326	5.987325168	0.119587564	50.06646	0	0	salmon	0.857838531	1.48E-46		AGI22790.1		hypothetical protein
Sapur.007G102300.1	611.8087942	12.52771892	0.30265788	41.39234	0	0	salmon	0.652429496	2.11E-20	GO:0005975;GO:0004553	AGI19620.1		Glycosyl hydrolase family protein
Sapur.008G087000.1	2279.279632	10.17717209	0.14696449	67.6503	0	0	salmon	0.826083884	1.50E-40		AGI20980.1		
Sapur.009G037300.1	1666.742626	5.017869971	0.089553283	56.032	0	0	salmon	0.858295566	9.12E-47	GO:2001070;GO:0008824	AGI51260.2		Carbohydrate-binding-like fold
Sapur.I59W100400.1	520.9997098	7.452890269	0.194946911	38.22667	0	0	salmon	0.726705848	4.62E-27	GO:0005975;GO:0004553	AGI24380.1		Glycosyl hydrolase family protein
Sapur.010G134000.1	1625.299089	6.274820488	0.117276619	53.50536	0	0	salmon	0.785588892	3.93E-34	GO:0016798;GO:0016020	AGI51250.2	AtGUS1,

Sapur.01G0370200.1	10.08634441	4.603570802	0.236357134	19.47718	1.71E-84	1.59E-83	salmon	0.748641162	1.92E-29			ATLG14750.1	SDS	Cyclin family protein	NA
Sapur.01G0245100.1	14.98903622	2.171098887	0.162834688	19.47434	1.81E-84	1.68E-83	salmon	0.604464434	5.05E-17			ATLG17030.1			NA
Sapur.01G0261300.1	17.89973948	3.08691546	0.158740604	19.4456	3.18E-84	2.95E-83	salmon	0.65087233	2.5E-18			ATLG19710.1	TBL42	TRICHOME BIREFRINGENCE-LIKE 42	Pmr5/CaLigo GDSL/SGNH-like acyl-esterase family protein
Sapur.01G0245000.1	155.9482608	5.96462702	0.101217468	19.40997	6.36E-84	5.86E-83	salmon	0.70202885	1.27E-24			ATLG21390.1	ATBAG7,BAG7	BCL-2-associated athanogene 7	BCL-2-associated athanogene protein, putative
Sapur.01G0405300.1	10.5613322	4.971292769	0.256456634	19.38593	9.52E-84	8.73E-83	salmon	0.64093681	9.26E-20	GO:0006355,GO:0003677		ATLG27160.1	anac086,NAC086	NAC domain containing protein 86	NA
Sapur.01G0870400.1	16.22772619	2.56523641	0.132988629	19.28914	6.63E-83	6.02E-82	salmon	0.70252605	1.14E-24	GO:0043565,GO:0006355,GO:0003700		ATLG5273.1	ATWRKY2,WRKY2	WRKY DNA-binding protein 2	NA
Sapur.00B0239300.1	114.8084604	3.353303303	0.070421195	19.24567	1.53E-82	1.38E-81	salmon	0.78626331	3.36E-34			ATLG27430.1		C2H2 and C2HC zinc fingers superfamily protein	C2H2-type zinc finger protein
Sapur.00G0188600.1	8.373312504	5.407783354	0.292078269	18.82285	4.91E-79	4.21E-78	salmon	0.56818879	1.57E-16	GO:0016020,GO:0016586,GO:0008519,GO:0072488		ATLG19110.1	AMT1;1,ATAMT1,ATAMT1	ammonium transporter 1;1	ammonium transporter 1 protein
Sapur.00G0207900.1	22.26513933	4.122054822	0.207415148	18.75865	1.65E-78	1.40E-77	salmon	0.657419188	8.57E-21	GO:0016747		ATLG26040.1	HXXXD-type acyl-transferase family protein		anthranilate N-benzoyltransferase, putative
Sapur.01G0260600.1	5.303260608	5.788330409	0.312961203	18.75679	1.8E-78	1.48E-77	salmon	0.729288399	3.46E-27	GO:0005488,GO:0006622		ATLG5145.2	Protein kinase superfamily	Protein kinase superfamily protein	tyrosine kinase family protein
Sapur.15W0110900.1	4.92005602	5.480391142	0.292515745	18.73273	2.68E-78	2.27E-77	salmon	0.6791782	1.42E-22	GO:0055085,GO:0046873,GO:0030001,GO:0016020		ATLG3160.1	ZIP10	zinc transporter 10 precursor	Fe(2+) transport 5
Sapur.01G0750300.1	103.2187368	2.5454941	0.150706689	18.73117	2.76E-78	2.34E-77	salmon	0.726464807	4.91E-27			ATLG4020.1			NA
Sapur.00G0672300.1	16.23685565	2.866104984	0.152883905	18.61612	2.38E-77	1.99E-76	salmon	0.675983823	2.65E-22			ATLG5340.1	BOB1	HSP20-like chaperones superfamily protein	p23-like N/UD (nuclear distribution) C-like domain protein
Sapur.00G0261000.1	462.3812218	2.538294208	0.08267948	18.59266	1.53E-76	1.22E-74	salmon	0.792904796	3.55E-36	GO:0006355,GO:0003700		ATLG7450.1		Integrase-type DNA-binding superfamily protein	dehydration responsive element-binding protein 2G, putative
Sapur.00G0298400.1	9.946792223	3.975837342	0.217261448	18.30147	8.06E-75	6.46E-74	salmon	0.661332417	4.22E-21	GO:0008233,GO:0006508		ATLG627330.1	BETA-VPE,BETAVPE	beta vacuolar processing enzyme	vacuolar processing enzyme, beta
Sapur.00G0250400.1	30.12826343	3.567387743	0.193486788	18.1065	2.63E-73	2.07E-72	salmon	0.70601527	2.07E-25			ATLG2136.1		VQ motif-containing protein	MKS1, putative
Sapur.15W0209800.1	1879.119542	6.640574413	0.035488713	18.05009	7.88E-73	6.17E-72	salmon	0.794617758	2.02E-35			ATLG24300.2	ATSS1,SS,SS1	Glycogen/starch synthases, ADP-glucose type	soluble starch synthase 1/amylopectin protein
Sapur.00G0292500.1	55.01008842	3.304062086	0.094296264	17.95566	4.27E-72	3.32E-71	salmon	0.77701592	9.42E-35			ATLG12210.2		DNA binding	DNA-binding protein
Sapur.00B0280300.1	759.8017671	5.730365658	0.04496467	17.93668	5.1E-72	4.76E-71	salmon	0.79439565	2.71E-33			ATLG03520.1	YqcH/sub-GKF domain of gyg1p superfamily protein	RsfdAY87AC domain protein	RsfdAY87AC domain protein
Sapur.01T0240300.1	119.310338	1.72385426	0.096497496	17.88466	1.54E-71	1.19E-70	salmon	0.718664819	3.08E-26	GO:0046983		ATLG34140.1	FMA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	transcription factor FAMA protein, putative
Sapur.00G0116700.1	99.73395769	1.388024008	0.07762268	17.88222	1.62E-71	1.25E-70	salmon	0.726883845	4.62E-27	GO:0045454,GO:0015035,GO:0009055,GO:0005556		ATLG11920.1		glutaredoxin-related	electron transporter, putative
Sapur.01G0151500.1	74.58496618	1.497135289	0.083832228	17.85956	2.44E-71	1.87E-70	salmon	0.73509055	5.96E-28						NA
Sapur.01G0250100.1	4.866330371	5.015156631	0.281216369	17.83124	4.04E-71	3.10E-70	salmon	0.688546679	2.35E-23						NA
Sapur.00G0621200.1	6.447092761	6.012735263	0.225632027	17.78521	9.20E-71	7.01E-70	salmon	0.746133519	3.54E-29			ATLG16030.1	AtMYB43,MYB43	myb domain protein 43	Myb-related transcription factor
Sapur.00G0298500.1	8.321108238	5.963885363	0.28477414	17.7174	1.4E-70	1.07E-69	salmon	0.59465861	2.9E-16	GO:0008544		ATLG11340.1		S-locus lectin protein kinase family protein	NA
Sapur.01G0104100.1	4.46412295	6.806985515	0.272380003	17.65805	8.82E-70	6.62E-69	salmon	0.72349539	1.13E-27	GO:0055085,GO:0046873,GO:0030001,GO:0016020		ATLG2460.1	ZIP7	zinc transporter 7 precursor	iron regulated transporter
Sapur.01G0250800.1	49.59478818	1.698880213	0.096939864	17.52788	8.78E-69	6.47E-68	salmon	0.795204164	1.68E-35			ATLG4240.1			WRC protein
Sapur.00S0260200.1	16.45103075	2.266407107	0.101140464	17.44582	3.75E-68	2.76E-67	salmon	0.65087233	2.97E-20	GO:0055114,GO:0020037,GO:0016705,GO:0005506		ATLG4640.1	CYP86A6	cytochrome P450, family 87, subfamily A, polypeptide 6	cytochrome P450 family protein
Sapur.01G0261100.1	123.9629269	2.945467802	0.16955146	17.37622	1.25E-67	9.05E-67	salmon	0.803302738	2.04E-36	GO:0046983,GO:0003677		ATLG4820.1	AGL48	AGAMOUS-like 48	MADS-box protein AGL85, putative
Sapur.01G0820500.1	56.03823873	2.324604201	0.136097911	17.28474	6.13E-67	4.40E-66	salmon	0.652708098	1.99E-20	GO:0003700,GO:0006355,GO:0009534		ATLG5667.1	PYR6	P-loop containing nucleoside triphosphate hydrolases superfamily protein	NA
Sapur.00T0271100.1	8.788690601	2.778197022	0.162326153	17.11512	1.14E-65	8.06E-65	salmon	0.79281847	6.92E-36						NA
Sapur.01G0270300.1	5.59404588	4.453819172	0.260342347	17.10777	1.16E-65	8.18E-65	salmon	0.75902102	4.54E-27	GO:0005634		ATLG14750.1	SDS	Cyclin family protein	cyclin, putative
Sapur.01G0141500.1	5.614163068	2.943081571	0.172187112	17.09235	1.68E-65	1.19E-64	salmon	0.76051474	7.15E-31						hypothetical protein
Sapur.00G0280100.1	20.63816569	2.360263271	0.13866195	16.92609	2.96E-64	2.06E-63	salmon	0.653905538	1.61E-20	GO:0005507,GO:0055114,GO:0016491		ATLMCO4,RX12,LAC4,LMC	Laccase/Diphenol oxidase family protein		laccase
Sapur.01G0284900.1	65.09822001	1.737440245	0.102739907	16.9127	3.63E-64	2.50E-63	salmon	0.760672132	6.84E-31	GO:0016887,GO:0005524,GO:0055085,GO:0042626,GO:0016021,GO:0006810		ATLG30410.1	ATMRP13,MRP13	multidrug resistance-associated protein 13	magnesium transporter MRS2-I
Sapur.01G0280800.1	496.8253158	1.730334009	0.043414117	16.85222	9.37E-64	6.45E-63	salmon	0.783674076	5.91E-34	GO:0016887,GO:0005524,GO:0046873,GO:0005385,GO:0016020		ATLG4560.1	ATMATR4,MATR,MRS2-2	magnesium transporter	breast carcinoma amplified sequence protein, putative
Sapur.15G0260700.1	256.1077746	5.245663223	0.031135793	16.8477	1.08E-63	7.45E-63	salmon	0.763823135	2.80E-31	GO:0006397		ATLG18165.1	MOS4	modifier of snc1,4	NA
Sapur.01B0261100.1	27.3947362	3.227260614	0.138240834	16.83489	1.35E-63	9.24E-63	salmon	0.708110842	3.37E-25	GO:0043565,GO:0006355,GO:0003700		ATLG27100.1	WRKY26	WRKY DNA-binding protein 26	WRKY transcription factor
Sapur.00G0279800.1	40.20865155	2.025351395	0.122553664	16.81338	1.96E-63	1.33E-62	salmon	0.662637142	2.32E-21	GO:0055085,GO:0055114,GO:0016491		ATLMCO4,RX12,LAC4,LMC	Laccase/Diphenol oxidase family protein		NA
Sapur.00G0280800.1	6.581840687	4.550155	0.276075507	16.7586	4.90E-62	3.31E-62	salmon	0.676689755	2.31E-22			ATLMCO4,RX12,LAC4,LMC			NA
Sapur.01G0211700.1	10.40097824	3.500425005	0.185534663	16.7572	5.02E-62	3.39E-62	salmon	0.694476237	8.56E-23						transmembrane protein, putative
Sapur.01G0261000.1	8.543177739	4.309447943	0.257360128	16.74682	6.18E-62	4.17E-62	salmon	0.518013059	1.70E-12	GO:0006468,GO:0006672		ATLG1760.1	ARK1,RR1	receptor kinase 1	NA
Sapur.01G0280500.1	115.4850317	2.814381145	0.098110708	16.5762	1.69E-61	1.08E-60	salmon	0.669972054	9E-24			ATLG4910.1			hypothetical protein
Sapur.00S0141900.1	44.28092173	3.571172361	0.094825609	16.56907	1.17E-61	7.73E-61	salmon	0.679619958	1.30E-22	GO:0003246,GO:0005975,GO:0004553		ATLG7410.1	BGAL16	beta-galactosidase 16	beta-galactosidase
Sapur.01G0280400.1	58.46622398	3.134341669	0.09260435	16.56663	1.21E-61	8.05E-61	salmon	0.753774607	4.60E-30	GO:0046983		ATLG10610.1		basic helix-loop-helix (bHLH) DNA-binding superfamily protein	NA
Sapur.01B0245100.1	5.362505853	5.341010059	0.322965567	16.5449	1.74E-61	1.15E-60	salmon	0.585709584	7.79E-16						NA
Sapur.01G0251100.1	45.98558709	2.018211811	0.09008287	16.51811	1.94E-61	1.28E-60	salmon	0.734576767	7.1E-27			ATLG2520.1	UDP-glucosyltransferase 72	UDP-glucosyltransferase 72	sulfoglucan 6-sulfotransferase
Sapur.00T0301000.1	153.5461702	1.418971278	0.08720136	16.30564	9.00E-60	5.79E-59	salmon	0.704858625	6.89E-25	GO:0016757		ATLG6240.1		F-box family protein	DUF563 family protein
Sapur.01G0970600.1	3092.419232	1.341101063	0.082303503	16.29713	1.03E-59	6.65E-59	salmon	0.732698919	1.08E-27	GO:0005507,GO:0055114,GO:0016491		ATLMCO4,RX12,LAC4,LMC	Laccase/Diphenol oxidase family protein		laccase 1a
Sapur.00G0134000.1	3.934410894	4.672167243	0.276254994	16.02601	8.41E-58	5.12E-57	salmon	0.712434306	1.28E-25	GO:0018024,GO:0005506,GO:0046872		ATLG4280.1	SDG31,SUVH4	SET-domain protein, putative	SET domain protein, putative
Sapur.01G0233300.1	27.08196342	1.941677163	0.121957334	15.92098	4.53E-57	2.79E-56	salmon	0.65838367	1.14E-20	GO:0004648,GO:0005524,GO:0006972,GO:0005634		ATLG5830.1		Concanavalin A-like lectin protein kinase family protein	lectin-domain receptor kinase
Sapur.01G0280200.1	169.10117	1.588605104	0.185534663	16.7572	5.02E-62	3.39E-62	salmon	0.694476237	8.56E-23	GO:0004412,GO:0005840,GO:0003735		ATLG6520.1		Ribosomal protein S10p/S20e family protein	40S ribosomal protein S10
Sapur.01G0261000.1	8.543177739	4.309447943	0.257360128	16.74682	6.18E-62	4.17E-62	salmon	0.518013059	1.70E-12	GO:0006468,GO:0006672		ATLG6190.1	RLA17	FASCICLIN-like arabinogalactan protein 17 precursor	fasciclin-like arabinogalactan protein
Sapur.01G0280100.1	115.4850317	2.814381145	0.098110708	16.5762	1.69E-61	1.08E-60	salmon	0.670839135	1.30E-22			ATLG8030.1	HCT	hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase
Sapur.01G0193000.1	9.997164305	3.104061836	0.197942557	16.68163	2.02E-55	1.21E-54	salmon	0.62471293	2.26E-18			ATLG8340.1	RLA7	FASCICLIN-like arabinogalactan protein 7	fasciclin-like arabinogalactan protein
Sapur.01G0261400.1	5.505503381	4.351723398	0.303740075	15.52349	1.36E-54	1.38E-53	salmon	0.611337651	1.86E-17			ATLG4440.1		VQ motif-containing protein	VQ motif protein
Sapur.01B0278800.1	1552.727864	1.074145825	0.069348626	15.48907	4.11E-54	2.42E-53	salmon	0.712286198	1.33E-25			ATLG8280.1		Tetratricopeptide repeat (TPR)-like superfamily protein	eukaryotic translation initiation factor 3 subunit, putative
Sapur.01G0134500.1	5.700291889	3.147545991	0.204785784	15.36994	2.68E-53	1.51E-52	salmon	0.69048951	1.46E-23	GO:0009731		ATLG5760.1		SAUR-like auxin-responsive protein family	SAUR family protein
Sapur.01G0461600.1	20.05631518	1.157674129	0.12968108	15.26859	1.24E-52	6.84E-52	salmon	0.684533332	4.88E-23						NA
Sapur.01G0240800.1	26.7010975	3.41162975	0.224329011	15.21493	2.83E-52	1.60E-51	salmon	0.549792369	8.82E-14	GO:0055114,GO:0020037,GO:0016705,GO:0005506		ATLG3720.1	CYP76C6	cytochrome P450, family 76, subfamily C, polypeptide 6	cytochrome P450 family protein
Sapur.01G0251100.1	32.93483225	2.688514	0.17668	15.18111	4.73E-52	2.68E-51	salmon	0.549578156	5.52E-14			ATLG2520.1	UDP-glucosyltransferase 72	UDP-glucosyltransferase 72	sulfoglucan 6-sulfotransferase
Sapur.01G0160600.1	3.98503939	4.19087325	0.27708742	15.12472	1.11E-51	6.27E-51	salmon	0.691420191	1.20E-23	GO:0005515		ATLG6240.1		F-box family protein	DUF563 family protein
Sapur.01G0261200.1	130.5852259	3.973817362	0.064879745	15.07197	2.48E-51	1.39E-50	salmon	0.712575833	1.26E-25	GO:0003723		ATLG5260.1	APUM12,PUM12	pumilio 12	pumilio family RNA binding repeat protein
Sapur.01G0280300.1	5.256782841	4.242638811	0.282406928	15.04228	3.88E-51	2.17E-50	salmon	0.663820252	2.66E-21						hypothetical protein
Sapur.01G0280600.1	282.2716948	3.814561404	0.081365157	14.85291	6.68E-50	3.61E-49	salmon	0.725247362	1.36E-25			ATLG7760.1	LAX3	like AUX1 3	auxin influx transporter
Sapur.03G0061200.1	2.866650066	8.872237968	0.328651642	14.82493	1.01E-49	5.52E-49	salmon	0.592911607	2.81E-16						B2 DA-binding domain protein
Sapur.01G0280300.1	3.768856527	4.443818689	0.300110074	14.32487	2.18E-49	1.29E-48	salmon	0.61173	1.77E-17			ATLG8450.1		VQ motif-containing protein	VQ motif protein
Sapur.01G0220800.1	444.4600625	6.483386907	0.032801505	14.73673	3.74E-49	2.02E-48	salmon	0.73435403	7.15E-28			ATLG2070.1			hypothetical protein
Sapur.01B0231300.1	491.1388359	8.153361320	0.058019341	14.70825	5.71E-49	3.07E-48	salmon	0.749887499	1.27E-28	GO:0055085,GO:0016020,GO:0006811,GO:0005216		ATLG03560.1	ATCICHLATTPC1,FOU2,TPC	two-pore channel 1	two pore calcium channel protein
Sapur.01G0882300.1	227.5189667	2.171239104	0.097640514	14.46697	1.88E-47	9.84E-47	salmon	0.669474425	2.21E-24	GO:0016020,GO:0010218		ATLG5700.1	IRX9	Nucleotide-diphosphate-sugar transferases superfamily protein	secondary cell wall-related glycosyltransferase family 43 protein
Sapur.01G0221200.1	298.8852254	1.238295281	0.085611699	14.46409	2.04E-47	1.07E-46	salmon	0.731674604	1.90E-25	GO:0016758,GO:0008152		ATLG2590.1		UDP-Glycosyltransferase superfamily protein	UDP-glucosyltransferase, putative
Sapur.01G0221700.1	741.0606934	1.152282092	0.063128343	14.45123	2.44E-47	1.28E-46	salmon	0.73462551	1.60E-28	GO:0016747		ATLG4890.1	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase
Sapur.01G0133400.1	189.127229	2.882806692	0.059927949	14.36403	8.70E-47	4.51E-46	salmon	0.72125937	1.36E-25			ATLG2470.1	FLA7	FASCICLIN-like arabinogalactan 7	fasciclin-like arabinogalactan protein
Sapur.01G0141800.1	22.24021856	2.481880327	0.16845352	14.35166	9.82E-47	5.09E-46	salmon	0.735351791	1.66E-28	GO:0006355,GO:0003700		ATLG2760.1		Integrase-type DNA-binding superfamily protein	AP2/EREBP domain transcription factor
Sapur.01G0243800.1	100.3324313	1.077195209	0.075661775	14.18075	1.21E-45	6.13E-45	salmon	0.708660005	3.40E-25	GO:0016020,GO:0006810,GO:0005215		ATLG4050.1	ATPTR3,PTR3	peptide transporter 3	peptide transporter PTR3-A
Sapur.00G0176500.1	14.66437816	2.05127405	0.14476464	13.98064	2.05E-44	9.68E-44	salmon	0.652564144	2.66E-20						hypothetical protein
Sapur.02G0687000.1	506.3557982	0.795974581	0.056978814	13.97088	2.35E-44	1.17E-43	salmon	0.753645427	5.77E-31			ATLG7670.1		Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	aspartate aminotransferase
Sapur.00T0242800.1	17.0863861	1.825881379	0.117476254	13.93276	4.54E-44	2.25E-43	salmon	0.68893997	2.90E-24			ATLG2943.1	NAPRT2	nicotinate phosphoribosyltransferase 2	nicotinate phosphoribosyltransferase family protein
Sapur.01G0261500.1	10.46197	5.080468086	0.218521216	13.86201	1.02E-43	4.97E-43	salmon	0.614457248	7.41E-19			ATLG3526.1	PMO1	Flavin-dependent monooxygenase 1	flavin containing monooxygenase, putative
Sapur.00G0680000.1	22.06713073	1.648092658	0.120749114	13.65582	1.88E-42	8.97E-42	salmon	0.658854029	6.63E-21			ATLG5560.1	TBL39	TRICHOME BIREFRINGENCE-LIKE 39	Pmr5/CaLigo GDSL/SGNH-like acyl-esterase family protein
Sapur.01G0270800.1	31.26274977	1.356414163	0.107286573	13.61823	2.07E-42	9.85E-42	salmon	0.650898555	1.05E-20	GO:0005524		ATLG5490.1	chr31	chromatin remodeling 31	NA
Sapur.00T0133300.1	2.14669918	3.876318673	0.296680651	13.61638	3.20E-42	1.53E-41	salmon	0.548456534	1.79E-13	GO:0003677					NA
Sapur.00G0140200.1	316.7667737	1.641884651	0.07273679	13.5705	9.45E-42	4.48E-41	salmon	0.74318625	5.62E-29	GO:0016021,GO:0006506,GO:0005789		ATLG16040.1			myo-inositol oxygenase 4
Sapur.01G0231400.1	509.3076642	0.558513221	0.041448893	13.4754	2.18E-41	1.03E-40	salmon	0.729090906	6.02E-27			ATLG5630.1			hypothetical protein
Sapur.01G0261900.1	3.031813551	3.715200992	0.275052921	13.46349	2.54E-41	1.21E-40	salmon	0.684203853	1.58E-23	GO:0006629		ATLG4930.1	SAG101	senescence-associated gene 101	NA
Sapur.15W0376800.1	9.817977384	2.285031378	0.17206053	13.2804	3.01E-40	1.39E-39	salmon	0.627610823	1.42E-18	GO:0012505,GO:0016049,GO:0010215		ATLG5130.1	COBRA,ATR6	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family	COBRA-like protein
Sapur.01G0261600.1	296.6298085	2.513690668	0.09029819	13.2093	5.88E-40	2.71E-39	salmon	0.667874412	2.52E-21	GO:0005515		ATLG2910.1	CCS52A1,FZR2	E2F/DP-like protein	cell cycle switch protein CCS52a
Sapur.01G0131400.1	5.947533011	3.063786888	0.2320618	13.2023	8.51E-40	3.91E-39	salmon	0.595303111	1.99E-16			ATLG2160.1		Protein of unknown function (DUF581)	DUF581 family protein
Sapur.00B0217200.1	1482.918092	0.743941149	0.056776238	13.09589	3.47E-39	1.58E-38	salmon	0.719346207	5.77E-26	GO:0055114,GO:0020037,GO:0016705,GO:0005506		ATLG0660.1	CYP77A4	cytochrome P450, family 77, subfamily A, polypeptide 4	cytochrome P450 family 77 protein
Sapur.01G0240500.1	31.53088775	1.800318012	0.138832504	12.96719	1.88E-38	8.06E-38	salmon	0.634573238	1.32E-19						transmembrane protein, putative
Sapur.01G0198300.1	135.3397687	1.498794294	0.118463366	12.65196	1.09E-36	4.72E-36	salmon	0.627167436	1.52E-18	GO:0008270,GO:0005622,GO:0005515		ATLG3500.1		B-box type zinc finger protein with CCT domain	zinc finger constans-like protein, putative
Sapur.01G0270500.1	293.7051392	1.267268404	0.034607092	12.60884	2.09E-36	8.96E-36	salmon	0.622836276	7.52E-18	GO:0008290,GO:0005737		ATLG3030.1		coenzyme Q (ubiquinone) / ubiquinone biosynthesis CoQ4 family protein	ubiquinone biosynthesis COQ4-like protein
Sapur.01G0120400.1	60.83563313	0.992895477	0.078024482	12.58032	2.71E-36	1.16E-35	salmon	0.60168886	7.81E-17			ATLG1440.1	ATMYB65,MYB65	myb domain protein 65	transcription factor Myb3, putative
Sapur.01T0288900.1	187.6216104	1.048899398	0.081604753	12.51118	3.91E-36	1.67E-35	salmon	0.719391205	1.30E-27	GO:0006562,GO:0004657		ATLG8710.1		Methylenetetrahydrofolate reductase family protein	proline dehydrogenase
Sapur.01G0899400.1	4.950667828	2.584786494	0.207662217	12.42888	1.82E-35	7.69E-35	salmon	0.624610307	2.92E-18			ATLG5740.1	SESA5	seed storage albumin 5	protease inhibitor/seed storage/LTP family protein
Sapur.01G0270400.1	4.801612203	2.010498308	0.174879719	12.35084	4.81E-35	2.01E-34	salmon	0.645281189	1.96E-21	GO:0005515		ATLG6620.1		Dicticocoagulase/Pro-Nem-Ep family protein	NA
Sapur.01G0094400.1	12.19451591	1.264562165	0.103338434	12.23733	1.96E-34	8.11E-34	salmon	0.638213934	2.44E-19			ATLG6778.1		Chaperone Dnaj-domain superfamily protein	NA
Sapur.01G0147000.1	5.112118848	2.176457033	0.179072456	12.14367	6.27E-34	2.57E-33	salmon	0.631134629	2.52E-19	GO:0009341,GO:0005975,GO:0004565,GO:0004553		ATLG6803.1	BGAL6,MUM2	Glycosyl hydrolase family 35 protein	NA
Sapur.01G0167000.1	80.21382087	1.285145247	0.106167761	12.10565	9.86E-34	4.02E-33	salmon	0.631377663	1.58E-17			ATLG3210.1	ATOPS6,OPS6	ovate family protein 16	ovate transcriptional repressor
Sapur.00G0171600.1	685.5098817	0.401283661	0.033348542	12.03305	2.38E-33	9.64E-33	salmon	0.64245819	3.40E-21	GO:0005515,GO:0005634,GO:0003677,GO:0006370,GO:0003676		ATLG3540.1	TFH5	transcript elongation factor 5	transcription elongation factor S-II
Sapur.01G0171400.1	8.090749411	2.442795257	0.203138081	12.02587	2.68E-33	1.05E-32	salmon	0.569393502	7.36E-15			ATLG2480.1		Protein of unknown function (DUF506)	plant/PBM4-180 protein
Sapur.00G0207700.1	48.73306952	1.593353331	0.1329168	11.98761	4.13E-33	1.66E-32	salmon	0.581383035	1.12E-15	GO:0016747		ATLG2640.1		HXXXD-type acyl-transferase family protein	anthranilate N-benzoyltransferase, putative
Sapur.00G0680.1001.1	182.6493232	0.48753188	0.040756337	11.96264	5.18E-33	2.24E-32	salmon	0.675739011	8.63E-21	GO:0016020		ATLG3620.1	ACYB-1,CYB-1	cytochrome b5 1	cytochrome b5 isoform b561
Sapur.02G0172800.1	2.761197607	3.248330732	0.271582243	11.96147	5.66E-33	2.27E-32	salmon	0.615621442	9.49E-18			ATLG4310.1		Calcium-binding EF-hand family protein	NA
Sapur.00G0151300.1	15.38505741	1.506324345	0.127861828	11.7765	1.59E-32	2.86E-31	salmon	0.642884958	4.57E-21			ATLG4680.1			hypothetical protein
Sapur.01G0120800.1	4.177561691	3.766050561	0.320647173	11.74515	7.48E-32	2.93E-31	salmon	0.446138016	4.74E-09	GO:0007165,GO:0005515,GO:0043531		ATLG4630.2		Disease resistance protein (TIR-NBS-LRR class) family	NA
Sapur.01G0261000.1	132.7558227	1.085685855	0.09009526	11.6623	1.98E-31	7.71E-31	salmon	0.605134114	4.26E-17	GO:0055114,GO:0020037,GO:0016705,GO:0005506		ATLG3060.1	CYP94B2	cytochrome P450 family 94, subfamily B, polypeptide 2	cytochrome P450 family protein
Sapur.01G0141400.1	3.429075912	2.870951351	0.248729136	11.54234	8.07E-31	2.89E-30	salmon	0.566730197	1.02E-14			ATG6030.1		Homeodomain-like superfamily protein	NA
Sapur.01G0139300.1	27.83729228	0.754231207	0.065498869	11.5473	1.13E-30	4.24E-30	salmon	0.6818914	8.62E-23			ATLG2810.1	ULT1,ULT1	Developmental regulator, ULTRAPETALA	transcription factor, putative
Sapur.01G0139000.1	23.31169949	0.925605553	0.080537487	11.49291	1.43E-30	5.45E-30	salmon	0.633697633	2.16E-19			ATLG2810.2	ULT1,ULT1	Developmental regulator, ULTRAPETALA	transcription factor, putative
Sapur.15W0203300.1	38.53514242	1.056372552	0.092498617	11.42522	3.12E-30	1.18E-29	salmon	0.649327742	3.61E-20			ATLG7950.1			NA
Sapur.01G0889900.1	145.6023672	1.213301794	0.112499519	11.37425	5.62E-30	2.11E-29	salmon	0.5190124	3.30E-12			ATLG0150.1	ATPP2-A10,PP2-A10	phloem protein 2-A10	NA
Sapur.01G0420900.1	474.4548609	1.112303742	0.099576871	11.1703	5.70E-29	2.10E-28	salmon	0.567690575	2.01E-14			ATLG4760.1			NA
Sapur.01G0261200.1	134.3638377	0.972848884	0.087625705	11.09319	1.35E-28	4.95E-28	salmon	0.633697633	2.16E-19			ATLG9160.1	AHL29,SOB3	Predicted AT-hook DNA-binding protein, putative	AT-hook DNA-binding protein, putative
Sapur.01G0139300.1	7.668025129	1.265669593	0.114321422	11.0709	1.74E-28	6.33E-28	salmon	0.631105053	1.39E-17	GO:0003677		ATLG2810.1	ULT1,ULT1	Developmental regulator, ULTRAPETALA	transcription factor, putative
Sapur.01G0122100.1	85.74482141	0.827008768	0.083766168	10.93788	7.60E-28	2.73E-27	salmon	0.664834566	1.16E-21	GO:0006887,GO:0000145		ATLG5270.1		Protein of unknown function (DUF607)	exocyst subunit exo70 E1
Sapur.00G0950000.1	14.4462

Sapur.009G112800.1	4.756814354	-0.963710692	0.229175215	-4.20513	2.63E-05	4.53E-05	white	-0.218776659	0.002598395	GO:0006355,GO:0003677	AT2G17040.1	anac036,NAC036	NAC domain containing protein 36	NAC transcription factor, putative
Sapur.001G177800.1	31.57547545	-0.608180882	0.148116153	-4.10627	4.02E-05	6.91E-05	white	-0.271757371	0.000575454	GO:0003677	AT1G12260.1	EDF4,RAV1	related to ABI3/VP1 1	B3 DNA-binding domain protein
Sapur.007G089700.1	9.973850673	-1.003806564	0.254168612	-3.9462	7.94E-05	0.000134169	white	-0.158381107	0.04757174	GO:0005488,GO:0005524,GO:0004672	AT5G60900.1	RLK1	receptor-like protein kinase 1	Serine/Threonine kinase domain protein
Sapur.013G005200.1	42.55501937	-0.863753828	0.228216164	-3.78481	0.000153829	0.000255652	white	-0.174112453	0.029192658	GO:0048046,GO:0016762,GO:0004073,GO:0005618,GO:0005975,GO:0004553	AT4G25830.1	XTH23,XTR6	xyloglucan endotransglycosylase 6	xyloglucan endotransglycosylase/hydrolase
Sapur.014G001600.4	2.592323816	-0.683319452	0.189445641	-3.60704	0.000309713	0.000501983	white	-0.09548917	0.985430202	GO:0006511	AT3G61415.1	ASK21,SK21	SKP1-like 21	SKP1-like protein
Sapur.001G177900.1	17.34727129	-0.460996798	0.143188456	-3.21965	0.001283473	0.002002737	white	-0.206614337	0.009434509	GO:0003677	AT1G12260.1	EDF4,RAV1	related to ABI3/VP1 1	B3 DNA-binding domain protein
Sapur.003G048700.1	20.71357919	-0.366559932	0.148731188	-2.46491	0.013704706	0.019027152	white	-0.12834993	0.1134358	GO:0003247	AT2G25430.1		RING/U-box superfamily protein	NA
Sapur.017G064100.1	7.742919718	-0.474822881	0.228888112	-2.07449	0.038033449	0.052986343	white	-0.117635263	0.14229815					transmembrane protein, putative
Sapur.010G015500.2	0.290229997	0.689656208	0.423483674	1.628531	0.103412383	0.134354447	white	-0.081608864	0.309590942		AT1G09020.1	ATSNF4,SNF4	homolog of yeast sucrose nonfermenting 4	AMP-activated kinase, gamma regulatory subunit%2C putative
Sapur.003G085800.1	1.545886611	-0.691966918	0.462424341	-1.06343	0.287586428	0.349025153	white	-0.133446919	0.095681779	GO:0006355,GO:0003700	AT5G02020.1		Integrase-type DNA-binding superfamily protein	AP2/EBF domain transcription factor
Sapur.009G012800.1	5.623495744	-0.187021945	0.2136687	-0.87529	0.381416468	0.451292107	white	-0.055703197	0.488339852		AT3G12460.1		hydroxyproline-rich glycoprotein family protein	harpin-induced protein, putative
Sapur.016G286700.1	0.305278123	0.364386544	0.504118124	0.722841	0.469377407	0.543970094	white	0.069360215	0.388039881	GO:0006468,GO:0004672	AT3G16030.1	CES101	lectin protein kinase family protein	NA
Sapur.008G087600.1	8.110066193	0.098616409	0.174928545	0.563749	0.573924759	0.648380273	white	0.040192989	0.617219933		AT1G13480.1		Protein of unknown function (DUF1262)	DUF1262 family protein
Sapur.004G037800.1	1.402534526	0.147907344	0.383446936	0.385566	0.699522113	0.768561086	white	0.008023168	0.92056064		AT4G18540.1			transmembrane-like protein
Sapur.002G149400.1	645.0138166	-0.047109435	0.192333331	-0.31337	0.754002205	0.816911879	white	-0.0196929	0.806547254		AT2G46140.1		Late embryogenesis abundant protein	late embryogenesis abundant protein Lea14-A
Sapur.019G116300.3	0.050329646	0.303394265	1.412556821	0.214772	0.829845027	0.879892354	white	-0.081608864	0.309590942		AT5G61820.1			stress up-regulated Nud 19 protein
Sapur.016G022600.1	0.071917381	-0.139854274	1.226353603	-0.11404	0.909205497	0.940426026	white	-0.12823081	0.133641457	GO:0031045,GO:0006364	AT3G60360.1	EDA14,U7P11	embryo sac development arrest 14	U3 small nucleolar RNA-associated protein, putative
Sapur.011G116800.1	0.127671561	0.035844891	0.751460374	0.0477	0.963955291	0.974835595	white	-0.081608864	0.309590942	GO:0006468,GO:0005524,GO:0004674,GO:0004672	AT4G14230.1		AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	Serine/Threonine-kinase-like protein
Sapur.016G286500.1	0.074691257	-0.001976784	1.517288828	-0.0013	0.998860498	0.999341754	white	-0.042684666	0.595153626		AT3G16030.1	CES101	lectin protein kinase family protein	NA
Sapur.010G119200.1	0.021796083	0.089337012	2.904822183	0.030755	0.975465146	NA	white	-0.001555124	0.984576905	GO:0005515,GO:0005634,GO:0003677	AT5G64230.1		Calmodulin-binding transcription activator protein with CG-1 and Ankyrin domains	calmodulin-binding transcription activator
Sapur.001G035700.2	0.005413001	0.05537013	2.904824396	0.01913	0.984737169	NA	white	-0.081608864	0.309590942	GO:0008168,GO:0008152	AT3G24410.1	APG1,E37,JJP37,YTE3	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	2-methyl-6-phytyl-1%2,4-benzoquinone methyltransferase
Sapur.005G035500.4	0.005413001	0.05537013	2.904824396	0.01913	0.984737169	NA	white	-0.081608864	0.309590942		AT1G54570.1		Esterase/lipase/thioesterase family protein	esterase/lipase/thioesterase family protein
Sapur.006G130200.1	0.005413001	0.05537013	2.904824396	0.01913	0.984737169	NA	white	-0.081608864	0.309590942		AT1G08080.1	ACA7,ATACA7	alpha carbonic anhydrase 7	carbonic anhydrase, putative